

cag acc ctg gct aag ggc ttt gtc cag ctg cac ggt ctg tcc tcc aag
 1267
 Gln Thr Leu Ala Lys Gly Phe Val Gln Leu His Gly Leu Ser Ser Lys
 375 380 385

atc gct aac aag cgc gat cgc gaa gct ggc aac aac taagccacct
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 Ile Ala Asn Lys Arg Asp Arg Glu Ala Gly Asn Asn
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 <213> Corynebacterium glutamicum

<400> 336
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Val Ser Leu Asp Leu Gly Gln Gly Gly Glu Asn Met Asp Asn Val Arg
 35 40 45

Gln Arg Ala Leu Asp Ala Gly Ala Ala Glu Ser Ile Val Val Asp Ala
 50 55 60

Lys Asp Glu Phe Ala Glu Glu Tyr Cys Leu Pro Thr Ile Lys Ala Asn
 65 70 75 80

Gly Met Tyr Met Lys Gln Tyr Pro Leu Val Ser Ala Ile Ser Arg Pro
 85 90 95

Leu Ile Val Lys His Leu Val Glu Ala Gly Lys Gln Phe Asn Gly Thr
 100 105 110

His Val Ala His Gly Cys Thr Gly Lys Gly Asn Asp Gln Val Arg Phe
 115 120 125

Glu Val Gly Phe Met Asp Thr Asp Pro Asn Leu Glu Ile Ile Ala Pro
 130 135 140

Ala Arg Asp Phe Ala Trp Thr Arg Asp Lys Ala Ile Ala Phe Ala Glu
 145 150 155 160

Glu Asn Asn Val Pro Ile Glu Gln Ser Val Lys Ser Pro Phe Ser Ile
 165 170 175

Asp Gln Asn Val Trp Gly Arg Ala Ile Glu Thr Gly Tyr Leu Glu Asp
 180 185 190

Leu Trp Asn Ala Pro Thr Lys Asp Ile Tyr Ala Tyr Thr Glu Asp Pro
 195 200 205

Ala Leu Gly Asn Ala Pro Asp Glu Val Ile Ile Ser Phe Glu Gly Gly
 210 215 220

Lys Pro Val Ser Ile Asp Gly Arg Pro Val Ser Val Leu Gln Ala Ile
 225 230 235 240
 Glu Glu Leu Asn Arg Arg Ala Gly Ala Gln Gly Val Gly Arg Leu Asp
 245 250 255
 Met Val Glu Asp Arg Leu Val Gly Ile Lys Ser Arg Glu Ile Tyr Glu
 260 265 270
 Ala Pro Gly Ala Ile Ala Leu Ile Lys Ala His Glu Ala Leu Glu Asp
 275 280 285
 Val Thr Ile Glu Arg Glu Leu Ala Arg Tyr Lys Arg Gly Val Asp Ala
 290 295 300
 Arg Trp Ala Glu Glu Val Tyr Asp Gly Leu Trp Phe Gly Pro Leu Lys
 305 310 315 320
 Arg Ser Leu Asp Ala Phe Ile Asp Ser Thr Gln Glu His Val Thr Gly
 325 330 335
 Asp Ile Arg Met Val Leu His Ala Gly Ser Ile Thr Ile Asn Gly Arg
 340 345 350
 Arg Ser Ser His Ser Leu Tyr Asp Phe Asn Leu Ala Thr Tyr Asp Thr
 355 360 365
 Gly Asp Thr Phe Asp Gln Thr Leu Ala Lys Gly Phe Val Gln Leu His
 370 375 380
 Gly Leu Ser Ser Lys Ile Ala Asn Lys Arg Asp Arg Glu Ala Gly Asn
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 Asn

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 <213> Corynebacterium glutamicum

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 <222> (101)..(1531)
 <223> RXN02162

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 Met Glu Gln His Gly
 1 5
 acc aat gaa ggt gcg ctg tgg ggc ggc cgc ttc tcc ggt gga ccc tcc 163
 Thr Asn Glu Gly Ala Leu Trp Gly Gly Arg Phe Ser Gly Gly Pro Ser
 10 15 20
 gag gcc atg ttc gcc ttg agt gtc tcc act cat ttc gac tgg gtt ttg 211
 Glu Ala Met Phe Ala Leu Ser Val Ser Thr His Phe Asp Trp Val Leu

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gcc cct tat gat gtg ttg gcc tcc aag gca cac gcc aag gtt ttg cac Ala Pro Tyr Asp Val Leu Ala Ser Lys Ala His Ala Lys Val Leu His 40 45 50			259
caa gca gat cta ctt tct gat gaa gat cta gcc acc atg ctg gct ggg Gln Ala Asp Leu Leu Ser Asp Glu Asp Leu Ala Thr Met Leu Ala Gly 55 60 65			307
ctt gat cag ctg ggc aag gat gtc gcc gac gga acc ttc ggt ccg ctg Leu Asp Gln Leu Gly Lys Asp Val Ala Asp Gly Thr Phe Gly Pro Leu 70 75 80 85			355
cct tct gat gag gat gtg cac ggc gcg atg gaa cgc ggt gtg att gac Pro Ser Asp Glu Asp Val His Gly Ala Met Glu Arg Gly Val Ile Asp 90 95 100			403
cgc gtt ggt cct gag gtg ggc ggc cgt ctg cgc gct ggt cgt tcc cgc Arg Val Gly Pro Glu Val Gly Gly Arg Leu Arg Ala Gly Arg Ser Arg 105 110 115			451
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cgc gac atc gcg ctg gga aca acc gag ctt gtc gac gcc ctc agc gcc Arg Asp Ile Ala Leu Gly Thr Thr Glu Leu Val Asp Ala Leu Ser Ala 135 140 145			547
caa gct aag gca cat gca ggc gcg atc atg cca ggc aag acc cac ttc Gln Ala Lys Ala His Ala Gly Ala Ile Met Pro Gly Lys Thr His Phe 150 155 160 165			595
cag gca gct cag ccg gtc ctt ctg gca cac cag ctg ctg gca cac gca Gln Ala Ala Gln Pro Val Leu Leu Ala His Gln Leu Leu Ala His Ala 170 175 180			643
cag cct ttg ctg cgc gat att gat cgt atc cgt gac ctg gac aag cgt Gln Pro Leu Leu Arg Asp Ile Asp Arg Ile Arg Asp Leu Asp Lys Arg 185 190 195			691
ctt gcg gtg tct cct tac ggt tcc ggc gca ctt gct ggt tcc tct ttg Leu Ala Val Ser Pro Tyr Gly Ser Gly Ala Leu Ala Gly Ser Ser Leu 200 205 210			739
aag ctc aac cct gaa gca atc gct gaa gaa ctc ggc ttt gat tcc gca Lys Leu Asn Pro Glu Ala Ile Ala Glu Glu Leu Gly Phe Asp Ser Ala 215 220 225			787
gca gat aac tcc att gat gcc acc agc tcc cgc gat ttc gca tct gaa Ala Asp Asn Ser Ile Asp Ala Thr Ser Ser Arg Asp Phe Ala Ser Glu 230 235 240 245			835
acc gcc ttc gtg ctg gcg cag ctt gca gtg gat atg tcc cgc ttg gct Thr Ala Phe Val Leu Ala Gln Leu Ala Val Asp Met Ser Arg Leu Ala 250 255 260			883
gaa gaa atc atc gca tgg tgc acc cca gaa ttt ggt tac atc acc ttg Glu Glu Ile Ile Ala Trp Cys Thr Pro Glu Phe Gly Tyr Ile Thr Leu 265 270 275			931

tct gat tcc tgg tcc aca ggc agc tca atc atg ccg cag aag aag aac 979
 Ser Asp Ser Trp Ser Thr Gly Ser Ser Ile Met Pro Gln Lys Lys Asn
 280 285 290

cct gac gtg gca gag ctg acc cgt ggc aag tct ggt cgc ttg atc ggt
 1027
 Pro Asp Val Ala Glu Leu Thr Arg Gly Lys Ser Gly Arg Leu Ile Gly
 295 300 305

aac ctc acc ggt ctg ctg gct acc ctg aag gca cag cct tta gcg tac
 1075
 Asn Leu Thr Gly Leu Leu Ala Thr Leu Lys Ala Gln Pro Leu Ala Tyr
 310 315 320 325

aac cgc gac ctg cag gaa gat aag gaa cca atc gta gat tcc gtg gcg
 1123
 Asn Arg Asp Leu Gln Glu Asp Lys Glu Pro Ile Val Asp Ser Val Ala
 330 335 340

cag ctc aac ctg ctg ctc cct gca atg act ggt ttg gtt tcc acc ttg
 1171
 Gln Leu Asn Leu Leu Leu Pro Ala Met Thr Gly Leu Val Ser Thr Leu
 345 350 355

acc ttc aac acc gag cgc atg cgt gaa ctt gca cca gca ggt ttc acc
 1219
 Thr Phe Asn Thr Glu Arg Met Arg Glu Leu Ala Pro Ala Gly Phe Thr
 360 365 370

ctt gcc acc gac ttg gct gag tgg atg gtg cgc cag ggc gtt cca ttc
 1267
 Leu Ala Thr Asp Leu Ala Glu Trp Met Val Arg Gln Gly Val Pro Phe
 375 380 385

cgt gag gca cac gaa gca tcc ggc gct tgc gtg cgg atc gcg gag tcc
 1315
 Arg Glu Ala His Glu Ala Ser Gly Ala Cys Val Arg Ile Ala Glu Ser
 390 395 400 405

agg gga gtg gac ctt atc gat ctc act gat gaa gaa ctc agt ggc gtt
 1363
 Arg Gly Val Asp Leu Ile Asp Leu Thr Asp Glu Glu Leu Ser Gly Val
 410 415 420

gat gca cgt ctg acc cca gag gta cgg gaa gtg ctc acc att gat ggt
 1411
 Asp Ala Arg Leu Thr Pro Glu Val Arg Glu Val Leu Thr Ile Asp Gly
 425 430 435

gca gtg gct tcc cgt gca acg cgc ggt gga acc gcg ggc gtg cgg gtt
 1459
 Ala Val Ala Ser Arg Ala Thr Arg Gly Gly Thr Ala Gly Val Arg Val
 440 445 450

gcg gag caa cgc gca cgt gtc gat gcc gca agt acc gct cac gcg gag
 1507
 Ala Glu Gln Arg Ala Arg Val Asp Ala Ala Ser Thr Ala His Ala Glu
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tgg gca cgt gcg ggg gta cgt cga taagcattag tttatggcct gtg
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 Trp Ala Arg Ala Gly Val Arg Arg
 470 475

<210> 338
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 <213> Corynebacterium glutamicum

<400> 338
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 Ser Gly Gly Pro Ser Glu Ala Met Phe Ala Leu Ser Val Ser Thr His
 20 25 30
 Phe Asp Trp Val Leu Ala Pro Tyr Asp Val Leu Ala Ser Lys Ala His
 35 40 45
 Ala Lys Val Leu His Gln Ala Asp Leu Leu Ser Asp Glu Asp Leu Ala
 50 55 60
 Thr Met Leu Ala Gly Leu Asp Gln Leu Gly Lys Asp Val Ala Asp Gly
 65 70 75 80
 Thr Phe Gly Pro Leu Pro Ser Asp Glu Asp Val His Gly Ala Met Glu
 85 90 95
 Arg Gly Val Ile Asp Arg Val Gly Pro Glu Val Gly Gly Arg Leu Arg
 100 105 110
 Ala Gly Arg Ser Arg Asn Asp Gln Val Ala Thr Leu Phe Arg Met Trp
 115 120 125
 Val Arg Asp Ala Val Arg Asp Ile Ala Leu Gly Thr Thr Glu Leu Val
 130 135 140
 Asp Ala Leu Ser Ala Gln Ala Lys Ala His Ala Gly Ala Ile Met Pro
 145 150 155 160
 Gly Lys Thr His Phe Gln Ala Ala Gln Pro Val Leu Leu Ala His Gln
 165 170 175
 Leu Leu Ala His Ala Gln Pro Leu Leu Arg Asp Ile Asp Arg Ile Arg
 180 185 190
 Asp Leu Asp Lys Arg Leu Ala Val Ser Pro Tyr Gly Ser Gly Ala Leu
 195 200 205
 Ala Gly Ser Ser Leu Lys Leu Asn Pro Glu Ala Ile Ala Glu Glu Leu
 210 215 220
 Gly Phe Asp Ser Ala Ala Asp Asn Ser Ile Asp Ala Thr Ser Ser Arg
 225 230 235 240
 Asp Phe Ala Ser Glu Thr Ala Phe Val Leu Ala Gln Leu Ala Val Asp
 245 250 255
 Met Ser Arg Leu Ala Glu Glu Ile Ile Ala Trp Cys Thr Pro Glu Phe

10										15										20									
gag	gcc	atg	ttc	gcc	ttg	agt	gtc	tcc	act	cat	ttc	gac	tgg	gtt	ttg					211									
Glu	Ala	Met	Phe	Ala	Leu	Ser	Val	Ser	Thr	His	Phe	Asp	Trp	Val	Leu														
			25					30					35																
gcc	cct	tat	gat	gtg	ttg	gcc	tcc	aag	gca	cac	gcc	aag	gtt	ttg	cac					259									
Ala	Pro	Tyr	Asp	Val	Leu	Ala	Ser	Lys	Ala	His	Ala	Lys	Val	Leu	His														
		40					45					50																	
caa	gca	gat	cta	ctt	tct	gat	gaa	gat	cta	gcc	acc	atg	ctg	gct	ggg					307									
Gln	Ala	Asp	Leu	Leu	Ser	Asp	Glu	Asp	Leu	Ala	Thr	Met	Leu	Ala	Gly														
		55				60					65																		
ctt	gat	cag	ctg	ggc	aag	gat	gtc	gcc	gac	gga	acc	ttc	ggg	ccg	ctg					355									
Leu	Asp	Gln	Leu	Gly	Lys	Asp	Val	Ala	Asp	Gly	Thr	Phe	Gly	Pro	Leu														
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cct	tct	gat	gag	gat	gtg	cac	ggc	gcg	atg	gaa	cgc	ggg	gtg	att	gac					403									
Pro	Ser	Asp	Glu	Asp	Val	His	Gly	Ala	Met	Glu	Arg	Gly	Val	Ile	Asp														
			90						95					100															
cgc	gtt	ggg	cct	gag	gtg	ggc	ggc	cgt	ctg	cgc	gct	ggg	cgt	tcc	cgc					451									
Arg	Val	Gly	Pro	Glu	Val	Gly	Gly	Arg	Leu	Arg	Ala	Gly	Arg	Ser	Arg														
			105					110					115																
aac	gac	cag	gtg	gca	acc	ctg	ttc	cgc	atg	tgg	gtc	cgc	gac	gca	gtg					499									
Asn	Asp	Gln	Val	Ala	Thr	Leu	Phe	Arg	Met	Trp	Val	Arg	Asp	Ala	Val														
		120					125					130																	
cgc	gac	atc	gcg	ctg	gga	aca	acc	gag	ctt	gtc	gac	gcc	ctc	agc	gcc					547									
Arg	Asp	Ile	Ala	Leu	Gly	Thr	Thr	Glu	Leu	Val	Asp	Ala	Leu	Ser	Ala														
		135				140						145																	
caa	gct	aag	gca	cat	gca	ggc	gcg	atc	atg	cca	ggc	aag	acc	cac	ttc					595									
Gln	Ala	Lys	Ala	His	Ala	Gly	Ala	Ile	Met	Pro	Gly	Lys	Thr	His	Phe														
		150				155				160					165														
cag	gca	gct	cag	ccg	gtc	ctt	ctg	gca	cac	cag	ctg	ctg	gca	cac	gca					643									
Gln	Ala	Ala	Gln	Pro	Val	Leu	Leu	Ala	His	Gln	Leu	Leu	Ala	His	Ala														
				170					175					180															
cag	cct	ttg	ctg	cgc	gat	att	gat	cgt	atc	cgt	gac	ctg	gac	aag	cgt					691									
Gln	Pro	Leu	Leu	Arg	Asp	Ile	Asp	Arg	Ile	Arg	Asp	Leu	Asp	Lys	Arg														
			185					190						195															
ctt	gcg	gtg	tct	cct	tac	ggg	tcc	ggc	gca	ctt	gct	ggg	tcc	tct	ttg					739									
Leu	Ala	Val	Ser	Pro	Tyr	Gly	Ser	Gly	Ala	Leu	Ala	Gly	Ser	Ser	Leu														
		200					205						210																
aag	ctc	aac	cct	gaa	gca	atc	gct	gaa	gaa	ctc	ggc	ttt	gat	tcc	gca					787									
Lys	Leu	Asn	Pro	Glu	Ala	Ile	Ala	Glu	Glu	Leu	Gly	Phe	Asp	Ser	Ala														
		215				220					225																		
gca	gat	aac	tcc	att	gat	gcc	acc	agc	tcc	cgc	gat	ttc	gca	tct	gaa					835									
Ala	Asp	Asn	Ser	Ile	Asp	Ala	Thr	Ser	Ser	Arg	Asp	Phe	Ala	Ser	Glu														
		230				235				240					245														
acc	gcc	ttc	gtg	ctg	gcg	cag	ctt	gca	ngt	gga	tat	gtc	ccg	ctt	ggc					883									
Thr	Ala	Phe	Val	Leu	Ala	Gln	Leu	Ala	Xaa	Gly	Tyr	Val	Pro	Leu	Gly														
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906

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<211> 261

<212> PRT

<213> Corynebacterium glutamicum

<400> 340

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Ser Gly Gly Pro Ser Glu Ala Met Phe Ala Leu Ser Val Ser Thr His
 20 25 30

Phe Asp Trp Val Leu Ala Pro Tyr Asp Val Leu Ala Ser Lys Ala His
 35 40 45

Ala Lys Val Leu His Gln Ala Asp Leu Leu Ser Asp Glu Asp Leu Ala
 50 55 60

Thr Met Leu Ala Gly Leu Asp Gln Leu Gly Lys Asp Val Ala Asp Gly
 65 70 75 80

Thr Phe Gly Pro Leu Pro Ser Asp Glu Asp Val His Gly Ala Met Glu
 85 90 95

Arg Gly Val Ile Asp Arg Val Gly Pro Glu Val Gly Gly Arg Leu Arg
 100 105 110

Ala Gly Arg Ser Arg Asn Asp Gln Val Ala Thr Leu Phe Arg Met Trp
 115 120 125

Val Arg Asp Ala Val Arg Asp Ile Ala Leu Gly Thr Thr Glu Leu Val
 130 135 140

Asp Ala Leu Ser Ala Gln Ala Lys Ala His Ala Gly Ala Ile Met Pro
 145 150 155 160

Gly Lys Thr His Phe Gln Ala Ala Gln Pro Val Leu Leu Ala His Gln
 165 170 175

Leu Leu Ala His Ala Gln Pro Leu Leu Arg Asp Ile Asp Arg Ile Arg
 180 185 190

Asp Leu Asp Lys Arg Leu Ala Val Ser Pro Tyr Gly Ser Gly Ala Leu
 195 200 205

Ala Gly Ser Ser Leu Lys Leu Asn Pro Glu Ala Ile Ala Glu Glu Leu
 210 215 220

Gly Phe Asp Ser Ala Ala Asp Asn Ser Ile Asp Ala Thr Ser Ser Arg
 225 230 235 240

Asp Phe Ala Ser Glu Thr Ala Phe Val Leu Ala Gln Leu Ala Xaa Gly
 245 250 255

Tyr Val Pro Leu Gly
 260

gca gtg gct tcc cgt gca acg cgc ggt gga acc gcg ggc gtg cgg gtt 691
 Ala Val Ala Ser Arg Ala Thr Arg Gly Gly Thr Ala Gly Val Arg Val
 185 190 195

gcg gag caa cgc gca cgt gtc gat gcc gca agt acc gct cac gcg gag 739
 Ala Glu Gln Arg Ala Arg Val Asp Ala Ala Ser Thr Ala His Ala Glu
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<210> 342

<211> 221

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 342

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 20 25 30

Pro Gln Lys Lys Asn Pro Asp Val Ala Glu Leu Thr Arg Gly Lys Ser
 35 40 45

Gly Arg Leu Ile Gly Asn Leu Thr Gly Leu Leu Ala Thr Leu Lys Ala
 50 55 60

Gln Pro Leu Ala Tyr Asn Arg Asp Leu Gln Glu Asp Lys Glu Pro Ile
 65 70 75 80

Val Asp Ser Val Ala Gln Leu Asn Leu Leu Leu Pro Ala Met Thr Gly
 85 90 95

Leu Val Ser Thr Leu Thr Phe Asn Thr Glu Arg Met Arg Glu Leu Ala
 100 105 110

Pro Ala Gly Phe Thr Leu Ala Thr Asp Leu Ala Glu Trp Met Val Arg
 115 120 125

Gln Gly Val Pro Phe Arg Glu Ala His Glu Ala Ser Gly Ala Cys Val
 130 135 140

Arg Ile Ala Glu Ser Arg Gly Val Asp Leu Ile Asp Leu Thr Asp Glu
 145 150 155 160

Glu Leu Ser Gly Val Asp Ala Arg Leu Thr Pro Glu Val Arg Glu Val
 165 170 175

Leu Thr Ile Asp Gly Ala Val Ala Ser Arg Ala Thr Arg Gly Gly Thr
 180 185 190

Ala Gly Val Arg Val Ala Glu Gln Arg Ala Arg Val Asp Ala Ala Ser
 195 200 205

Thr Ala His Ala Glu Trp Ala Arg Ala Gly Val Arg Arg
 210 215 220

	170	175	180	
cgc cca gga atc acc acc atc aag atc aag gga cgc agc gaa cgc ggc				691
Arg Pro Gly Ile Thr Thr Ile Lys Ile Lys Gly Arg Ser Glu Arg Gly				
	185	190	195	
atc aac gcc ttt gca aca tgg gcg ttg gaa aaa ttc ccc gag atc gaa				739
Ile Asn Ala Phe Ala Thr Trp Ala Leu Glu Lys Phe Pro Glu Ile Glu				
	200	205	210	
gtg gtc gcc gtc gga tct gaa gaa gac gtg gtc aaa gac gcc gac atc				787
Val Val Ala Val Gly Ser Glu Glu Asp Val Val Lys Asp Ala Asp Ile				
	215	220	225	
gtc atc gcc gcc acc acc acg gac gcc gcc ggc tcc tcc gcc ttc cca				835
Val Ile Ala Ala Thr Thr Thr Asp Ala Ala Gly Ser Ser Ala Phe Pro				
	230	235	240	245
tac ttc aaa aaa gaa tgg ctc aag ccg ggc gca ttg ctg ctg ctt cca				883
Tyr Phe Lys Lys Glu Trp Leu Lys Pro Gly Ala Leu Leu Leu Leu Pro				
	250	255	260	
gcc gcc ggt cgc ttc gac gac gct tat ttg ctt gac gac gcc cgc ctc				931
Ala Ala Gly Arg Phe Asp Asp Ala Tyr Leu Leu Asp Asp Ala Arg Leu				
	265	270	275	
gtt gtt gac tac atg ggg ctc tac gaa gcc tgg gca gaa gaa tac ggc				979
Val Val Asp Tyr Met Gly Leu Tyr Glu Ala Trp Ala Glu Glu Tyr Gly				
	280	285	290	
cca cag gcc tac caa cta ctc ggc att cca gga acc cac tgg tac gac				
1027				
Pro Gln Ala Tyr Gln Leu Leu Gly Ile Pro Gly Thr His Trp Tyr Asp				
	295	300	305	
ctg gcg ctg caa gga aaa ctc gac ctt gca aag att tcc cag att ggc				
1075				
Leu Ala Leu Gln Gly Lys Leu Asp Leu Ala Lys Ile Ser Gln Ile Gly				
	310	315	320	325
gat atc tgc tcc ggc aag cta ccc gga cgc acc aac gat gag gaa atc				
1123				
Asp Ile Cys Ser Gly Lys Leu Pro Gly Arg Thr Asn Asp Glu Glu Ile				
	330	335	340	
atc ctc tat tcc gtc ggc ggc atg cca gta gaa gac gtc gcc tgg gca				
1171				
Ile Leu Tyr Ser Val Gly Gly Met Pro Val Glu Asp Val Ala Trp Ala				
	345	350	355	
acc caa gtg tat gaa aac gcc ctg gaa aaa ggc gtc ggc acc aca ttg				
1219				
Thr Gln Val Tyr Glu Asn Ala Leu Glu Lys Gly Val Gly Thr Thr Leu				
	360	365	370	
aac ctg tgg gaa tca ccc gca ctg gct tgagagaaga aacaacaatg				
1266				
Asn Leu Trp Glu Ser Pro Ala Leu Ala				
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aaa
1269

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<213> *Corynebacterium glutamicum*

<400> 344

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Ser	Glu	Pro	Asp	Met	Ile	Ala	Ala	Gly	Val	Lys	Asp	Val	Ala	Gln	Cys	20	25	30	
Val	Asp	Val	Met	Glu	Glu	Thr	Leu	Val	Leu	Leu	Ala	Gln	Gly	Asp	Tyr	35	40	45	
Lys	Met	Ala	Gly	Leu	Asn	Ser	Asn	Ser	His	Gly	Ala	Met	Ile	Thr	Phe	50	55	60	
Pro	Glu	Asn	Pro	Glu	Phe	Glu	Gly	Met	Pro	Lys	Asp	Gly	Pro	Asp	Arg	65	70	75	80
Arg	Phe	Met	Ala	Met	Pro	Ala	Tyr	Leu	Gly	Gly	Arg	Phe	Lys	Asn	Thr	85	90	95	
Gly	Val	Lys	Trp	Tyr	Gly	Ser	Asn	Ala	Glu	Asn	Lys	Ala	Ser	Gly	Leu	100	105	110	
Pro	Arg	Ser	Ile	His	Thr	Phe	Val	Leu	Asn	Asp	Thr	Val	Thr	Gly	Ala	115	120	125	
Pro	Lys	Ala	Ile	Met	Ser	Ala	Asn	Leu	Leu	Ser	Ala	Tyr	Arg	Thr	Gly	130	135	140	
Ala	Val	Pro	Gly	Val	Gly	Val	Lys	His	Leu	Ala	Val	Ala	Asp	Ala	Thr	145	150	155	160
Thr	Leu	Ala	Val	Val	Gly	Pro	Gly	Val	Met	Ala	Lys	Thr	Ile	Thr	Glu	165	170	175	
Ala	Cys	Ile	Ala	Glu	Arg	Pro	Gly	Ile	Thr	Thr	Ile	Lys	Ile	Lys	Gly	180	185	190	
Arg	Ser	Glu	Arg	Gly	Ile	Asn	Ala	Phe	Ala	Thr	Trp	Ala	Leu	Glu	Lys	195	200	205	
Phe	Pro	Glu	Ile	Glu	Val	Val	Ala	Val	Gly	Ser	Glu	Glu	Asp	Val	Val	210	215	220	
Lys	Asp	Ala	Asp	Ile	Val	Ile	Ala	Ala	Thr	Thr	Thr	Asp	Ala	Ala	Gly	225	230	235	240
Ser	Ser	Ala	Phe	Pro	Tyr	Phe	Lys	Lys	Glu	Trp	Leu	Lys	Pro	Gly	Ala	245	250	255	
Leu	Leu	Leu	Leu	Pro	Ala	Ala	Gly	Arg	Phe	Asp	Asp	Ala	Tyr	Leu	Leu	260	265	270	

Asp Asp Ala Arg Leu Val Val Asp Tyr Met Gly Leu Tyr Glu Ala Trp
 275 280 285
 Ala Glu Glu Tyr Gly Pro Gln Ala Tyr Gln Leu Leu Gly Ile Pro Gly
 290 295 300
 Thr His Trp Tyr Asp Leu Ala Leu Gln Gly Lys Leu Asp Leu Ala Lys
 305 310 315 320
 Ile Ser Gln Ile Gly Asp Ile Cys Ser Gly Lys Leu Pro Gly Arg Thr
 325 330 335
 Asn Asp Glu Glu Ile Ile Leu Tyr Ser Val Gly Gly Met Pro Val Glu
 340 345 350
 Asp Val Ala Trp Ala Thr Gln Val Tyr Glu Asn Ala Leu Glu Lys Gly
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 Val Gly Thr Thr Leu Asn Leu Trp Glu Ser Pro Ala Leu Ala
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 <213> *Corynebacterium glutamicum*

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 <222> (101)..(1042)
 <223> RXA00219

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 Val Ala Arg Lys Lys
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 aac acg tcc gat caa tcc cgc tcc caa gct gcc aac acg ccc att gct 163
 Asn Thr Ser Asp Gln Ser Arg Ser Gln Ala Ala Asn Thr Pro Ile Ala
 10 15 20
 ggc acc tat gag ggt gaa tat tcc gtc atc gag ttg gag gcc gat tcc 211
 Gly Thr Tyr Glu Gly Glu Tyr Ser Val Ile Glu Leu Glu Ala Asp Ser
 25 30 35
 tac acc acc gat ggc tgg ttg atc agc att aat ggc gtg ccc agc tct 259
 Tyr Thr Thr Asp Gly Trp Leu Ile Ser Ile Asn Gly Val Pro Ser Ser
 40 45 50
 cat att gtc ctg ggg caa ccg cag gca ctg gaa ttt gag tac atg cgg 307
 His Ile Val Leu Gly Gln Pro Gln Ala Leu Glu Phe Glu Tyr Met Arg
 55 60 65
 tgg atc gct acc ggc gct cgg gcg ttc atc gat gcg cat cag gat gca 355
 Trp Ile Ala Thr Gly Ala Arg Ala Phe Ile Asp Ala His Gln Asp Ala
 70 75 80 85
 tcc aag ctg cgg att act cac ctc ggc ggc ggt gcg tgc acg atg gcc 403
 Ser Lys Leu Arg Ile Thr His Leu Gly Gly Gly Ala Cys Thr Met Ala

90										95					100					
agg	tat	ttc	gcg	gat	gtt	tac	ccg	cag	tca	cgc	aac	act	gtc	gtg	gaa	451				
Arg	Tyr	Phe	Ala	Asp	Val	Tyr	Pro	Gln	Ser	Arg	Asn	Thr	Val	Val	Glu					
			105					110					115							
ttg	gat	gca	gag	ctt	gcc	cgc	ctg	tcg	cgt	gaa	tgg	ttc	gac	att	ccg	499				
Leu	Asp	Ala	Glu	Leu	Ala	Arg	Leu	Ser	Arg	Glu	Trp	Phe	Asp	Ile	Pro					
		120					125					130								
cgc	gcg	cca	cgg	gta	aag	att	cgt	gtg	gat	gat	gcc	cga	atg	gtg	gca	547				
Arg	Ala	Pro	Arg	Val	Lys	Ile	Arg	Val	Asp	Asp	Ala	Arg	Met	Val	Ala					
	135					140					145									
gaa	tct	ttc	act	ccc	gca	agc	cgc	gat	gtg	atc	atc	cgt	gac	gtt	ttt	595				
Glu	Ser	Phe	Thr	Pro	Ala	Ser	Arg	Asp	Val	Ile	Ile	Arg	Asp	Val	Phe					
150					155					160					165					
gcc	gga	gct	atc	acg	ccg	cag	aac	ttc	acc	acc	gtg	gag	ttc	ttt	gag	643				
Ala	Gly	Ala	Ile	Thr	Pro	Gln	Asn	Phe	Thr	Thr	Val	Glu	Phe	Phe	Glu					
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cac	tgt	cac	cgt	ggc	ctt	gct	ccc	ggc	gga	ttg	tac	gtt	gcc	aac	tgt	691				
His	Cys	His	Arg	Gly	Leu	Ala	Pro	Gly	Gly	Leu	Tyr	Val	Ala	Asn	Cys					
			185					190					195							
ggc	gat	cat	tcg	gat	ctg	cgc	gga	gct	aaa	tct	gag	ctc	gcg	gga	atg	739				
Gly	Asp	His	Ser	Asp	Leu	Arg	Gly	Ala	Lys	Ser	Glu	Leu	Ala	Gly	Met					
		200					205					210								
atg	gag	gtg	ttc	gag	cac	gtc	gcg	gtc	atc	gcc	gat	ccc	ccg	atg	ctt	787				
Met	Glu	Val	Phe	Glu	His	Val	Ala	Val	Ile	Ala	Asp	Pro	Pro	Met	Leu					
	215					220					225									
aaa	ggg	cgc	cgt	tac	ggc	aac	atc	att	ttg	atg	ggg	tca	gac	acc	gag	835				
Lys	Gly	Arg	Arg	Tyr	Gly	Asn	Ile	Ile	Leu	Met	Gly	Ser	Asp	Thr	Glu					
230					235					240					245					
ttc	ttt	agc	tcc	aac	agc	acg	gaa	gcg	tcc	gcg	att	acc	cgt	gag	ctt	883				
Phe	Phe	Ser	Ser	Asn	Ser	Thr	Glu	Ala	Ser	Ala	Ile	Thr	Arg	Glu	Leu					
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ctt	ggc	ggc	ggc	gtt	cca	gcg	cag	tac	aag	gat	gaa	tcc	tgg	gtg	cgg	931				
Leu	Gly	Gly	Gly	Val	Pro	Ala	Gln	Tyr	Lys	Asp	Glu	Ser	Trp	Val	Arg					
			265				270						275							
aaa	ttc	gcc	tcg	gga	gcc	cag	gcc	cgc	cac	gat	ggg	gtc	tct	acc	ctc	979				
Lys	Phe	Ala	Ser	Gly	Ala	Gln	Ala	Arg	His	Asp	Gly	Val	Ser	Thr	Leu					
		280				285						290								
caa	atg	ccg	agt	gat	act	cca	caa	cac	cct	gcg	gaa	acg	ccg	gag	cat					
1027																				
Gln	Met	Pro	Ser	Asp	Thr	Pro	Gln	His	Pro	Ala	Glu	Thr	Pro	Glu	His					
	295					300					305									
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1065																				
Ser	Asn	Thr	Gln	Pro																
310																				

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 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 346

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Asn	Thr	Pro	Ile	Ala	Gly	Thr	Tyr	Glu	Gly	Glu	Tyr	Ser	Val	Ile	Glu	20	25	30	
Leu	Glu	Ala	Asp	Ser	Tyr	Thr	Thr	Asp	Gly	Trp	Leu	Ile	Ser	Ile	Asn	35	40	45	
Gly	Val	Pro	Ser	Ser	His	Ile	Val	Leu	Gly	Gln	Pro	Gln	Ala	Leu	Glu	50	55	60	
Phe	Glu	Tyr	Met	Arg	Trp	Ile	Ala	Thr	Gly	Ala	Arg	Ala	Phe	Ile	Asp	65	70	75	80
Ala	His	Gln	Asp	Ala	Ser	Lys	Leu	Arg	Ile	Thr	His	Leu	Gly	Gly	Gly	85	90	95	
Ala	Cys	Thr	Met	Ala	Arg	Tyr	Phe	Ala	Asp	Val	Tyr	Pro	Gln	Ser	Arg	100	105	110	
Asn	Thr	Val	Val	Glu	Leu	Asp	Ala	Glu	Leu	Ala	Arg	Leu	Ser	Arg	Glu	115	120	125	
Trp	Phe	Asp	Ile	Pro	Arg	Ala	Pro	Arg	Val	Lys	Ile	Arg	Val	Asp	Asp	130	135	140	
Ala	Arg	Met	Val	Ala	Glu	Ser	Phe	Thr	Pro	Ala	Ser	Arg	Asp	Val	Ile	145	150	155	160
Ile	Arg	Asp	Val	Phe	Ala	Gly	Ala	Ile	Thr	Pro	Gln	Asn	Phe	Thr	Thr	165	170	175	
Val	Glu	Phe	Phe	Glu	His	Cys	His	Arg	Gly	Leu	Ala	Pro	Gly	Gly	Leu	180	185	190	
Tyr	Val	Ala	Asn	Cys	Gly	Asp	His	Ser	Asp	Leu	Arg	Gly	Ala	Lys	Ser	195	200	205	
Glu	Leu	Ala	Gly	Met	Met	Glu	Val	Phe	Glu	His	Val	Ala	Val	Ile	Ala	210	215	220	
Asp	Pro	Pro	Met	Leu	Lys	Gly	Arg	Arg	Tyr	Gly	Asn	Ile	Ile	Leu	Met	225	230	235	240
Gly	Ser	Asp	Thr	Glu	Phe	Phe	Ser	Ser	Asn	Ser	Thr	Glu	Ala	Ser	Ala	245	250	255	
Ile	Thr	Arg	Glu	Leu	Leu	Gly	Gly	Gly	Val	Pro	Ala	Gln	Tyr	Lys	Asp	260	265	270	
Glu	Ser	Trp	Val	Arg	Lys	Phe	Ala	Ser	Gly	Ala	Gln	Ala	Arg	His	Asp	275	280	285	
Gly	Val	Ser	Thr	Leu	Gln	Met	Pro	Ser	Asp	Thr	Pro	Gln	His	Pro	Ala				

150	155	160	165	
ctg ccg tgg ctt ggc atg atg cgc ggt gcc gca gca gcc gga atg atc				643
Leu Pro Trp Leu Gly Met Met Arg Gly Ala Ala Ala Ala Gly Met Ile				
	170	175	180	
aac ctc gtt gca gca cta ttc gtg ggc tgt gtg ctg ctg cga cat ttg				691
Asn Leu Val Ala Ala Leu Phe Val Gly Cys Val Leu Leu Arg His Leu				
	185	190	195	
ctt ccg cgc acc cac ttc ttc gta tcc gtg gtg gcg ctt ctt ctc gcg				739
Leu Pro Arg Thr His Phe Phe Val Ser Val Val Ala Leu Leu Leu Ala				
	200	205	210	
atc gca gcg cta gcc acc gtg ttg gtg aaa tcc gac ggg atc gtt gcc				787
Ile Ala Ala Leu Ala Thr Val Leu Val Lys Ser Asp Gly Ile Val Ala				
	215	220	225	
acc gcc cgc gca cag ctc tac cgc gac ccc gtg atc tat tca cac caa				835
Thr Ala Arg Ala Gln Leu Tyr Arg Asp Pro Val Ile Tyr Ser His Gln				
	230	235	240	245
tct gac tac caa gac atc gta gtg aca gaa cga ggc aaa gac cga cgc				883
Ser Asp Tyr Gln Asp Ile Val Val Thr Glu Arg Gly Lys Asp Arg Arg				
	250	255	260	
ctc tac ctc aat ggc ggt ttg cag tat tcc act cgt gac cag cat aga				931
Leu Tyr Leu Asn Gly Gly Leu Gln Tyr Ser Thr Arg Asp Gln His Arg				
	265	270	275	
tat aca gaa tca ctg gtg tat cca agc ctt aat cca gag gca gaa tcg				979
Tyr Thr Glu Ser Leu Val Tyr Pro Ser Leu Asn Pro Glu Ala Glu Ser				
	280	285	290	
gtg tta atc atc ggc ggt ggc gat ggc ctc gca gca cgg gaa ctc ctc				
1027				
Val Leu Ile Ile Gly Gly Gly Asp Gly Leu Ala Ala Arg Glu Leu Leu				
	295	300	305	
cga ttc cca tca atg cag atc acc caa gtt gaa tta gac cca gaa gtc				
1075				
Arg Phe Pro Ser Met Gln Ile Thr Gln Val Glu Leu Asp Pro Glu Val				
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atc gaa gta gcc aac aca gtg ctg cgc tct gac aat ggg gga gcg atg				
1123				
Ile Glu Val Ala Asn Thr Val Leu Arg Ser Asp Asn Gly Gly Ala Met				
	330	335	340	
gaa gat ccc cgc gtc tcc atc atc gtt gac gac gct ttc acc tgg ctg				
1171				
Glu Asp Pro Arg Val Ser Ile Ile Val Asp Asp Ala Phe Thr Trp Leu				
	345	350	355	
cgc tcc ggc gga aat aat ggc gaa act tac gat tcc atc atc atc gat				
1219				
Arg Ser Gly Gly Asn Asn Gly Glu Thr Tyr Asp Ser Ile Ile Ile Asp				
	360	365	370	
ctt ccc gac cca aac aac gac acc atg gcc agg ctg tat tca gaa gag				
1267				

Leu Pro Asp Pro Asn Asn Asp Thr Met Ala Arg Leu Tyr Ser Glu Glu
 375 380 385

ttc tac acc ttg gcc cga gca cga ctg aac gaa caa ggc cgc atg gtg
 1315

Phe Tyr Thr Leu Ala Arg Ala Arg Leu Asn Glu Gln Gly Arg Met Val
 390 395 400 405

gtg caa tcc tcc agc gcc tac acc act cca gat gtg ttc tgg cga gtt
 1363

Val Gln Ser Ser Ser Ala Tyr Thr Thr Pro Asp Val Phe Trp Arg Val
 410 415 420

gga gca acc ttg aaa tcg gcg ggc tgt gaa caa gtc atc cca tat cac
 1411

Gly Ala Thr Leu Lys Ser Ala Gly Cys Glu Gln Val Ile Pro Tyr His
 425 430 435

gtg cat gtt ccc aca ttt ggc gac tgg ggc ttc caa ctg tgt ggc cct
 1459

Val His Val Pro Thr Phe Gly Asp Trp Gly Phe Gln Leu Cys Gly Pro
 440 445 450

gcc gac atg gaa tta gag ctt cgg gaa gac acc ccg cca ctg act ttc
 1507

Ala Asp Met Glu Leu Glu Leu Arg Glu Asp Thr Pro Pro Leu Thr Phe
 455 460 465

ctt aat gat gaa gtt ctg gtg gct gct ggg gtg ttt ggg ttg gat aat
 1555

Leu Asn Asp Glu Val Leu Val Ala Ala Gly Val Phe Gly Leu Asp Asn
 470 475 480 485

cag cct cgt gaa ttg gaa cct tcc acg ctg gat cat ccc cgc gtg gtg
 1603

Gln Pro Arg Glu Leu Glu Pro Ser Thr Leu Asp His Pro Arg Val Val
 490 495 500

gag gat ctg cgc aag gga tac cgc gaa tca ggc gac tagctgcaac
 1649

Glu Asp Leu Arg Lys Gly Tyr Arg Glu Ser Gly Asp
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gatgcgctgt gtg
 1662

<210> 348

<211> 513

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<213> Corynebacterium glutamicum

<400> 348

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Leu Ser Thr Ser Leu Asn Gly Gly Gly Ile Val Glu Thr Ser Leu Ile
 35 40 45

Val Ala Gly Tyr Val Ala Ala Leu Gly Leu Gly Ala Leu Leu Val Lys
 50 55 60
 Pro Phe Leu Asn Trp Pro Ala Gln Thr Phe Leu Gly Val Glu Thr Leu
 65 70 75 80
 Leu Gly Leu Ile Gly Gly Cys Ser Ala Leu Val Leu Tyr Phe Thr Phe
 85 90 95
 Ala Thr Ile Gly Gln Ser Leu Trp Ile Leu Val Ile Ala Thr Ala Ala
 100 105 110
 Ile Gly Ile Leu Val Gly Ala Glu Leu Pro Leu Leu Met Thr Met Ile
 115 120 125
 Gln Gln Gly Arg Leu Ala Asp Ala Lys Thr Thr Gly Ser Leu Val Ala
 130 135 140
 Thr Leu Asn Ala Ala Asp Tyr Leu Gly Ala Leu Leu Gly Gly Leu Ala
 145 150 155 160
 Trp Pro Phe Val Leu Leu Pro Trp Leu Gly Met Met Arg Gly Ala Ala
 165 170 175
 Ala Ala Gly Met Ile Asn Leu Val Ala Ala Leu Phe Val Gly Cys Val
 180 185 190
 Leu Leu Arg His Leu Leu Pro Arg Thr His Phe Phe Val Ser Val Val
 195 200 205
 Ala Leu Leu Leu Ala Ile Ala Ala Leu Ala Thr Val Leu Val Lys Ser
 210 215 220
 Asp Gly Ile Val Ala Thr Ala Arg Ala Gln Leu Tyr Arg Asp Pro Val
 225 230 235 240
 Ile Tyr Ser His Gln Ser Asp Tyr Gln Asp Ile Val Val Thr Glu Arg
 245 250 255
 Gly Lys Asp Arg Arg Leu Tyr Leu Asn Gly Gly Leu Gln Tyr Ser Thr
 260 265 270
 Arg Asp Gln His Arg Tyr Thr Glu Ser Leu Val Tyr Pro Ser Leu Asn
 275 280 285
 Pro Glu Ala Glu Ser Val Leu Ile Ile Gly Gly Gly Asp Gly Leu Ala
 290 295 300
 Ala Arg Glu Leu Leu Arg Phe Pro Ser Met Gln Ile Thr Gln Val Glu
 305 310 315 320
 Leu Asp Pro Glu Val Ile Glu Val Ala Asn Thr Val Leu Arg Ser Asp
 325 330 335
 Asn Gly Gly Ala Met Glu Asp Pro Arg Val Ser Ile Ile Val Asp Asp
 340 345 350
 Ala Phe Thr Trp Leu Arg Ser Gly Gly Asn Asn Gly Glu Thr Tyr Asp
 355 360 365

Ser Ile Ile Ile Asp Leu Pro Asp Pro Asn Asn Asp Thr Met Ala Arg
 370 375 380

Leu Tyr Ser Glu Glu Phe Tyr Thr Leu Ala Arg Ala Arg Leu Asn Glu
 385 390 395 400

Gln Gly Arg Met Val Val Gln Ser Ser Ser Ala Tyr Thr Thr Pro Asp
 405 410 415

Val Phe Trp Arg Val Gly Ala Thr Leu Lys Ser Ala Gly Cys Glu Gln
 420 425 430

Val Ile Pro Tyr His Val His Val Pro Thr Phe Gly Asp Trp Gly Phe
 435 440 445

Gln Leu Cys Gly Pro Ala Asp Met Glu Leu Glu Leu Arg Glu Asp Thr
 450 455 460

Pro Pro Leu Thr Phe Leu Asn Asp Glu Val Leu Val Ala Ala Gly Val
 465 470 475 480

Phe Gly Leu Asp Asn Gln Pro Arg Glu Leu Glu Pro Ser Thr Leu Asp
 485 490 495

His Pro Arg Val Val Glu Asp Leu Arg Lys Gly Tyr Arg Glu Ser Gly
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Asp

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 <213> Corynebacterium glutamicum

<220>
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 <223> RXA01757

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 Met Pro Thr Ala Ser
 1 5

cca att tat gat gtc gtt gtc gtc gga gcc ggc att tct ggc ctc atc 163
 Pro Ile Tyr Asp Val Val Val Val Gly Ala Gly Ile Ser Gly Leu Ile
 10 15 20

gcc acg caa ctg ttg gac cgc gca ggt cta aac atc aaa tgc ttc gaa 211
 Ala Thr Gln Leu Leu Asp Arg Ala Gly Leu Asn Ile Lys Cys Phe Glu
 25 30 35

gcc tgc tca aga gtt ggc ggc cga gca gtg tct gtc caa cag tcc gat 259
 Ala Cys Ser Arg Val Gly Gly Arg Ala Val Ser Val Gln Gln Ser Asp
 40 45 50

ttg ttc ctg gac ctc ggc gca aca tgg ttc tgg ctc aac gaa cca ctt 307

Leu	Phe	Leu	Asp	Leu	Gly	Ala	Thr	Trp	Phe	Trp	Leu	Asn	Glu	Pro	Leu	
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gtg	cag	caa	ctc	gtc	aat	aat	ctc	ggc	ctc	ggc	aca	ttc	cct	cag	gcc	355
Val	Gln	Gln	Leu	Val	Asn	Asn	Leu	Gly	Leu	Gly	Thr	Phe	Pro	Gln	Ala	
70					75					80					85	
atc	gag	ggg	gat	gcg	ctt	ttt	gag	acg	ctt	gtc	gac	gcc	ccg	agc	cgc	403
Ile	Glu	Gly	Asp	Ala	Leu	Phe	Glu	Thr	Leu	Val	Asp	Ala	Pro	Ser	Arg	
				90					95					100		
ctg	cgg	ggg	aac	ccc	ata	gac	gct	gct	tca	ggc	agg	ttc	caa	gca	ggg	451
Leu	Arg	Gly	Asn	Pro	Ile	Asp	Ala	Ala	Ser	Gly	Arg	Phe	Gln	Ala	Gly	
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gcc	tcc	tcg	ctt	gcg	ctc	ggg	ctt	gca	gcc	cag	ctc	aag	cca	gga	gtt	499
Ala	Ser	Ser	Leu	Ala	Leu	Gly	Leu	Ala	Ala	Gln	Leu	Lys	Pro	Gly	Val	
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tta	gaa	ctc	ggg	gac	ccc	gtc	cat	tct	ctc	agt	gag	gaa	gat	ggg	gaa	547
Leu	Glu	Leu	Gly	Asp	Pro	Val	His	Ser	Leu	Ser	Glu	Glu	Asp	Gly	Glu	
	135					140					145					
atc	gtt	gtg	aag	tct	tcc	aaa	cag	att	gtg	agg	gca	aag	cac	gtc	atc	595
Ile	Val	Val	Lys	Ser	Ser	Lys	Gln	Ile	Val	Arg	Ala	Lys	His	Val	Ile	
150					155					160					165	
att	gcg	gtt	cca	ccg	gca	ctc	gct	gcc	gag	ttg	att	ggg	ttc	acc	cta	643
Ile	Ala	Val	Pro	Pro	Ala	Leu	Ala	Ala	Glu	Leu	Ile	Gly	Phe	Thr	Leu	
				170					175					180		
gat	tta	cca	gct	gac	gtg	cga	aaa	gca	gcg	cat	cca	caa	cat	ata	gct	691
Asp	Leu	Pro	Ala	Asp	Val	Arg	Lys	Ala	Ala	His	Pro	Gln	His	Ile	Ala	
			185					190					195			
gtg	atg	aat	tgg	gca	aag	gag	aaa	tac	acc	tta	ccc	aca	caa	gcc	gca	739
Val	Met	Asn	Trp	Ala	Lys	Glu	Lys	Tyr	Thr	Leu	Pro	Thr	Gln	Ala	Ala	
		200					205					210				
tcg	gct	ggg	ggg	ttt	ggg	cat	gag	ctg	ttc	caa	caa	cca	ctc	gga	cat	787
Ser	Ala	Gly	Gly	Phe	Gly	His	Glu	Leu	Phe	Gln	Gln	Pro	Leu	Gly	His	
	215					220					225					
ggg	cga	att	cat	tgg	gca	tca	acg	gaa	gtt	gcc	act	gag	ttt	ggg	gga	835
Gly	Arg	Ile	His	Trp	Ala	Ser	Thr	Glu	Val	Ala	Thr	Glu	Phe	Gly	Gly	
230					235					240				245		
cac	ctt	gaa	ggc	gca	gtt	cgt	gca	gga	att	cag	gct	gcg	ctt	caa	aca	883
His	Leu	Glu	Gly	Ala	Val	Arg	Ala	Gly	Ile	Gln	Ala	Ala	Leu	Gln	Thr	
				250					255					260		
gga	ttt	aat	cta	aaa	tct	taa	ac	ctc	gt	att	tt	cc	ctg	ata		924
Gly	Phe	Asn	Leu	Lys	Ser											
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<212> PRT

<213> Corynebacterium glutamicum

<400> 350

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Ile Lys Cys Phe Glu Ala Cys Ser Arg Val Gly Gly Arg Ala Val Ser
 35 40 45

Val Gln Gln Ser Asp Leu Phe Leu Asp Leu Gly Ala Thr Trp Phe Trp
 50 55 60

Leu Asn Glu Pro Leu Val Gln Gln Leu Val Asn Asn Leu Gly Leu Gly
 65 70 75 80

Thr Phe Pro Gln Ala Ile Glu Gly Asp Ala Leu Phe Glu Thr Leu Val
 85 90 95

Asp Ala Pro Ser Arg Leu Arg Gly Asn Pro Ile Asp Ala Ala Ser Gly
 100 105 110

Arg Phe Gln Ala Gly Ala Ser Ser Leu Ala Leu Gly Leu Ala Ala Gln
 115 120 125

Leu Lys Pro Gly Val Leu Glu Leu Gly Asp Pro Val His Ser Leu Ser
 130 135 140

Glu Glu Asp Gly Glu Ile Val Val Lys Ser Ser Lys Gln Ile Val Arg
 145 150 155 160

Ala Lys His Val Ile Ile Ala Val Pro Pro Ala Leu Ala Ala Glu Leu
 165 170 175

Ile Gly Phe Thr Leu Asp Leu Pro Ala Asp Val Arg Lys Ala Ala His
 180 185 190

Pro Gln His Ile Ala Val Met Asn Trp Ala Lys Glu Lys Tyr Thr Leu
 195 200 205

Pro Thr Gln Ala Ala Ser Ala Gly Gly Phe Gly His Glu Leu Phe Gln
 210 215 220

Gln Pro Leu Gly His Gly Arg Ile His Trp Ala Ser Thr Glu Val Ala
 225 230 235 240

Thr Glu Phe Gly Gly His Leu Glu Gly Ala Val Arg Ala Gly Ile Gln
 245 250 255

Ala Ala Leu Gln Thr Gly Phe Asn Leu Lys Ser
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<211> 636

<212> DNA

<213> *Corynebacterium glutamicum*

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<222> (101)..(613)

<223> RXA02159

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 Met Ser Leu Gly Ser
 1 5

acc ccg tca aca ccg gaa aac tta aat ccc gtg act cgc act gca cgc 163
 Thr Pro Ser Thr Pro Glu Asn Leu Asn Pro Val Thr Arg Thr Ala Arg
 10 15 20

caa gct ctc att ttg cag att ttg gac aaa caa aaa gtc acc agc cag 211
 Gln Ala Leu Ile Leu Gln Ile Leu Asp Lys Gln Lys Val Thr Ser Gln
 25 30 35

gta caa ctg tct gaa ttg ctg ctg gat gaa ggc atc gat atc acc cag 259
 Val Gln Leu Ser Glu Leu Leu Leu Asp Glu Gly Ile Asp Ile Thr Gln
 40 45 50

gcc acc ttg tcc cga gat ctc gat gaa ctc ggt gca cgc aag gtt cgc 307
 Ala Thr Leu Ser Arg Asp Leu Asp Glu Leu Gly Ala Arg Lys Val Arg
 55 60 65

ccc gat ggg gga cgc gcc tac tac gcg gtc ggc cca gta gat agc atc 355
 Pro Asp Gly Gly Arg Ala Tyr Tyr Ala Val Gly Pro Val Asp Ser Ile
 70 75 80 85

gcc cgc gaa gat ctc cgg ggt ccg tcg gag aag ctg cgc cgc atg ctt 403
 Ala Arg Glu Asp Leu Arg Gly Pro Ser Glu Lys Leu Arg Arg Met Leu
 90 95 100

gat gaa ctg ctg gtt tct aca gat cat tcc ggc aac atc gcg atg ctg 451
 Asp Glu Leu Leu Val Ser Thr Asp His Ser Gly Asn Ile Ala Met Leu
 105 110 115

cgc acc ccg ccg gga gct gcc cag tac ctg gca agt ttc atc gat agg 499
 Arg Thr Pro Pro Gly Ala Ala Gln Tyr Leu Ala Ser Phe Ile Asp Arg
 120 125 130

gtg ggg ctg aaa gaa gtc gtt ggc acc atc gct ggt gat gac acc gtt 547
 Val Gly Leu Lys Glu Val Val Gly Thr Ile Ala Gly Asp Asp Thr Val
 135 140 145

ttc gtt ctc gcc cgt gat ccg ctc aca ggt aaa gaa cta ggt gaa tta 595
 Phe Val Leu Ala Arg Asp Pro Leu Thr Gly Lys Glu Leu Gly Glu Leu
 150 155 160 165

ctc agc ggg cgc acc act taaagcgccc ctagttcaag gct 636
 Leu Ser Gly Arg Thr Thr
 170

<210> 352

<211> 171

<212> PRT

<213> Corynebacterium glutamicum

<400> 352

Met Ser Leu Gly Ser Thr Pro Ser Thr Pro Glu Asn Leu Asn Pro Val

290

295

300

Glu Thr Pro Glu His Ser Asn Thr Gln Pro
 305 310

<210> 347

<211> 1662

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1639)

<223> RXA01508

<400> 347

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ttccgggacg tttccgtgat ctcgtggaag atcccaaact ccgttccggt gccgtcgtgg 60
ccgccgtcat cttgatcgtg gtgggaaccg taaacgctgc atg tct gat tta gga 115
                                         Met Ser Asp Leu Gly
                                         1 5

ccc atc tgg cgc tgg ctg tta tta gtt tcc gtc tcc att tgt gcg gca 163
Pro Ile Trp Arg Trp Leu Leu Leu Val Ser Val Ser Ile Cys Ala Ala
                        10 15 20

tcg ggg ctg gtc tat gag cta gcc ctg gta tcg ctt tcc acc agc ttg 211
Ser Gly Leu Val Tyr Glu Leu Ala Leu Val Ser Leu Ser Thr Ser Leu
                        25 30 35

aac ggt ggc gga att gta gaa acc tcc ctc atc gtc gca ggt tat gta 259
Asn Gly Gly Gly Ile Val Glu Thr Ser Leu Ile Val Ala Gly Tyr Val
                        40 45 50

gct gcc ctt gga ctt ggt gca ctg ctg gtc aag ccg ttt ctc aac tgg 307
Ala Ala Leu Gly Leu Gly Ala Leu Leu Val Lys Pro Phe Leu Asn Trp
                        55 60 65

cct gcg caa acc ttc ctc ggt gtg gaa acc ctc ctt gga ctt att ggt 355
Pro Ala Gln Thr Phe Leu Gly Val Glu Thr Leu Leu Gly Leu Ile Gly
                        70 75 80 85

ggt tgt tcc gcg ctg gtg ctg tat ttc acc ttc gcg acc atc ggc caa 403
Gly Cys Ser Ala Leu Val Leu Tyr Phe Thr Phe Ala Thr Ile Gly Gln
                        90 95 100

tcc ctg tgg att ctg gtg att gcc acc gct gca att ggc atc ctg gtc 451
Ser Leu Trp Ile Leu Val Ile Ala Thr Ala Ala Ile Gly Ile Leu Val
                        105 110 115

ggc gct gaa ctt cca ctg ctg atg acc atg atc cag caa ggc cgc ctc 499
Gly Ala Glu Leu Pro Leu Leu Met Thr Met Ile Gln Gln Gly Arg Leu
                        120 125 130

gcc gac gcc aaa acc aca gga tct ctg gtt gcc acc ttg aat gct gct 547
Ala Asp Ala Lys Thr Thr Gly Ser Leu Val Ala Thr Leu Asn Ala Ala
                        135 140 145

gat tac ctt ggc gca ctt tta ggt ggc ctg gcc tgg cct ttt gtg ttg 595
Asp Tyr Leu Gly Ala Leu Leu Gly Gly Leu Ala Trp Pro Phe Val Leu

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1				5					10					15		
Thr	Arg	Thr	Ala	Arg	Gln	Ala	Leu	Ile	Leu	Gln	Ile	Leu	Asp	Lys	Gln	
			20					25					30			
Lys	Val	Thr	Ser	Gln	Val	Gln	Leu	Ser	Glu	Leu	Leu	Leu	Asp	Glu	Gly	
		35					40					45				
Ile	Asp	Ile	Thr	Gln	Ala	Thr	Leu	Ser	Arg	Asp	Leu	Asp	Glu	Leu	Gly	
	50					55					60					
Ala	Arg	Lys	Val	Arg	Pro	Asp	Gly	Gly	Arg	Ala	Tyr	Tyr	Ala	Val	Gly	
65					70					75					80	
Pro	Val	Asp	Ser	Ile	Ala	Arg	Glu	Asp	Leu	Arg	Gly	Pro	Ser	Glu	Lys	
				85					90					95		
Leu	Arg	Arg	Met	Leu	Asp	Glu	Leu	Leu	Val	Ser	Thr	Asp	His	Ser	Gly	
			100					105					110			
Asn	Ile	Ala	Met	Leu	Arg	Thr	Pro	Pro	Gly	Ala	Ala	Gln	Tyr	Leu	Ala	
		115					120					125				
Ser	Phe	Ile	Asp	Arg	Val	Gly	Leu	Lys	Glu	Val	Val	Gly	Thr	Ile	Ala	
	130					135					140					
Gly	Asp	Asp	Thr	Val	Phe	Val	Leu	Ala	Arg	Asp	Pro	Leu	Thr	Gly	Lys	
145					150					155					160	
Glu	Leu	Gly	Glu	Leu	Leu	Ser	Gly	Arg	Thr	Thr						
				165					170							

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<210> 353
<211> 414
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(391)  
<223> RXN02154
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<400> 353																
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caccggttacc	tgcggaattc	tcaccactgc	aaccgcacct	ttg	aaa	gaa	ggc	gtt	115							
				Leu	Lys	Glu	Gly	Val								
				1				5								
acc	gca	gaa	cag	gct	cgc	gca	gta	tat	gaa	gag	ttc	tat	gca	cag	gaa	163
Thr	Ala	Glu	Gln	Ala	Arg	Ala	Val	Tyr	Glu	Glu	Phe	Tyr	Ala	Gln	Glu	
			10					15						20		
acc	ttc	gtg	cat	gtt	ctt	cca	gaa	ggc	gca	cag	cca	caa	acc	caa	gca	211
Thr	Phe	Val	His	Val	Leu	Pro	Glu	Gly	Ala	Gln	Pro	Gln	Thr	Gln	Ala	
			25					30					35			
gtt	ctt	ggc	tcc	aac	atg	tgc	cac	gtg	cag	gta	gaa	att	gat	gag	gaa	259
Val	Leu	Gly	Ser	Asn	Met	Cys	His	Val	Gln	Val	Glu	Ile	Asp	Glu	Glu	
		40					45				50					

gca	ggc	aaa	gtc	ctt	gtt	acc	tcc	gca	atc	gat	aac	ctc	acc	aag	gga	307
Ala	Gly	Lys	Val	Leu	Val	Thr	Ser	Ala	Ile	Asp	Asn	Leu	Thr	Lys	Gly	
	55						60					65				
act	gcc	ggc	gcc	gct	gtt	cag	tgc	atg	aac	tta	agc	gtt	ggg	ttt	gat	355
Thr	Ala	Gly	Ala	Ala	Val	Gln	Cys	Met	Asn	Leu	Ser	Val	Gly	Phe	Asp	
	70					75					80				85	
gag	gca	gca	ggc	ctg	cca	cag	gtc	ggc	gtc	gca	cct	taaagtagcg				401
Glu	Ala	Ala	Gly	Leu	Pro	Gln	Val	Gly	Val	Ala	Pro					
				90					95							
ccttaaagcg gcg															414	

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<210> 354
<211> 97
<212> PRT
<213> Corynebacterium glutamicum
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<400> 354
Leu Lys Glu Gly Val Thr Ala Glu Gln Ala Arg Ala Val Tyr Glu Glu
  1                      5                      10                      15

Phe Tyr Ala Gln Glu Thr Phe Val His Val Leu Pro Glu Gly Ala Gln
                20                      25                      30

Pro Gln Thr Gln Ala Val Leu Gly Ser Asn Met Cys His Val Gln Val
      35                      40                      45

Glu Ile Asp Glu Glu Ala Gly Lys Val Leu Val Thr Ser Ala Ile Asp
  50                      55                      60

Asn Leu Thr Lys Gly Thr Ala Gly Ala Ala Val Gln Cys Met Asn Leu
  65                      70                      75                      80

Ser Val Gly Phe Asp Glu Ala Ala Gly Leu Pro Gln Val Gly Val Ala
                85                      90                      95

Pro

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<210> 355
<211> 1302
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(1279)  
<223> RXS00147
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<400> 355
attgcatata atgcaatgaa ttgaataaac tacattcagg gttatcaacc agccaatttc 60

ttttaaaaag gcagacacac gaaaggcgac aacagtcacc gtg agt aaa gac acc 115
              Val Ser Lys Asp Thr
              1             5

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acc acc tac cag gga gtc acc gag atc gga tcc gtt ccg gca tac ctg	163
Thr Thr Tyr Gln Gly Val Thr Glu Ile Gly Ser Val Pro Ala Tyr Leu	
10 15 20	
gtt ctt gca gac gga cgt acc ttc acc gga ttt ggc ttt gga gct atc	211
Val Leu Ala Asp Gly Arg Thr Phe Thr Gly Phe Gly Phe Gly Ala Ile	
25 30 35	
ggc acc acc ctt ggt gag gca gtg ttc act acc gcc atg acc ggt tac	259
Gly Thr Thr Leu Gly Glu Ala Val Phe Thr Thr Ala Met Thr Gly Tyr	
40 45 50	
caa gaa acc atg acc gat cct tcc tat cac cgc cag att gtt gtg gct	307
Gln Glu Thr Met Thr Asp Pro Ser Tyr His Arg Gln Ile Val Val Ala	
55 60 65	
acc gca cca cag atc ggc aac acc ggc tgg aac gat gag gac aac gag	355
Thr Ala Pro Gln Ile Gly Asn Thr Gly Trp Asn Asp Glu Asp Asn Glu	
70 75 80 85	
tcc cgc gac ggc aag att tgg gtt gca ggc ctt gtt atc cgc gac ctc	403
Ser Arg Asp Gly Lys Ile Trp Val Ala Gly Leu Val Ile Arg Asp Leu	
90 95 100	
gca gca cgt gtg tcc aac tgg cgc gcc acc acc tcc ttg cag cag gaa	451
Ala Ala Arg Val Ser Asn Trp Arg Ala Thr Thr Ser Leu Gln Gln Glu	
105 110 115	
atg gca ggc cag ggc atc gtc ggc atc ggc gga atc gac acc cgc gca	499
Met Ala Gly Gln Gly Ile Val Gly Ile Gly Gly Ile Asp Thr Arg Ala	
120 125 130	
ctg gtt cgc cac ctg cgc aat gaa ggt tcc att gca gcg ggc atc ttc	547
Leu Val Arg His Leu Arg Asn Glu Gly Ser Ile Ala Ala Gly Ile Phe	
135 140 145	
tcc ggc gct gac gca cag cgc cca gtt gaa gaa ctc gta gag atc gtc	595
Ser Gly Ala Asp Ala Gln Arg Pro Val Glu Glu Leu Val Glu Ile Val	
150 155 160 165	
aag aat cag cca gca atg acc ggc gca aac ctc tcc gtt gag gtc tct	643
Lys Asn Gln Pro Ala Met Thr Gly Ala Asn Leu Ser Val Glu Val Ser	
170 175 180	
gct gat gaa acc tac gtc atc gaa gct gaa ggc gaa gag cgc cac acc	691
Ala Asp Glu Thr Tyr Val Ile Glu Ala Glu Gly Glu Glu Arg His Thr	
185 190 195	
gtc gtg gcc tac gac ctg ggc att aag caa aac acc cca cgt cgt ttc	739
Val Val Ala Tyr Asp Leu Gly Ile Lys Gln Asn Thr Pro Arg Arg Phe	
200 205 210	
tct gca cgc ggt gtt cgc acc gtc atc gtg cct gct gaa acc cca ttc	787
Ser Ala Arg Gly Val Arg Thr Val Ile Val Pro Ala Glu Thr Pro Phe	
215 220 225	
gag gat atc aag cag tac aac cca tca ggc gtg ttc atc tcc aac ggc	835
Glu Asp Ile Lys Gln Tyr Asn Pro Ser Gly Val Phe Ile Ser Asn Gly	
230 235 240 245	
cct ggc gat cct gca gca gca gac gtc atg gtt gat atc gtc cgc gaa	883

Pro Gly Asp Pro Ala Ala Ala Asp Val Met Val Asp Ile Val Arg Glu
 250 255 260
 gtt ctt gaa gcc gac att cca ttc ttt ggc atc tgc ttc ggc aac cag 931
 Val Leu Glu Ala Asp Ile Pro Phe Phe Gly Ile Cys Phe Gly Asn Gln
 265 270 275
 att ctt ggc cgc gca ttc ggc atg gag acc tac aag ctg aag ttc ggc 979
 Ile Leu Gly Arg Ala Phe Gly Met Glu Thr Tyr Lys Leu Lys Phe Gly
 280 285 290
 cac cgc ggc atc aac gtt cca gtg aag aac cac atc acc ggc aag atc
 1027
 His Arg Gly Ile Asn Val Pro Val Lys Asn His Ile Thr Gly Lys Ile
 295 300 305
 gac atc acc gcc cag aac cac ggc ttc gca ctc aag ggt gaa gca ggc
 1075
 Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu Lys Gly Glu Ala Gly
 310 315 320 325
 cag gaa ttc gag acc gat ttc ggc act gca att gtc acc cac acc tgc
 1123
 Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile Val Thr His Thr Cys
 330 335 340
 ctc aac gac ggc gtc gtt gaa ggt att gcg ctg aag tcc gga cgc gca
 1171
 Leu Asn Asp Gly Val Val Glu Gly Ile Ala Leu Lys Ser Gly Arg Ala
 345 350 355
 tac tcc gtt cag tac cac cca gag gcc gct gcc ggc cca aat gat gca
 1219
 Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala Gly Pro Asn Asp Ala
 360 365 370
 agc ccc ctg ttt gac cag ttt gtt gag ctg atg gat gca gac gct cag
 1267
 Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met Asp Ala Asp Ala Gln
 375 380 385
 aag aaa ggc gca taaataacat gccaaagcgt tca
 1302
 Lys Lys Gly Ala
 390

<210> 356

<211> 393

<212> PRT

<213> Corynebacterium glutamicum

<400> 356

Val Ser Lys Asp Thr Thr Thr Tyr Gln Gly Val Thr Glu Ile Gly Ser
 1 5 10 15
 Val Pro Ala Tyr Leu Val Leu Ala Asp Gly Arg Thr Phe Thr Gly Phe
 20 25 30
 Gly Phe Gly Ala Ile Gly Thr Thr Leu Gly Glu Ala Val Phe Thr Thr
 35 40 45

Ala Met Thr Gly Tyr Gln Glu Thr Met Thr Asp Pro Ser Tyr His Arg
 50 55 60
 Gln Ile Val Val Ala Thr Ala Pro Gln Ile Gly Asn Thr Gly Trp Asn
 65 70 75 80
 Asp Glu Asp Asn Glu Ser Arg Asp Gly Lys Ile Trp Val Ala Gly Leu
 85 90 95
 Val Ile Arg Asp Leu Ala Ala Arg Val Ser Asn Trp Arg Ala Thr Thr
 100 105 110
 Ser Leu Gln Gln Glu Met Ala Gly Gln Gly Ile Val Gly Ile Gly Gly
 115 120 125
 Ile Asp Thr Arg Ala Leu Val Arg His Leu Arg Asn Glu Gly Ser Ile
 130 135 140
 Ala Ala Gly Ile Phe Ser Gly Ala Asp Ala Gln Arg Pro Val Glu Glu
 145 150 155 160
 Leu Val Glu Ile Val Lys Asn Gln Pro Ala Met Thr Gly Ala Asn Leu
 165 170 175
 Ser Val Glu Val Ser Ala Asp Glu Thr Tyr Val Ile Glu Ala Glu Gly
 180 185 190
 Glu Glu Arg His Thr Val Val Ala Tyr Asp Leu Gly Ile Lys Gln Asn
 195 200 205
 Thr Pro Arg Arg Phe Ser Ala Arg Gly Val Arg Thr Val Ile Val Pro
 210 215 220
 Ala Glu Thr Pro Phe Glu Asp Ile Lys Gln Tyr Asn Pro Ser Gly Val
 225 230 235 240
 Phe Ile Ser Asn Gly Pro Gly Asp Pro Ala Ala Ala Asp Val Met Val
 245 250 255
 Asp Ile Val Arg Glu Val Leu Glu Ala Asp Ile Pro Phe Phe Gly Ile
 260 265 270
 Cys Phe Gly Asn Gln Ile Leu Gly Arg Ala Phe Gly Met Glu Thr Tyr
 275 280 285
 Lys Leu Lys Phe Gly His Arg Gly Ile Asn Val Pro Val Lys Asn His
 290 295 300
 Ile Thr Gly Lys Ile Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu
 305 310 315 320
 Lys Gly Glu Ala Gly Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile
 325 330 335
 Val Thr His Thr Cys Leu Asn Asp Gly Val Val Glu Gly Ile Ala Leu
 340 345 350
 Lys Ser Gly Arg Ala Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala
 355 360 365

Gly Pro Asn Asp Ala Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met
 370 375 380

Asp Ala Asp Ala Gln Lys Lys Gly Ala
 385 390

<210> 357

<211> 924

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(901)

<223> RXS00905

<400> 357

cgctgccccct ctatgctgct cctagttacc cctgcacaaa tagcgggtttt tctcagcat 60

tctgcatcga gtcgggtcga cgtatataag gtggaaaggc atg acc caa ttc gaa 115
 Met Thr Gln Phe Glu
 1 5

aac gcg caa gta ctt aaa gag aac atc gaa aac caa cgc gag cag atc 163
 Asn Ala Gln Val Leu Lys Glu Asn Ile Glu Asn Gln Arg Glu Gln Ile
 10 15 20

ttt acc cag ttg aaa gaa att gtg tct ttc aac tcc gtg cac agc gat 211
 Phe Thr Gln Leu Lys Glu Ile Val Ser Phe Asn Ser Val His Ser Asp
 25 30 35

cca aac cta ctg gag gac tac gcc ggc gcg aaa gaa tgg gta aaa gaa 259
 Pro Asn Leu Leu Glu Asp Tyr Ala Gly Ala Lys Glu Trp Val Lys Glu
 40 45 50

aca ctg acc aac gca ggt ctc acc gtc agc gaa ttc gct gcc gaa gat 307
 Thr Leu Thr Asn Ala Gly Leu Thr Val Ser Glu Phe Ala Ala Glu Asp
 55 60 65

gga acc acc aac ttc atc ggc acc cgc aag ggc tcc gaa ggt gca cca 355
 Gly Thr Thr Asn Phe Ile Gly Thr Arg Lys Gly Ser Glu Gly Ala Pro
 70 75 80 85

aag gta ctg ctg tac agc cac ttc gac gtt gtc cca tcc ggc cct ttg 403
 Lys Val Leu Leu Tyr Ser His Phe Asp Val Val Pro Ser Gly Pro Leu
 90 95 100

gat ctc tgg gac acc aat cct ttt gaa ctc acc gag cgc gac gct ggc 451
 Asp Leu Trp Asp Thr Asn Pro Phe Glu Leu Thr Glu Arg Asp Ala Gly
 105 110 115

cac ggc acc cgc tgg tac ggc cgc ggc gcc gct gac tgc aag ggc aac 499
 His Gly Thr Arg Trp Tyr Gly Arg Gly Ala Ala Asp Cys Lys Gly Asn
 120 125 130

ctg gtc atg cac ctc gca gca ctg cgc gcc gtc gaa gcc agc ggc gac 547
 Leu Val Met His Leu Ala Ala Leu Arg Ala Val Glu Ala Ser Gly Asp
 135 140 145

acc aca ctc aac ctc acc tac gtg gtc gag ggc tcc gag gaa atg gga 595

Thr Thr Leu Asn Leu Thr Tyr Val Val Glu Gly Ser Glu Glu Met Gly
 150 155 160 165
 ggc gga gcg ctc agc gcg ctc atc aag gac aag cct gag ctt ttc gac 643
 Gly Gly Ala Leu Ser Ala Leu Ile Lys Asp Lys Pro Glu Leu Phe Asp 180
 170 175
 gca gat gtc atc ttg att gca gac agc gga aac gct tcc gtg ggc acc 691
 Ala Asp Val Ile Leu Ile Ala Asp Ser Gly Asn Ala Ser Val Gly Thr 195
 185 190
 cca acc ttg acc act acc ctg cgc ggt ggc gga cag gtc acc gtc acc 739
 Pro Thr Leu Thr Thr Thr Leu Arg Gly Gly Gly Gln Val Thr Val Thr 210
 200 205
 gtg gac acc ctt gaa ggc gct gtt cac tcc ggc cag aac ggt ggc gct 787
 Val Asp Thr Leu Glu Gly Ala Val His Ser Gly Gln Asn Gly Gly Ala 225
 215 220
 gcc cca gat gct gtt gct gct ctc gtg cgc gtt ctg gat act ttg cgc 835
 Ala Pro Asp Ala Val Ala Ala Leu Val Arg Val Leu Asp Thr Leu Arg 245
 230 235 240
 gat gaa cac gga cgc acc gtt atc gac ggc tgt caa cac cac cgc aaa 883
 Asp Glu His Gly Arg Thr Val Ile Asp Gly Cys Gln His His Arg Lys 260
 250 255
 ctg gaa ggg cga gcc tta tgatccagag actttccgca gcg 924
 Leu Glu Gly Arg Ala Leu 265

<210> 358

<211> 267

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 358

Met Thr Gln Phe Glu Asn Ala Gln Val Leu Lys Glu Asn Ile Glu Asn
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 Gln Arg Glu Gln Ile Phe Thr Gln Leu Lys Glu Ile Val Ser Phe Asn
 20 25 30
 Ser Val His Ser Asp Pro Asn Leu Leu Glu Asp Tyr Ala Gly Ala Lys
 35 40 45
 Glu Trp Val Lys Glu Thr Leu Thr Asn Ala Gly Leu Thr Val Ser Glu
 50 55 60
 Phe Ala Ala Glu Asp Gly Thr Thr Asn Phe Ile Gly Thr Arg Lys Gly
 65 70 75 80
 Ser Glu Gly Ala Pro Lys Val Leu Leu Tyr Ser His Phe Asp Val Val
 85 90 95
 Pro Ser Gly Pro Leu Asp Leu Trp Asp Thr Asn Pro Phe Glu Leu Thr
 100 105 110
 Glu Arg Asp Ala Gly His Gly Thr Arg Trp Tyr Gly Arg Gly Ala Ala
 115 120 125

Asp Cys Lys Gly Asn Leu Val Met His Leu Ala Ala Leu Arg Ala Val
 130 135 140
 Glu Ala Ser Gly Asp Thr Thr Leu Asn Leu Thr Tyr Val Val Glu Gly
 145 150 155 160
 Ser Glu Glu Met Gly Gly Gly Ala Leu Ser Ala Leu Ile Lys Asp Lys
 165 170 175
 Pro Glu Leu Phe Asp Ala Asp Val Ile Leu Ile Ala Asp Ser Gly Asn
 180 185 190
 Ala Ser Val Gly Thr Pro Thr Leu Thr Thr Thr Leu Arg Gly Gly Gly
 195 200 205
 Gln Val Thr Val Thr Val Asp Thr Leu Glu Gly Ala Val His Ser Gly
 210 215 220
 Gln Asn Gly Gly Ala Ala Pro Asp Ala Val Ala Ala Leu Val Arg Val
 225 230 235 240
 Leu Asp Thr Leu Arg Asp Glu His Gly Arg Thr Val Ile Asp Gly Cys
 245 250 255
 Gln His His Arg Lys Leu Glu Gly Arg Ala Leu
 260 265

<210> 359

<211> 627

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(604)

<223> RXS00906

<400> 359

accgtggaca cccttgaagg cgctgttcac tccggccaga acggtggcgc tgccccagat 60
 gctgttgctg ctctcgtgcg cgttctggat actttgcgcg atg aac acg gac gca 115
 Met Asn Thr Asp Ala
 1 5
 ccg tta tcg acg gct gtc aac acc acc gca aac tgg -aag ggc gag cct 163
 Pro Leu Ser Thr Ala Val Asn Thr Thr Ala Asn Trp Lys Gly Glu Pro
 10 15 20
 tat gat cca gag act ttc cgc agc gat gcc ggc atc ctc gac ggt gta 211
 Tyr Asp Pro Glu Thr Phe Arg Ser Asp Ala Gly Ile Leu Asp Gly Val
 25 30 35
 gac atc atg ggc gac ggc gac aac cca gca agc atg ctg tgg tcc agg 259
 Asp Ile Met Gly Asp Gly Asp Asn Pro Ala Ser Met Leu Trp Ser Arg
 40 45 50
 cct gca atc tcc atc acc gga ttc act tcc acc cca gtg gca gaa gca 307
 Pro Ala Ile Ser Ile Thr Gly Phe Thr Ser Thr Pro Val Ala Glu Ala
 55 60 65

ctc aac gca gtg ccc gca acg gcg tcc gcc aag cta aac ctt cgc gtg 355
 Leu Asn Ala Val Pro Ala Thr Ala Ser Ala Lys Leu Asn Leu Arg Val
 70 75 80 85

cca gca ggc ctg gaa gca aac gat gtg gcc gag aag ctg aag cag cac 403
 Pro Ala Gly Leu Glu Ala Asn Asp Val Ala Glu Lys Leu Lys Gln His
 90 95 100

ctg atc aat cac aca cct tgg ggc gca aag atc acg gtg gag atc gat 451
 Leu Ile Asn His Thr Pro Trp Gly Ala Lys Ile Thr Val Glu Ile Asp
 105 110 115

gac att aac caa ccg ttc tcc acc gat att acc ggc cct gca atg tcc 499
 Asp Ile Asn Gln Pro Phe Ser Thr Asp Ile Thr Gly Pro Ala Met Ser
 120 125 130

acc ctg gcg tcc tgc ctg agc gct gcg tac gag ggc aag gat ctt gtc 547
 Thr Leu Ala Ser Cys Leu Ser Ala Ala Tyr Glu Gly Lys Asp Leu Val
 135 140 145

acc gaa ggc agc ggc gga tcc att cca ctg tgt acc gaa ctg att gag 595
 Thr Glu Gly Ser Gly Ser Ile Pro Leu Cys Thr Glu Leu Ile Glu
 150 155 160 165

gtc aac cca taagcagaat tggcactcta cgg 627
 Val Asn Pro

<210> 360

<211> 168

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 360

Met Asn Thr Asp Ala Pro Leu Ser Thr Ala Val Asn Thr Thr Ala Asn
 1 5 10 15

Trp Lys Gly Glu Pro Tyr Asp Pro Glu Thr Phe Arg Ser Asp Ala Gly
 20 25 30

Ile Leu Asp Gly Val Asp Ile Met Gly Asp Gly Asp Asn Pro Ala Ser
 35 40 45

Met Leu Trp Ser Arg Pro Ala Ile Ser Ile Thr Gly Phe Thr Ser Thr
 50 55 60

Pro Val Ala Glu Ala Leu Asn Ala Val Pro Ala Thr Ala Ser Ala Lys
 65 70 75 80

Leu Asn Leu Arg Val Pro Ala Gly Leu Glu Ala Asn Asp Val Ala Glu
 85 90 95

Lys Leu Lys Gln His Leu Ile Asn His Thr Pro Trp Gly Ala Lys Ile
 100 105 110

Thr Val Glu Ile Asp Asp Ile Asn Gln Pro Phe Ser Thr Asp Ile Thr
 115 120 125

Gly Pro Ala Met Ser Thr Leu Ala Ser Cys Leu Ser Ala Ala Tyr Glu

130 135 140
 Gly Lys Asp Leu Val Thr Glu Gly Ser Gly Gly Ser Ile Pro Leu Cys
 145 150 155 160
 Thr Glu Leu Ile Glu Val Asn Pro
 165

<210> 361
 <211> 246
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(223)
 <223> RXS00907

<400> 361
 cctgagcgcgt gcgtacgagg gcaaggatct tgtcaccgaa ggcagcggcg gatccattcc 60
 actgtgtacc gaactgattg aggtcaaccc ataagcagaa ttg gca ctc tac ggt 115
 Leu Ala Leu Tyr Gly
 1 5
 gtg gaa gaa ccc ctc acc gtt atc cac tcc gct aat gaa tct gtt gac 163
 Val Glu Glu Pro Leu Thr Val Ile His Ser Ala Asn Glu Ser Val Asp
 10 15 20
 ccc aat gag att cgc gat atc gcc acc gca gaa gca ttg ttc ctg ctc 211
 Pro Asn Glu Ile Arg Asp Ile Ala Thr Ala Glu Ala Leu Phe Leu Leu
 25 30 35
 aac tac acc aag tagacccaaa agcaggcgtt aac 246
 Asn Tyr Thr Lys
 40

<210> 362
 <211> 41
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 362
 Leu Ala Leu Tyr Gly Val Glu Glu Pro Leu Thr Val Ile His Ser Ala
 1 5 10 15
 Asn Glu Ser Val Asp Pro Asn Glu Ile Arg Asp Ile Ala Thr Ala Glu
 20 25 30
 Ala Leu Phe Leu Leu Asn Tyr Thr Lys
 35 40

<210> 363
 <211> 1281
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1258)

<223> RXS02001

<400> 363

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gcggtttcgt catggataag gactgtgttc gggaccattg cgatactcgt gtcaaaaggc 60
gatagtccag catagaccgt gctttatcga aggtgaaccc atg ccc gtt atc aat 115
                                         Met Pro Val Ile Asn
                                         1 5

agt atc gcc agt ttt tcc gac gag atg acc cgc tgg cgg cgt cac ctg 163
Ser Ile Ala Ser Phe Ser Asp Glu Met Thr Arg Trp Arg Arg His Leu
                        10                        15                        20

cat caa aac ccc gaa atc agc ttt gat tgt gtg gaa act gcg gcc ttc 211
His Gln Asn Pro Glu Ile Ser Phe Asp Cys Val Glu Thr Ala Ala Phe
                        25                        30                        35

gtg gcc gag cag ctg cgc agc ttc ggg gtg gat gaa att cac acc ggc 259
Val Ala Glu Gln Leu Arg Ser Phe Gly Val Asp Glu Ile His Thr Gly
                        40                        45                        50

atc gcg aaa acc ggt atc atc gcc ctg att cac ggg cgc gag gct ggc 307
Ile Ala Lys Thr Gly Ile Ile Ala Leu Ile His Gly Arg Glu Ala Gly
                        55                        60                        65

ccc gtc gtc ggc ctg cgc gcc gat atg gac gcg ctg ccg ctg acc gag 355
Pro Val Val Gly Leu Arg Ala Asp Met Asp Ala Leu Pro Leu Thr Glu
                        70                        75                        80                        85

att acc ggc gtc gac tat gcc tcg acc acc ccc gga aaa atg cac gcc 403
Ile Thr Gly Val Asp Tyr Ala Ser Thr Thr Pro Gly Lys Met His Ala
                        90                        95                        100

tgc ggc cac gac ggc cac acg acc atg ctg ctg ggc gcc gcc aaa tat 451
Cys Gly His Asp Gly His Thr Thr Met Leu Leu Gly Ala Ala Lys Tyr
                        105                        110                        115

ctg gcc gag acg cgc aat ttc gca ggt acc gtc gcg ctg atc ttc cag 499
Leu Ala Glu Thr Arg Asn Phe Ala Gly Thr Val Ala Leu Ile Phe Gln
                        120                        125                        130

cct gcg gaa gaa aac ggc ggc ggc gcg ggc gtt atg gtc gat gaa ggc 547
Pro Ala Glu Glu Asn Gly Gly Gly Ala Gly Val Met Val Asp Glu Gly
                        135                        140                        145

gtc ctc gac cgc ttt gcc atc gcc gaa gtc tac gcc ctg cac aac cag 595
Val Leu Asp Arg Phe Ala Ile Ala Glu Val Tyr Ala Leu His Asn Gln
                        150                        155                        160                        165

ccc ggc ctg ccg ctt ggc cat ttt atg acg aca gcc ggc ccg atc atg 643
Pro Gly Leu Pro Leu Gly His Phe Met Thr Thr Ala Gly Pro Ile Met
                        170                        175                        180

gcc gct gtc gac acg ttc gac atc aac att acc gga cgc ggc ggc cac 691
Ala Ala Val Asp Thr Phe Asp Ile Asn Ile Thr Gly Arg Gly Gly His
                        185                        190                        195

ggg gcc aaa ccg cac caa acc cgc gac ccc atc gtc gca gcc gtc gga 739
Gly Ala Lys Pro His Gln Thr Arg Asp Pro Ile Val Ala Ala Val Gly

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200	205	210	
att gtc caa gcg ttt caa acg ata gtc agc cgg aat cac aat ccg gtc			787
Ile Val Gln Ala Phe Gln Thr Ile Val Ser Arg Asn His Asn Pro Val			
215	220	225	
gag gac ctt gtc gtg tcg gtc acg caa atc cac acc ggc agc gcc gat			835
Glu Asp Leu Val Val Ser Val Thr Gln Ile His Thr Gly Ser Ala Asp			
230	235	240	245
aat atc atc ccc gaa acc gcc tat atc aac ggc act gtc cgc acc ttc			883
Asn Ile Ile Pro Glu Thr Ala Tyr Ile Asn Gly Thr Val Arg Thr Phe			
	250	255	260
aac aaa gac gtg cag gcc atg gtc atc acg cgg atg gaa gaa atc gtc			931
Asn Lys Asp Val Gln Ala Met Val Ile Thr Arg Met Glu Glu Ile Val			
	265	270	275
gcg ggc caa gct gca gcc tat ggg gtc gag gcg acg ctg acc tac aac			979
Ala Gly Gln Ala Ala Ala Tyr Gly Val Glu Ala Thr Leu Thr Tyr Asn			
	280	285	290
cgc aac tat ccc gcc acc att aac gac gcc gcc aaa gcc gcc atc gct			
1027			
Arg Asn Tyr Pro Ala Thr Ile Asn Asp Ala Ala Lys Ala Ala Ile Ala			
	295	300	305
gcc gaa gtc gcg ggc gag gtc ggc ctc ggg gtc aac ccg aac ggc tcg			
1075			
Ala Glu Val Ala Gly Glu Val Gly Leu Gly Val Asn Pro Asn Gly Ser			
310	315	320	325
cgc ggg atg ggg gcc gag gat ttc tcg tat ttc ctc gaa aag cgc ccg			
1123			
Arg Gly Met Gly Ala Glu Asp Phe Ser Tyr Phe Leu Glu Lys Arg Pro			
	330	335	340
ggt gcc tac ctg ttc gtc ggt aat ggc gac agc gcg ggc ctt cac aac			
1171			
Gly Ala Tyr Leu Phe Val Gly Asn Gly Asp Ser Ala Gly Leu His Asn			
	345	350	355
ccc gcc tat aat ttc aac gac gag gcc gcg ccc tac ggc gca tcg ttc			
1219			
Pro Ala Tyr Asn Phe Asn Asp Glu Ala Ala Pro Tyr Gly Ala Ser Phe			
	360	365	370
ttg gcc cgc atg gca gaa cgc ccc ttg ccg tta aag ggc tgatccatgg			
1268			
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cgctcgaaga tgc			
1281			

<210> 364

<211> 386

<212> PRT

<213> Corynebacterium glutamicum

<400> 364

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 Trp Arg Arg His Leu His Gln Asn Pro Glu Ile Ser Phe Asp Cys Val
 20 25 30
 Glu Thr Ala Ala Phe Val Ala Glu Gln Leu Arg Ser Phe Gly Val Asp
 35 40 45
 Glu Ile His Thr Gly Ile Ala Lys Thr Gly Ile Ile Ala Leu Ile His
 50 55 60
 Gly Arg Glu Ala Gly Pro Val Val Gly Leu Arg Ala Asp Met Asp Ala
 65 70 75 80
 Leu Pro Leu Thr Glu Ile Thr Gly Val Asp Tyr Ala Ser Thr Thr Pro
 85 90 95
 Gly Lys Met His Ala Cys Gly His Asp Gly His Thr Thr Met Leu Leu
 100 105 110
 Gly Ala Ala Lys Tyr Leu Ala Glu Thr Arg Asn Phe Ala Gly Thr Val
 115 120 125
 Ala Leu Ile Phe Gln Pro Ala Glu Glu Asn Gly Gly Gly Ala Gly Val
 130 135 140
 Met Val Asp Glu Gly Val Leu Asp Arg Phe Ala Ile Ala Glu Val Tyr
 145 150 155 160
 Ala Leu His Asn Gln Pro Gly Leu Pro Leu Gly His Phe Met Thr Thr
 165 170 175
 Ala Gly Pro Ile Met Ala Ala Val Asp Thr Phe Asp Ile Asn Ile Thr
 180 185 190
 Gly Arg Gly Gly His Gly Ala Lys Pro His Gln Thr Arg Asp Pro Ile
 195 200 205
 Val Ala Ala Val Gly Ile Val Gln Ala Phe Gln Thr Ile Val Ser Arg
 210 215 220
 Asn His Asn Pro Val Glu Asp Leu Val Val Ser Val Thr Gln Ile His
 225 230 235 240
 Thr Gly Ser Ala Asp Asn Ile Ile Pro Glu Thr Ala Tyr Ile Asn Gly
 245 250 255
 Thr Val Arg Thr Phe Asn Lys Asp Val Gln Ala Met Val Ile Thr Arg
 260 265 270
 Met Glu Glu Ile Val Ala Gly Gln Ala Ala Ala Tyr Gly Val Glu Ala
 275 280 285
 Thr Leu Thr Tyr Asn Arg Asn Tyr Pro Ala Thr Ile Asn Asp Ala Ala
 290 295 300
 Lys Ala Ala Ile Ala Ala Glu Val Ala Gly Glu Val Gly Leu Gly Val
 305 310 315 320

Lys Gly
385

atg cgt ccg cat gat ggg gca aat gtc cat gtc atg cac gca tgc ggc 451
Met Arg Pro His Asp Gly Ala Asn Val His Val Met His Ala Cys Gly
105 110 115

cac gat gtc cac gtc acc gcg ctg ctt ggt gcg tgt gcc att tta gat	499
His Asp Val His Val Thr Ala Leu Leu Gly Ala Cys Ala Ile Leu Asp	
120 125 130	
gag cgt cgc gat gca tgg gaa ggc acg ttc atc gcg ttg ttc cag cca	547
Glu Arg Arg Asp Ala Trp Glu Gly Thr Phe Ile Ala Leu Phe Gln Pro	
135 140 145	
tcg gag gaa aac tcc caa ggc gct aac aag atg gtc gcc ggc ggt tta	595
Ser Glu Glu Asn Ser Gln Gly Ala Asn Lys Met Val Ala Gly Gly Leu	
150 155 160 165	
gtt gat ctg atc cca cgc cct gat gtg tgc ttt ggc cag cat gta gtc	643
Val Asp Leu Ile Pro Arg Pro Asp Val Cys Phe Gly Gln His Val Val	
170 175 180	
ccc ggt gct gca gga acc gtg atg agc atg cct ggc ggt gct ctc gct	691
Pro Gly Ala Ala Gly Thr Val Met Ser Met Pro Gly Gly Ala Leu Ala	
185 190 195	
gcc tgc gat tcc att gaa atc cgc att cag ggt cgc agc gcc cat ggt	739
Ala Cys Asp Ser Ile Glu Ile Arg Ile Gln Gly Arg Ser Ala His Gly	
200 205 210	
tcc atg cct cat aat tcc atc gat ccc act tat gtt gca gcg atg att	787
Ser Met Pro His Asn Ser Ile Asp Pro Thr Tyr Val Ala Ala Met Ile	
215 220 225	
gtc gtg cga ctc caa gga atc gtg ggc cgc gag gtt tct cca gag gat	835
Val Val Arg Leu Gln Gly Ile Val Gly Arg Glu Val Ser Pro Glu Asp	
230 235 240 245	
ttc gcc gtt att tct gtg ggc acc ctc cag tgc ggc aac acc aac aac	883
Phe Ala Val Ile Ser Val Gly Thr Leu Gln Ser Gly Asn Thr Asn Asn	
250 255 260	
acc att cca gca agt gct cgt ttg gtg ttg aac tgc cgt ttc tac aac	931
Thr Ile Pro Ala Ser Ala Arg Leu Val Leu Asn Cys Arg Phe Tyr Asn	
265 270 275	
gac aaa gtc aag cac aag gtc tac cga gcc atc gaa cgt gtt gtc cgt	979
Asp Lys Val Lys His Lys Val Tyr Arg Ala Ile Glu Arg Val Val Arg	
280 285 290	
ggt gaa tgc ctt gct tcc ggt att gag gaa gaa cct gtc att gag tac	
1027	
Gly Glu Cys Leu Ala Ser Gly Ile Glu Glu Glu Pro Val Ile Glu Tyr	
295 300 305	
ttc gcc cac ggt gat ctc acc aac aac acc cct gtt gtc ttc gat act	
1075	
Phe Ala His Gly Asp Leu Thr Asn Asn Thr Pro Val Val Phe Asp Thr	
310 315 320 325	
gtg cgc cct gtc ttc gac gat gtt ttc ggc gag gat tct att gac gct	
1123	
Val Arg Pro Val Phe Asp Asp Val Phe Gly Glu Asp Ser Ile Asp Ala	
330 335 340	
tac cgg tgg act gcg tcg gag gat ttc ccc tcc att cct aag gca ttc	
1171	

Tyr Arg Trp Thr Ala Ser Glu Asp Phe Pro Ser Ile Pro Lys Ala Phe
 345 350 355
 aac agc cct tac ctg tac tgg acg att ggt gtc acg ccg cgc gat cag
 1219
 Asn Ser Pro Tyr Leu Tyr Trp Thr Ile Gly Val Thr Pro Arg Asp Gln
 360 365 370
 tgg aca gaa gcc gta gaa aga gac cgc gtg gca tcg gat gtg cca gcc
 1267
 Trp Thr Glu Ala Val Glu Arg Asp Arg Val Ala Ser Asp Val Pro Ala
 375 380 385
 aat cac atg gga gat ttc ctc cct gat tat gcg ccg acg atg tcc gct
 1315
 Asn His Met Gly Asp Phe Leu Pro Asp Tyr Ala Pro Thr Met Ser Ala
 390 395 400 405
 gcc acc cgc gca gcc gca gcc gcg ctg ctg acc tac ttg gga act aac
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<210> 366

<211> 421

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<213> Corynebacterium glutamicum

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 Gly Phe Glu Ser Glu Thr Ala Asp Arg Ile Gln Lys Tyr Leu Glu Arg
 35 40 45
 Phe Asp Cys Glu Val Ile Pro Asn Val Gly Gly Tyr Gly Ile Leu Ala
 50 55 60
 Val Phe Arg Asn Gly Ser Thr Asp Pro Gly Ala Pro Val Ala Leu Met
 65 70 75 80
 Arg Ala Asp Phe Asp Gly Leu Pro Val Lys Glu Ile Thr Gly Val Pro
 85 90 95
 Phe Ala Ser Thr Arg Met Arg Pro His Asp Gly Ala Asn Val His Val
 100 105 110
 Met His Ala Cys Gly His Asp Val His Val Thr Ala Leu Leu Gly Ala
 115 120 125
 Cys Ala Ile Leu Asp Glu Arg Arg Asp Ala Trp Glu Gly Thr Phe Ile
 130 135 140
 Ala Leu Phe Gln Pro Ser Glu Glu Asn Ser Gln Gly Ala Asn Lys Met

145		150		155		160									
Val	Ala	Gly	Gly	Leu	Val	Asp	Leu	Ile	Pro	Arg	Pro	Asp	Val	Cys	Phe
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Gly	Gln	His	Val	Val	Pro	Gly	Ala	Ala	Gly	Thr	Val	Met	Ser	Met	Pro
			180					185					190		
Gly	Gly	Ala	Leu	Ala	Ala	Cys	Asp	Ser	Ile	Glu	Ile	Arg	Ile	Gln	Gly
		195					200					205			
Arg	Ser	Ala	His	Gly	Ser	Met	Pro	His	Asn	Ser	Ile	Asp	Pro	Thr	Tyr
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Val	Ala	Ala	Met	Ile	Val	Val	Arg	Leu	Gln	Gly	Ile	Val	Gly	Arg	Glu
225					230					235					240
Val	Ser	Pro	Glu	Asp	Phe	Ala	Val	Ile	Ser	Val	Gly	Thr	Leu	Gln	Ser
				245					250					255	
Gly	Asn	Thr	Asn	Asn	Thr	Ile	Pro	Ala	Ser	Ala	Arg	Leu	Val	Leu	Asn
			260					265					270		
Cys	Arg	Phe	Tyr	Asn	Asp	Lys	Val	Lys	His	Lys	Val	Tyr	Arg	Ala	Ile
		275					280					285			
Glu	Arg	Val	Val	Arg	Gly	Glu	Cys	Leu	Ala	Ser	Gly	Ile	Glu	Glu	Glu
	290					295					300				
Pro	Val	Ile	Glu	Tyr	Phe	Ala	His	Gly	Asp	Leu	Thr	Asn	Asn	Thr	Pro
305					310					315					320
Val	Val	Phe	Asp	Thr	Val	Arg	Pro	Val	Phe	Asp	Asp	Val	Phe	Gly	Glu
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Asp	Ser	Ile	Asp	Ala	Tyr	Arg	Trp	Thr	Ala	Ser	Glu	Asp	Phe	Pro	Ser
			340					345					350		
Ile	Pro	Lys	Ala	Phe	Asn	Ser	Pro	Tyr	Leu	Tyr	Trp	Thr	Ile	Gly	Val
		355					360					365			
Thr	Pro	Arg	Asp	Gln	Trp	Thr	Glu	Ala	Val	Glu	Arg	Asp	Arg	Val	Ala
	370					375					380				
Ser	Asp	Val	Pro	Ala	Asn	His	Met	Gly	Asp	Phe	Leu	Pro	Asp	Tyr	Ala
385					390					395					400
Pro	Thr	Met	Ser	Ala	Ala	Thr	Arg	Ala	Ala	Ala	Ala	Ala	Leu	Leu	Thr
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Tyr	Leu	Gly	Thr	Asn											
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<211> 3462

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(3439)

<223> RXS02234

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Met Pro Lys Arg Ser
1 5

gat att aac cac gtc ctc gtc atc ggt tcc ggc ccc atc gtc att ggc 163
Asp Ile Asn His Val Leu Val Ile Gly Ser Gly Pro Ile Val Ile Gly
10 15 20

cag gca tgt gaa ttc gac tac tcc ggc acc cag gct tgc cgc gtg ctg 211
Gln Ala Cys Glu Phe Asp Tyr Ser Gly Thr Gln Ala Cys Arg Val Leu
25 30 35

aag gaa gag gga ctg cgc gtc acc ctc atc aac tcc aac cca gca acg 259
Lys Glu Glu Gly Leu Arg Val Thr Leu Ile Asn Ser Asn Pro Ala Thr
40 45 50

atc atg acc gac cca gaa atg gct gac cac acc tac gtg gag cca atc 307
Ile Met Thr Asp Pro Glu Met Ala Asp His Thr Tyr Val Glu Pro Ile
55 60 65

gag ccg gaa tac atc gac aag att ttc gct aag gaa atc gag cag ggc 355
Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala Lys Glu Ile Glu Gln Gly
70 75 80 85

cac cca atc gac gcc gtc ctg gca acc ctt ggt ggc cag act gca ctt 403
His Pro Ile Asp Ala Val Leu Ala Thr Leu Gly Gly Gln Thr Ala Leu
90 95 100

aac gca gct atc cag ctg gat cgc ctc ggc atc ctg gaa aag tac ggc 451
Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly Ile Leu Glu Lys Tyr Gly
105 110 115

gtt gaa ctc atc ggt gca gac atc gat gcc att gag cgc ggc gaa gat 499
Val Glu Leu Ile Gly Ala Asp Ile Asp Ala Ile Glu Arg Gly Glu Asp
120 125 130

cgc cag aag ttc aag gat att gtc acc acc atc ggt ggc gaa tcc gcg 547
Arg Gln Lys Phe Lys Asp Ile Val Thr Thr Ile Gly Gly Glu Ser Ala
135 140 145

cgt tcc cgc gtc tgc cac aac atg gaa gaa gtc cac gag act gtc gca 595
Arg Ser Arg Val Cys His Asn Met Glu Glu Val His Glu Thr Val Ala
150 155 160 165

gaa ctc ggc ctt cca gta gtc gtg cgt cca tcc ttc act atg ggt ggc 643
Glu Leu Gly Leu Pro Val Val Val Arg Pro Ser Phe Thr Met Gly Gly
170 175 180

ctg ggc tcc ggt ctt gca tac aac acc gaa gac ctt gag cgc atc gct 691
Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu Asp Leu Glu Arg Ile Ala
185 190 195

ggt ggc gga ctt gct gca tct cct gaa gca aac gtc ttg atc gaa gaa 739
Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala Asn Val Leu Ile Glu Glu
200 205 210

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tcc atc ctt ggt tgg aag gaa ttc gag ctc gag ctc atg cgc gat acc	787
Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu Glu Leu Met Arg Asp Thr	
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Ala Asp Asn Val Val Val Ile Cys Ser Ile Glu Asn Val Asp Ala Leu	
230 235 240 245	
ggc gtg cac acc ggc gac tct gtc acc gtg gca cct gcc ctg acc ctg	883
Gly Val His Thr Gly Asp Ser Val Thr Val Ala Pro Ala Leu Thr Leu	
250 255 260	
act gac cgt gaa ttc cag aag atg cgc gat cag ggt atc gcc atc atc	931
Thr Asp Arg Glu Phe Gln Lys Met Arg Asp Gln Gly Ile Ala Ile Ile	
265 270 275	
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Asn Pro Val Asp Gly Arg Ile Ile Thr Ile Glu Met Asn Pro Arg Val	
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tct cgt tcc tcc gct ctg gca tcc aag gca acg ggc ttc cca att gcc	
1075	
Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala Thr Gly Phe Pro Ile Ala	
310 315 320 325	
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1123	
Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr Thr Leu Asp Glu Ile Thr	
330 335 340	
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1171	
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345 350 355	
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1267	
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1315	
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1363	
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 425 430 435

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 1459
 Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val Glu Leu Ala Met Arg Leu
 440 445 450

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 455 460 465

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 1555
 Phe Leu Ala Glu Leu Glu Ala Leu Val Gln Phe Arg Gln Lys Leu Val
 470 475 480 485

gac gca cca ttc cta aac gaa gat ctc ctg cgc gaa gca aag ttc atg
 1603
 Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu Arg Glu Ala Lys Phe Met
 490 495 500

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 Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu Arg Pro Glu Phe Ala Gly
 505 510 515

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 1699
 Glu Asp Gly Val Arg Thr Leu Arg Leu Ser Leu Gly Ile Arg Pro Val
 520 525 530

ttc aag act gtg gat acc tgt gca gca gag ttt gaa gct aag act ccg
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 Phe Lys Thr Val Asp Thr Cys Ala Ala Glu Phe Glu Ala Lys Thr Pro
 535 540 545

tac cac tac tcc gca tac gag ctg gat cca gca gct gag tct gag gtc
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 Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro Ala Ala Glu Ser Glu Val
 550 555 560 565

gca cca cag act gag cgt gaa aag gtc ctg atc ttg ggc tcc ggt cca
 1843
 Ala Pro Gln Thr Glu Arg Glu Lys Val Leu Ile Leu Gly Ser Gly Pro
 570 575 580

aac cgc atc ggc cag ggc atc gag ttc gac tac tcc tgt gtt cac gca
 1891
 Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp Tyr Ser Cys Val His Ala
 585 590 595

gct ctt gag ctc tcc cgc gtc ggc tac gaa act gtc atg gtc aac tgc
 1939
 Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu Thr Val Met Val Asn Cys
 600 605 610

aac cca gag acc gtg tcc acc gac tac gac acc gct gac cgc ctg tac
 1987
 Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp Thr Ala Asp Arg Leu Tyr
 615 620 625

ttc gag cca ctg acc ttc gaa gac gtc atg gag gtc tac cac gct gag
 2035
 Phe Glu Pro Leu Thr Phe Glu Asp Val Met Glu Val Tyr His Ala Glu
 630 635 640 645

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 Ala Gln Ser Gly Thr Val Ala Gly Val Ile Val Gln Leu Gly Gly Gln
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 2131
 Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys Lys Ala Gly Val Pro Val
 665 670 675

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 2179
 Ile Gly Thr Ser Pro Glu Ala Ile Asp Met Ala Glu Asp Arg Gly Glu
 680 685 690

ttc ggt gca ctg ctg aac cgc gag cag ctt cct gct cca gca ttc ggc
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 Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu Pro Ala Pro Ala Phe Gly
 695 700 705

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 Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr Val Ala Asp Glu Ile Ser
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tac cca gtg ctg gtt cgc cct tcc tac gtc ttg ggt ggc cgt ggc atg
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 Tyr Pro Val Leu Val Arg Pro Ser Tyr Val Leu Gly Gly Arg Gly Met
 730 735 740

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 Glu Ile Val Tyr Asp Glu Ala Ser Leu Glu Asp Tyr Ile Asn Arg Ala
 745 750 755

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 Thr Glu Leu Ser Ser Asp His Pro Val Leu Val Asp Arg Phe Leu Asp
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 2467
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 775 780 785

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 2515
 Tyr Leu Ala Gly Val Met Glu His Ile Glu Glu Ala Gly Ile His Ser
 790 795 800 805

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 2563
 Gly Asp Ser Ala Cys Ala Leu Pro Pro Met Thr Leu Gly Ala Gln Asp
 810 815 820

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 2611
 Ile Glu Lys Val Arg Glu Ala Thr Lys Lys Leu Ala Leu Gly Ile Gly
 825 830 835

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 2659
 Val Gln Gly Leu Met Asn Val Gln Tyr Ala Leu Lys Asp Asp Ile Leu
 840 845 850

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 870 875 880 885

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 Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp Ala Pro Ile Ala Val Lys
 905 910 915

gaa gca gtg ttg ccg ttc aac cgc ttc cgt cgc cca gat gga aag acc
 2899
 Glu Ala Val Leu Pro Phe Asn Arg Phe Arg Arg Pro Asp Gly Lys Thr
 920 925 930

ctg gac acc ctg ctt tcc cca gag atg aag tcc act ggc gag gtc atg
 2947
 Leu Asp Thr Leu Leu Ser Pro Glu Met Lys Ser Thr Gly Glu Val Met
 935 940 945

ggc ttg gcc aac aac ttc ggc gct gca tat gca aag gct gaa gct ggc
 2995
 Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr Ala Lys Ala Glu Ala Gly
 950 955 960 965

gcg ttt ggt gca ttg cca acc gaa ggc acc gtc ttc gtg acc gtg gct
 3043
 Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr Val Phe Val Thr Val Ala
 970 975 980

aac cgc gac aag cgc acc ctg atc ctg cca atc cag cgc ctg gcg ttg
 3091
 Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro Ile Gln Arg Leu Ala Leu
 985 990 995

atg ggc tac aag atc ctc gcc acc gaa ggc acc gca ggc atg ctg cgc
 3139
 Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly Thr Ala Gly Met Leu Arg
 1000 1005 1010

 cgc aac ggc att gag tgt gaa gtt gtg ctc aag gct tcc gac atc cgc
 3187
 Arg Asn Gly Ile Glu Cys Glu Val Val Leu Lys Ala Ser Asp Ile Arg
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 gaa ggt gta gag ggc aag tcc atc gtg gat cgt atc cgc gaa ggc gaa
 3235
 Glu Gly Val Glu Gly Lys Ser Ile Val Asp Arg Ile Arg Glu Gly Glu
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 gtt gac ctc atc ctc aac acc cca gct ggt tct gct ggc gct cgc cac
 3283
 Val Asp Leu Ile Leu Asn Thr Pro Ala Gly Ser Ala Gly Ala Arg His
 1050 1055 1060

 gat ggc tac gat atc cgc gca gca gca gtg acc gtg ggt gtt ccg ctg
 3331
 Asp Gly Tyr Asp Ile Arg Ala Ala Ala Val Thr Val Gly Val Pro Leu
 1065 1070 1075

 atc acc act gtt cag ggt gtc acc gca gct gtc cag ggc ata gag gcc
 3379
 Ile Thr Thr Val Gln Gly Val Thr Ala Ala Val Gln Gly Ile Glu Ala
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 3427
 Leu Arg Glu Gly Val Val Ser Val Arg Ala Leu Gln Glu Leu Asp His
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 Ala Val Lys Ala
 1110

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<400> 368
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 35 40 45

 Ser Asn Pro Ala Thr Ile Met Thr Asp Pro Glu Met Ala Asp His Thr
 50 55 60

 Tyr Val Glu Pro Ile Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala Lys
 65 70 75 80

Glu	Ile	Glu	Gln	Gly	His	Pro	Ile	Asp	Ala	Val	Leu	Ala	Thr	Leu	Gly	
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Gly	Gln	Thr	Ala	Leu	Asn	Ala	Ala	Ile	Gln	Leu	Asp	Arg	Leu	Gly	Ile	
				100					105					110		
Leu	Glu	Lys	Tyr	Gly	Val	Glu	Leu	Ile	Gly	Ala	Asp	Ile	Asp	Ala	Ile	
				115					120					125		
Glu	Arg	Gly	Glu	Asp	Arg	Gln	Lys	Phe	Lys	Asp	Ile	Val	Thr	Thr	Ile	
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Gly	Gly	Glu	Ser	Ala	Arg	Ser	Arg	Val	Cys	His	Asn	Met	Glu	Glu	Val	
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His	Glu	Thr	Val	Ala	Glu	Leu	Gly	Leu	Pro	Val	Val	Val	Arg	Pro	Ser	
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Phe	Thr	Met	Gly	Gly	Leu	Gly	Ser	Gly	Leu	Ala	Tyr	Asn	Thr	Glu	Asp	
				180					185					190		
Leu	Glu	Arg	Ile	Ala	Gly	Gly	Gly	Leu	Ala	Ala	Ser	Pro	Glu	Ala	Asn	
				195					200					205		
Val	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Gly	Trp	Lys	Glu	Phe	Glu	Leu	Glu	
				210					215					220		
Leu	Met	Arg	Asp	Thr	Ala	Asp	Asn	Val	Val	Val	Ile	Cys	Ser	Ile	Glu	
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Asn	Val	Asp	Ala	Leu	Gly	Val	His	Thr	Gly	Asp	Ser	Val	Thr	Val	Ala	
				245					250					255		
Pro	Ala	Leu	Thr	Leu	Thr	Asp	Arg	Glu	Phe	Gln	Lys	Met	Arg	Asp	Gln	
				260					265					270		
Gly	Ile	Ala	Ile	Ile	Arg	Glu	Val	Gly	Val	Asp	Thr	Gly	Gly	Cys	Asn	
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Met	Asn	Pro	Arg	Val	Ser	Arg	Ser	Ser	Ala	Leu	Ala	Ser	Lys	Ala	Thr	
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Gly	Phe	Pro	Ile	Ala	Lys	Met	Ala	Ala	Lys	Leu	Ala	Ile	Gly	Tyr	Thr	
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Leu	Asp	Glu	Ile	Thr	Asn	Asp	Ile	Thr	Gly	Glu	Thr	Pro	Ala	Ala	Phe	
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Glu	Pro	Thr	Ile	Asp	Tyr	Val	Val	Val	Lys	Ala	Pro	Arg	Phe	Ala	Phe	
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Glu	Lys	Phe	Val	Gly	Ala	Asp	Asp	Thr	Leu	Thr	Thr	Thr	Met	Lys	Ser	
				370					375					380		
Val	Gly	Glu	Val	Met	Ser	Leu	Gly	Arg	Asn	Tyr	Ile	Ala	Ala	Leu	Asn	
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Lys Ala Leu Arg Ser Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr Lys
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 Pro Asp Glu Phe Phe Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala Val
 420 425 430
 Leu Glu Asp Leu Lys Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val Glu
 435 440 445
 Leu Ala Met Arg Leu Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala Ser
 450 455 460
 Ser Ile Asp Pro Trp Phe Leu Ala Glu Leu Glu Ala Leu Val Gln Phe
 465 470 475 480
 Arg Gln Lys Leu Val Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu Arg
 485 490 495
 Glu Ala Lys Phe Met Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu Arg
 500 505 510
 Pro Glu Phe Ala Gly Glu Asp Gly Val Arg Thr Leu Arg Leu Ser Leu
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 Gly Ile Arg Pro Val Phe Lys Thr Val Asp Thr Cys Ala Ala Glu Phe
 530 535 540
 Glu Ala Lys Thr Pro Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro Ala
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 Ala Glu Ser Glu Val Ala Pro Gln Thr Glu Arg Glu Lys Val Leu Ile
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 Leu Gly Ser Gly Pro Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp Tyr
 580 585 590
 Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu Thr
 595 600 605
 Val Met Val Asn Cys Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp Thr
 610 615 620
 Ala Asp Arg Leu Tyr Phe Glu Pro Leu Thr Phe Glu Asp Val Met Glu
 625 630 635 640
 Val Tyr His Ala Glu Ala Gln Ser Gly Thr Val Ala Gly Val Ile Val
 645 650 655
 Gln Leu Gly Gly Gln Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys Lys
 660 665 670
 Ala Gly Val Pro Val Ile Gly Thr Ser Pro Glu Ala Ile Asp Met Ala
 675 680 685
 Glu Asp Arg Gly Glu Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu Pro
 690 695 700
 Ala Pro Ala Phe Gly Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr Val
 705 710 715 720
 Ala Asp Glu Ile Ser Tyr Pro Val Leu Val Arg Pro Ser Tyr Val Leu

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Tyr	Ile	Asn	Arg	Ala	Thr	Glu	Leu	Ser	Ser	Asp	His	Pro	Val	Leu	Val				
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Asp	Gly	Asp	Glu	Val	Tyr	Leu	Ala	Gly	Val	Met	Glu	His	Ile	Glu	Glu				
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Ala	Gly	Ile	His	Ser	Gly	Asp	Ser	Ala	Cys	Ala	Leu	Pro	Pro	Met	Thr				
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Ala	Leu	Gly	Ile	Gly	Val	Gln	Gly	Leu	Met	Asn	Val	Gln	Tyr	Ala	Leu				
		835					840					845							
Lys	Asp	Asp	Ile	Leu	Tyr	Val	Ile	Glu	Ala	Asn	Pro	Arg	Ala	Ser	Arg				
	850					855					860								
Thr	Val	Pro	Phe	Val	Ser	Lys	Ala	Thr	Gly	Val	Asn	Leu	Ala	Lys	Ala				
865					870					875				880					
Ala	Ser	Arg	Ile	Ala	Val	Gly	Ala	Thr	Ile	Lys	Asp	Leu	Gln	Asp	Glu				
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Gly	Met	Ile	Pro	Thr	Glu	Tyr	Asp	Gly	Gly	Ser	Leu	Pro	Leu	Asp	Ala				
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Pro	Ile	Ala	Val	Lys	Glu	Ala	Val	Leu	Pro	Phe	Asn	Arg	Phe	Arg	Arg				
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Pro	Asp	Gly	Lys	Thr	Leu	Asp	Thr	Leu	Leu	Ser	Pro	Glu	Met	Lys	Ser				
	930					935					940								
Thr	Gly	Glu	Val	Met	Gly	Leu	Ala	Asn	Asn	Phe	Gly	Ala	Ala	Tyr	Ala				
945					950					955				960					
Lys	Ala	Glu	Ala	Gly	Ala	Phe	Gly	Ala	Leu	Pro	Thr	Glu	Gly	Thr	Val				
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Phe	Val	Thr	Val	Ala	Asn	Arg	Asp	Lys	Arg	Thr	Leu	Ile	Leu	Pro	Ile				
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Gln	Arg	Leu	Ala	Leu	Met	Gly	Tyr	Lys	Ile	Leu	Ala	Thr	Glu	Gly	Thr				
		995					1000						1005						
Ala	Gly	Met	Leu	Arg	Arg	Asn	Gly	Ile	Glu	Cys	Glu	Val	Val	Leu	Lys				
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Ile	Arg	Glu	Gly	Glu	Val	Asp	Leu	Ile	Leu	Asn	Thr	Pro	Ala	Gly	Ser				
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Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Ala Val Thr
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Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala Val
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Gln Glu Leu Asp His Ala Val Lys Ala
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<223> FRXA02234

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acc tac gtg gag cca atc gag ccg gaa tac atc gac aag att ttc gct 96
 Thr Tyr Val Glu Pro Ile Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala
 20 25 30

aag gaa atc gag cag ggc cac cca atc gac gcc gtc ctg gca acc ctt 144
 Lys Glu Ile Glu Gln Gly His Pro Ile Asp Ala Val Leu Ala Thr Leu
 35 40 45

ggc ggc cag act gca ctt aac gca gct atc cag ctg gat cgc ctc ggc 192
 Gly Gly Gln Thr Ala Leu Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly
 50 55 60

atc ctg gaa aag tac ggc gtt gaa ctc atc ggt gca gac atc gat gcc 240
 Ile Leu Glu Lys Tyr Gly Val Glu Leu Ile Gly Ala Asp Ile Asp Ala
 65 70 75 80

att gag cgc ggc gaa gat cgc cag aag ttc aag gat att gtc acc acc 288
 Ile Glu Arg Gly Glu Asp Arg Gln Lys Phe Lys Asp Ile Val Thr Thr
 85 90 95

atc ggt ggc gaa tcc gcg cgt tcc cgc gtc tgc cac aac atg gaa gaa 336
 Ile Gly Gly Glu Ser Ala Arg Ser Arg Val Cys His Asn Met Glu Glu
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 Val His Glu Thr Val Ala Glu Leu Gly Leu Pro Val Val Val Arg Pro
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 Ser Phe Thr Met Gly Gly Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu
 130 135 140

gac ctt gag cgc atc gct ggt ggc gga ctt gct gca tct cct gaa gca	480
Asp Leu Glu Arg Ile Ala Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala	
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Asn Val Leu Ile Glu Glu Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu	
165 170 175	
gag ctc atg cgc gat acc gca gac aac gtt gtg gtt atc tgc tcc att	576
Glu Leu Met Arg Asp Thr Ala Asp Asn Val Val Val Ile Cys Ser Ile	
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Glu Asn Val Asp Ala Leu Gly Val His Thr Gly Asp Ser Val Thr Val	
195 200 205	
gca cct gcc ctg acc ctg act gac cgt gaa ttc cag aag atg cgc gat	672
Ala Pro Ala Leu Thr Leu Thr Asp Arg Glu Phe Gln Lys Met Arg Asp	
210 215 220	
cag ggt atc gcc atc atc cgc gag gtc ggc gtg gac acc ggt gga tgt	720
Gln Gly Ile Ala Ile Ile Arg Glu Val Gly Val Asp Thr Gly Gly Cys	
225 230 235 240	
aac atc cag ttc gcc atc aac cca gtt gat ggc cgc atc atc acc att	768
Asn Ile Gln Phe Ala Ile Asn Pro Val Asp Gly Arg Ile Ile Thr Ile	
245 250 255	
gag atg aac cca cgt gtg tct cgt tcc tcc gct ctg gca tcc aag gca	816
Glu Met Asn Pro Arg Val Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala	
260 265 270	
acg ggc ttc cca att gcc aag atg gct gcc aag ctg gct atc gga tac	864
Thr Gly Phe Pro Ile Ala Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr	
275 280 285	
acc ctg gat gag atc acc aac gac atc act ggt gaa acc cca gct gcg	912
Thr Leu Asp Glu Ile Thr Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala	
290 295 300	
ttt gag ccc acc atc gac tac gtc gtg gtc aag gcc cca cgc ttt gct	960
Phe Glu Pro Thr Ile Asp Tyr Val Val Val Lys Ala Pro Arg Phe Ala	
305 310 315 320	
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1008	
Phe Glu Lys Phe Val Gly Ala Asp Asp Thr Leu Thr Thr Thr Met Lys	
325 330 335	
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1056	
Ser Val Gly Glu Val Met Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu	
340 345 350	
aac aag gca ctg cgt tcc ctg gaa acc aag cag cag ggt ttc tgg acc	
1104	
Asn Lys Ala Leu Arg Ser Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr	
355 360 365	
aag cct gat gag ttc ttc gca ggg gag cgc gct acc gat aag gca gct	
1152	

Lys Pro Asp Glu Phe Phe Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala
 370 375 380
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 1200
 Val Leu Glu Asp Leu Lys Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val
 385 390 395 400
 gag ctg gca atg cgc ctt ggc gca agc gtg gaa gaa ctc tac gaa gca
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 Glu Leu Ala Met Arg Leu Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala
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 1296
 Ser Ser Ile Asp Pro Trp Phe Leu Ala Glu Leu Glu Ala Leu Val Gln
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 1344
 Phe Arg Gln Lys Leu Val Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu
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 1392
 Arg Glu Ala Lys Phe Met Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu
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 465 470 475 480
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 1488
 Leu Gly Ile Arg Pro Val Phe Lys Thr Val Asp Thr Cys Ala Ala Glu
 485 490 495
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 1536
 Phe Glu Ala Lys Thr Pro Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro
 500 505 510
 gca gct gag tct gag gtc gca cca cag act gag cgt gaa aag gtc ctg
 1584
 Ala Ala Glu Ser Glu Val Ala Pro Gln Thr Glu Arg Glu Lys Val Leu
 515 520 525
 atc ttg ggc tcc ggt cca aac cgc atc ggc cag ggc atc gag ttc gac
 1632
 Ile Leu Gly Ser Gly Pro Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp
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 1680
 Tyr Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu
 545 550 555 560
 act gtc atg gtc aac tgc aac cca gag acc gtg tcc acc gac tac gac
 1728
 Thr Val Met Val Asn Cys Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp

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1776																			
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gtc cag ctt ggt ggc cag act cct ctg ggc ttg gca gat cgt ttg aag																			
1872																			
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	610					615					620								
aag gct ggc gtc cct gtc att ggt acc tcc cca gag gca atc gac atg																			
1920																			
Lys	Ala	Gly	Val	Pro	Val	Ile	Gly	Thr	Ser	Pro	Glu	Ala	Ile	Asp	Met				
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Ala	Glu	Asp	Arg	Gly	Glu	Phe	Gly	Ala	Leu	Leu	Asn	Arg	Glu	Gln	Leu				
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2016																			
Pro	Ala	Pro	Ala	Phe	Gly	Thr	Ala	Thr	Ser	Phe	Glu	Glu	Ala	Arg	Thr				
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gta gcc gat gag atc agc tac cca gtg ctg gtt cgc cct tcc tac gtc																			
2064																			
Val	Ala	Asp	Glu	Ile	Ser	Tyr	Pro	Val	Leu	Val	Arg	Pro	Ser	Tyr	Val				
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2112																			
Leu	Gly	Gly	Arg	Gly	Met	Glu	Ile	Val	Tyr	Asp	Glu	Ala	Ser	Leu	Glu				
	690					695					700								
gat tac atc aac cgc gca act gag ttg tct tct gac cac cca gtg ctg																			
2160																			
Asp	Tyr	Ile	Asn	Arg	Ala	Thr	Glu	Leu	Ser	Ser	Asp	His	Pro	Val	Leu				
	705				710					715				720					
gtt gac cgc ttc cta gac aac gct att gag atc gac gtc gac gca ctg																			
2208																			
Val	Asp	Arg	Phe	Leu	Asp	Asn	Ala	Ile	Glu	Ile	Asp	Val	Asp	Ala	Leu				
				725					730					735					
tgc gac ggc gac gag gtc tac ctg gca ggc gtc atg gag cac atc gag																			
2256																			
Cys	Asp	Gly	Asp	Glu	Val	Tyr	Leu	Ala	Gly	Val	Met	Glu	His	Ile	Glu				
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gaa gcc ggc att cac tcc ggt gac tcc gca tgt gca ctt cct cca atg																			
2304																			
Glu	Ala	Gly	Ile	His	Ser	Gly	Asp	Ser	Ala	Cys	Ala	Leu	Pro	Pro	Met				
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 Thr Leu Gly Ala Gln Asp Ile Glu Lys Val Arg Glu Ala Thr Lys Lys
 770 775 780

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 2400
 Leu Ala Leu Gly Ile Gly Val Gln Gly Leu Met Asn Val Gln Tyr Ala
 785 790 795 800

ctc aag gac gac atc ctc tac gtc atc gag gca aac cca cgt gca tcc
 2448
 Leu Lys Asp Asp Ile Leu Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser
 805 810 815

cgc acc gtg ccg ttc gtc tcc aag gca acg ggc gtc aac ctg gcc aag
 2496
 Arg Thr Val Pro Phe Val Ser Lys Ala Thr Gly Val Asn Leu Ala Lys
 820 825 830

gca gca tcc cgt atc gca gtg ggc gcc acc atc aag gat ctc caa gat
 2544
 Ala Ala Ser Arg Ile Ala Val Gly Ala Thr Ile Lys Asp Leu Gln Asp
 835 840 845

gag ggc atg att cct acc gag tac gac ggc ggc tcc ttg cca ctg gac
 2592
 Glu Gly Met Ile Pro Thr Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp
 850 855 860

gct cca atc gct gtg aag gaa gca gtg ttg ccg ttc aac cgc ttc cgt
 2640
 Ala Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Asn Arg Phe Arg
 865 870 875 880

cgc cca gat gga aag acc ctg gac acc ctg ctt tcc cca gag atg aag
 2688
 Arg Pro Asp Gly Lys Thr Leu Asp Thr Leu Leu Ser Pro Glu Met Lys
 885 890 895

tcc act ggc gag gtc atg ggc ttg gcc aac aac ttc ggc gct gca tat
 2736
 Ser Thr Gly Glu Val Met Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr
 900 905 910

gca aag gct gaa gct ggc gcg ttt ggt gca ttg cca acc gaa ggc acc
 2784
 Ala Lys Ala Glu Ala Gly Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr
 915 920 925

gtc ttc gtg acc gtg gct aac cgc gac aag cgc acc ctg atc ctg cca
 2832
 Val Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro
 930 935 940

atc cag cgc ctg gcg ttg atg ggc tac aag atc ctc gcc acc gaa ggc
 2880
 Ile Gln Arg Leu Ala Leu Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly
 945 950 955 960

acc gca ggc atg ctg cgc cgc aac ggc att gag tgt gaa gtt gtg ctc
2928

Thr Ala Gly Met Leu Arg Arg Asn Gly Ile Glu Cys Glu Val Val Leu
965 970 975

aag gct tcc gac atc cgc gaa ggt gta gag ggc aag tcc atc gtg gat
2976

Lys Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp
980 985 990

cgt atc cgc gaa ggc gaa gtt gac ctc atc ctc aac acc cca gct ggt
3024

Arg Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly
995 1000 1005

tct gct ggc gct cgc cac gat ggc tac gat atc cgc gca gca gca gtg
3072

Ser Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Ala Val
1010 1015 1020

acc gtg ggt gtt ccg ctg atc acc act gtt cag ggt gtc acc gca gct
3120

Thr Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala
1025 1030 1035 1040

gtc cag ggc ata gag gcc ctg cgt gag ggc gtt gtc agc gtc cgc gcg
3168

Val Gln Gly Ile Glu Ala Leu Arg Glu Gly Val Val Ser Val Arg Ala
1045 1050 1055

ctg cag gaa ctc gac cac gca gtc aag gct taagccctat gacattcggc
3218

Leu Gln Glu Leu Asp His Ala Val Lys Ala
1060 1065

gag
3221

<210> 370

<211> 1066

<212> PRT

<213> Corynebacterium glutamicum

<400> 370

Gly Ser Asn Pro Ala Thr Ile Met Thr Asp Pro Glu Met Ala Asp His
1 5 10 15

Thr Tyr Val Glu Pro Ile Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala
20 25 30

Lys Glu Ile Glu Gln Gly His Pro Ile Asp Ala Val Leu Ala Thr Leu
35 40 45

Gly Gly Gln Thr Ala Leu Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly
50 55 60

Ile Leu Glu Lys Tyr Gly Val Glu Leu Ile Gly Ala Asp Ile Asp Ala
65 70 75 80

Ile Glu Arg Gly Glu Asp Arg Gln Lys Phe Lys Asp Ile Val Thr Thr

85					90					95					
Ile	Gly	Gly	Glu	Ser	Ala	Arg	Ser	Arg	Val	Cys	His	Asn	Met	Glu	Glu
			100					105					110		
Val	His	Glu	Thr	Val	Ala	Glu	Leu	Gly	Leu	Pro	Val	Val	Val	Arg	Pro
		115					120					125			
Ser	Phe	Thr	Met	Gly	Gly	Leu	Gly	Ser	Gly	Leu	Ala	Tyr	Asn	Thr	Glu
	130					135					140				
Asp	Leu	Glu	Arg	Ile	Ala	Gly	Gly	Gly	Leu	Ala	Ala	Ser	Pro	Glu	Ala
145					150					155					160
Asn	Val	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Gly	Trp	Lys	Glu	Phe	Glu	Leu
				165					170					175	
Glu	Leu	Met	Arg	Asp	Thr	Ala	Asp	Asn	Val	Val	Val	Ile	Cys	Ser	Ile
			180					185					190		
Glu	Asn	Val	Asp	Ala	Leu	Gly	Val	His	Thr	Gly	Asp	Ser	Val	Thr	Val
		195					200					205			
Ala	Pro	Ala	Leu	Thr	Leu	Thr	Asp	Arg	Glu	Phe	Gln	Lys	Met	Arg	Asp
	210					215					220				
Gln	Gly	Ile	Ala	Ile	Ile	Arg	Glu	Val	Gly	Val	Asp	Thr	Gly	Gly	Cys
225					230					235					240
Asn	Ile	Gln	Phe	Ala	Ile	Asn	Pro	Val	Asp	Gly	Arg	Ile	Ile	Thr	Ile
				245					250					255	
Glu	Met	Asn	Pro	Arg	Val	Ser	Arg	Ser	Ser	Ala	Leu	Ala	Ser	Lys	Ala
			260					265					270		
Thr	Gly	Phe	Pro	Ile	Ala	Lys	Met	Ala	Ala	Lys	Leu	Ala	Ile	Gly	Tyr
		275					280					285			
Thr	Leu	Asp	Glu	Ile	Thr	Asn	Asp	Ile	Thr	Gly	Glu	Thr	Pro	Ala	Ala
	290					295					300				
Phe	Glu	Pro	Thr	Ile	Asp	Tyr	Val	Val	Val	Lys	Ala	Pro	Arg	Phe	Ala
305					310					315					320
Phe	Glu	Lys	Phe	Val	Gly	Ala	Asp	Asp	Thr	Leu	Thr	Thr	Thr	Met	Lys
				325					330					335	
Ser	Val	Gly	Glu	Val	Met	Ser	Leu	Gly	Arg	Asn	Tyr	Ile	Ala	Ala	Leu
			340					345					350		
Asn	Lys	Ala	Leu	Arg	Ser	Leu	Glu	Thr	Lys	Gln	Gln	Gly	Phe	Trp	Thr
		355					360					365			
Lys	Pro	Asp	Glu	Phe	Phe	Ala	Gly	Glu	Arg	Ala	Thr	Asp	Lys	Ala	Ala
	370					375					380				
Val	Leu	Glu	Asp	Leu	Lys	Arg	Pro	Thr	Glu	Gly	Arg	Leu	Tyr	Asp	Val
385					390					395					400
Glu	Leu	Ala	Met	Arg	Leu	Gly	Ala	Ser	Val	Glu	Glu	Leu	Tyr	Glu	Ala
				405					410					415	

Cys Asp Gly Asp Glu Val Tyr Leu Ala Gly Val Met Glu His Ile Glu
 740 745 750
 Glu Ala Gly Ile His Ser Gly Asp Ser Ala Cys Ala Leu Pro Pro Met
 755 760 765
 Thr Leu Gly Ala Gln Asp Ile Glu Lys Val Arg Glu Ala Thr Lys Lys
 770 775 780
 Leu Ala Leu Gly Ile Gly Val Gln Gly Leu Met Asn Val Gln Tyr Ala
 785 790 795 800
 Leu Lys Asp Asp Ile Leu Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser
 805 810 815
 Arg Thr Val Pro Phe Val Ser Lys Ala Thr Gly Val Asn Leu Ala Lys
 820 825 830
 Ala Ala Ser Arg Ile Ala Val Gly Ala Thr Ile Lys Asp Leu Gln Asp
 835 840 845
 Glu Gly Met Ile Pro Thr Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp
 850 855 860
 Ala Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Asn Arg Phe Arg
 865 870 875 880
 Arg Pro Asp Gly Lys Thr Leu Asp Thr Leu Leu Ser Pro Glu Met Lys
 885 890 895
 Ser Thr Gly Glu Val Met Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr
 900 905 910
 Ala Lys Ala Glu Ala Gly Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr
 915 920 925
 Val Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro
 930 935 940
 Ile Gln Arg Leu Ala Leu Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly
 945 950 955 960
 Thr Ala Gly Met Leu Arg Arg Asn Gly Ile Glu Cys Glu Val Val Leu
 965 970 975
 Lys Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp
 980 985 990
 Arg Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly
 995 1000 1005
 Ser Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Val
 1010 1015 1020
 Thr Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala
 1025 1030 1035 1040
 Val Gln Gly Ile Glu Ala Leu Arg Glu Gly Val Val Ser Val Arg Ala
 1045 1050 1055
 Leu Gln Glu Leu Asp His Ala Val Lys Ala

Asp	Ala	Val	Val	Ile	Asn	Val	Gly	Glu	Lys	Gly	Ala	Ala	Gln	Arg	Arg		
				170					175					180			
att	cac	gtc	aat	ggc	gat	gct	ggt	cat	ggg	tcc	att	cct	ttc	gac	cgt	691	
Ile	His	Val	Asn	Gly	Asp	Ala	Gly	His	Gly	Ser	Ile	Pro	Phe	Asp	Arg		
			185					190					195				
gac	agc	gct	att	gtc	aag	atc	ggg	gaa	gtc	gcc	cgc	cga	atc	gct	gcc	739	
Asp	Ser	Ala	Ile	Val	Lys	Ile	Gly	Glu	Val	Ala	Arg	Arg	Ile	Ala	Ala		
		200					205					210					
gcc	gat	ctg	aag	gta	gcc	aag	gac	gat	atc	tgg	caa	ggc	ttc	gtc	caa	787	
Ala	Asp	Leu	Lys	Val	Ala	Lys	Asp	Asp	Ile	Trp	Gln	Gly	Phe	Val	Gln		
	215					220					225						
gcg	cac	cgt	ttc	gac	cca	gaa	acg	gag	cag	gcg	ctt	ctt	agc	ggg	acc	835	
Ala	His	Arg	Phe	Asp	Pro	Glu	Thr	Glu	Gln	Ala	Leu	Leu	Ser	Gly	Thr		
	230				235					240					245		
tcc	cct	gag	gcc	tac	gca	gag	ttc	ggc	gga	ctc	tcc	cgc	ttc	gcc	cac	883	
Ser	Pro	Glu	Ala	Tyr	Ala	Glu	Phe	Gly	Gly	Leu	Ser	Arg	Phe	Ala	His		
			250					255						260			
gcg	gtg	tct	cat	ctc	acg	atc	gcc	caa	act	gtg	gtt	cgt	gca	ggg	caa	931	
Ala	Val	Ser	His	Leu	Thr	Ile	Ala	Gln	Thr	Val	Val	Arg	Ala	Gly	Gln		
			265					270					275				
gcc	atc	aat	gta	ttg	cca	tcg	cat	gcg	tac	ttg	gaa	ctg	gat	atc	cgt	979	
Ala	Ile	Asn	Val	Leu	Pro	Ser	His	Ala	Tyr	Leu	Glu	Leu	Asp	Ile	Arg		
		280					285					290					
acc	ctt	cca	ggc	caa	acc	aat	gac	tat	gtt	gat	gac	acc	ctg	cgt	gct		
	1027																
Thr	Leu	Pro	Gly	Gln	Thr	Asn	Asp	Tyr	Val	Asp	Asp	Thr	Leu	Arg	Ala		
	295					300					305						
gct	ctg	ggc	gat	ctt	gcc	gat	gaa	gta	gaa	atc	gaa	cac	ctc	atc	tct		
	1075																
Ala	Leu	Gly	Asp	Leu	Ala	Asp	Glu	Val	Glu	Ile	Glu	His	Leu	Ile	Ser		
	310				315				320					325			
gaa	gaa	gca	acg	gtg	agc	cca	act	gat	tcc	agg	ttg	tat	aac	acc	ttg		
	1123																
Glu	Glu	Ala	Thr	Val	Ser	Pro	Thr	Asp	Ser	Arg	Leu	Tyr	Asn	Thr	Leu		
			330					335						340			
gaa	aaa	gtt	ctt	ggt	gat	ttc	ttc	ccc	gat	gcg	cct	gtg	gtc	cca	att		
	1171																
Glu	Lys	Val	Leu	Gly	Asp	Phe	Phe	Pro	Asp	Ala	Pro	Val	Val	Pro	Ile		
			345					350					355				
att	tcc	tct	ggt	ggc	tct	gac	ctg	cgc	ttt	ggt	cgt	cga	cta	ggc	ggt		
	1219																
Ile	Ser	Ser	Gly	Gly	Ser	Asp	Leu	Arg	Phe	Gly	Arg	Arg	Leu	Gly	Gly		
		360					365					370					
ggt	ggt	tat	ggt	ttt	gca	gtt	cat	gca	cgt	gaa	cga	act	ttg	gcg	gaa		
	1267																
Val	Gly	Tyr	Gly	Phe	Ala	Val	His	Ala	Arg	Glu	Arg	Thr	Leu	Ala	Glu		
	375					380					385						

gca atg ggg caa ctt cac tcc cat gac gag gcg ctg tac ctg gaa gat
 1315
 Ala Met Gly Gln Leu His Ser His Asp Glu Ala Leu Tyr Leu Glu Asp
 390 395 400 405

ctt gaa ctg act gtt cgg ggt tat gac tcc gtc gtg cgt gaa ttc cta
 1363
 Leu Glu Leu Thr Val Arg Gly Tyr Asp Ser Val Val Arg Glu Phe Leu
 410 415 420

ggc taaaaacatg aagcaggagt ctt
 1389
 Gly

<210> 372
 <211> 422
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 372
 Val Asn Asp Leu Thr Pro Asp Ser Gly Gln Glu Ile Arg Asn Ala Glu
 1 5 10 15
 Ser Leu Glu Arg Phe Phe Glu Gly Thr Pro Asn Val Lys Ile Thr Lys
 20 25 30
 Leu Glu Pro His Pro Gly Arg Thr Ser Ile Ile Val Thr Val Pro Gly
 35 40 45
 Ser Asp Pro Asp Ala Glu Pro Leu Thr Leu Leu Gly His Thr Asp Val
 50 55 60
 Val Pro Val Asp Leu Pro Lys Trp Thr Lys Asp Pro Phe Gly Ala Glu
 65 70 75 80
 Ile Ser Asp Gly Gln Ile Trp Gly Arg Gly Ser Val Asp Met Leu Phe
 85 90 95
 Ile Thr Ala Thr Gln Ala Ala Val Thr Arg Gln Val Ala Arg Glu Gly
 100 105 110
 Gly Leu Arg Gly Thr Leu Thr Phe Val Gly Val Ala Asp Glu Glu Ala
 115 120 125
 Arg Gly Gly Leu Gly Ala Lys Trp Leu Ser Glu Glu His Gln Asn Leu
 130 135 140
 Phe Ser Trp Lys Asn Cys Leu Ser Glu Ser Gly Gly Ser His Leu Pro
 145 150 155 160
 Val His Asp Gly Ser Asp Ala Val Val Ile Asn Val Gly Glu Lys Gly
 165 170 175
 Ala Ala Gln Arg Arg Ile His Val Asn Gly Asp Ala Gly His Gly Ser
 180 185 190
 Ile Pro Phe Asp Arg Asp Ser Ala Ile Val Lys Ile Gly Glu Val Ala
 195 200 205

Arg Arg Ile Ala Ala Ala Asp Leu Lys Val Ala Lys Asp Asp Ile Trp
 210 215 220
 Gln Gly Phe Val Gln Ala His Arg Phe Asp Pro Glu Thr Glu Gln Ala
 225 230 235 240
 Leu Leu Ser Gly Thr Ser Pro Glu Ala Tyr Ala Glu Phe Gly Gly Leu
 245 250 255
 Ser Arg Phe Ala His Ala Val Ser His Leu Thr Ile Ala Gln Thr Val
 260 265 270
 Val Arg Ala Gly Gln Ala Ile Asn Val Leu Pro Ser His Ala Tyr Leu
 275 280 285
 Glu Leu Asp Ile Arg Thr Leu Pro Gly Gln Thr Asn Asp Tyr Val Asp
 290 295 300
 Asp Thr Leu Arg Ala Ala Leu Gly Asp Leu Ala Asp Glu Val Glu Ile
 305 310 315 320
 Glu His Leu Ile Ser Glu Glu Ala Thr Val Ser Pro Thr Asp Ser Arg
 325 330 335
 Leu Tyr Asn Thr Leu Glu Lys Val Leu Gly Asp Phe Phe Pro Asp Ala
 340 345 350
 Pro Val Val Pro Ile Ile Ser Ser Gly Gly Ser Asp Leu Arg Phe Gly
 355 360 365
 Arg Arg Leu Gly Gly Val Gly Tyr Gly Phe Ala Val His Ala Arg Glu
 370 375 380
 Arg Thr Leu Ala Glu Ala Met Gly Gln Leu His Ser His Asp Glu Ala
 385 390 395 400
 Leu Tyr Leu Glu Asp Leu Glu Leu Thr Val Arg Gly Tyr Asp Ser Val
 405 410 415
 Val Arg Glu Phe Leu Gly
 420

<210> 373
 <211> 525
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(502)
 <223> RXS02937

<400> 373
 gctaccgcga agaactgtac tagttcttcc atcagcaccc gcagttgtct ttgcaagagt 60
 tcgaaacatc caacgcattg gtgacaccgg tgttgctcgcg gtg atc agc aat ggg 115
 Val Ile Ser Asn Gly
 1 5
 gaa ggt ccg gtt gtt gcg ctt cgt ggc gac att gat gcg ttg ccc atg 163

100	105	110	
Met Gln Pro Thr Leu Asp Arg Gly Val Glu Ala Leu Val Val Ala Ala			
115	120	125	
Ser Ala Trp Leu Val Lys			
130			
<210> 375			
<211> 966			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(943)			
<223> RXA02194			
<400> 375			
gaaatctccc agctcatttta ttggacccag gtcatcatgg ttgctcgcg cctgaagcca 60			
gaagatatct acaagaacct gtaggagttt taaagcaatc atg ttg aaa atc gct 115			
		Met Leu Lys Ile Ala	
		1 5	
gtc cca aac aaa ggc tcg ctg tcc gag cgc gcc atg gaa atc ctc gcc 163			
Val Pro Asn Lys Gly Ser Leu Ser Glu Arg Ala Met Glu Ile Leu Ala			
10	15	20	
gaa gca ggc tac gca ggc cgt gga gat tcc aaa tcc ctc aac gtt ttt 211			
Glu Ala Gly Tyr Ala Gly Arg Gly Asp Ser Lys Ser Leu Asn Val Phe			
25	30	35	
gat gaa gca aac aac gtt gaa ttc ttc ttc ctt cgc cct aaa gat atc 259			
Asp Glu Ala Asn Asn Val Glu Phe Phe Phe Leu Arg Pro Lys Asp Ile			
40	45	50	
gcc atc tac gtt gct ggt ggc cag ctc gat ttg ggt atc acc ggc cgc 307			
Ala Ile Tyr Val Ala Gly Gly Gln Leu Asp Leu Gly Ile Thr Gly Arg			
55	60	65	
gac ctt gct cgc gat tcc cag gct gat gtc cac gaa gtt ctt tcc ctc 355			
Asp Leu Ala Arg Asp Ser Gln Ala Asp Val His Glu Val Leu Ser Leu			
70	75	80	85
ggc ttc ggt tcc tcc act ttc cgt tac gca gca cca gct gat gaa gag 403			
Gly Phe Gly Ser Ser Thr Phe Arg Tyr Ala Ala Pro Ala Asp Glu Glu			
90	95	100	
tgg agc atc gaa aag ctc gac ggc aag cgc atc gct acc tct tac ccc 451			
Trp Ser Ile Glu Lys Leu Asp Gly Lys Arg Ile Ala Thr Ser Tyr Pro			
105	110	115	
aac ctt gtt cgc gat gac ctc gca gca cgt ggg ctt tcc gct gag gtg 499			
Asn Leu Val Arg Asp Asp Leu Ala Ala Arg Gly Leu Ser Ala Glu Val			
120	125	130	
ctc cgc ctc gac ggt gca gta gag gta tcc atc aag ctt ggt gtc gca 547			
Leu Arg Leu Asp Gly Ala Val Glu Val Ser Ile Lys Leu Gly Val Ala			
135	140	145	

gat gcc atc gcc gat gtt gta tcc acc ggc cgc acg ctg cgt cag caa 595
 Asp Ala Ile Ala Asp Val Val Ser Thr Gly Arg Thr Leu Arg Gln Gln
 150 155 160 165

 ggt ctt gca cct ttc ggc gag gtt ctg tgc acc tct gag gct gtc att 643
 Gly Leu Ala Pro Phe Gly Glu Val Leu Cys Thr Ser Glu Ala Val Ile
 170 175 180

 gtt ggc cgc aag gat gaa aag gtc acc cca gag cag cag atc ctg ctt 691
 Val Gly Arg Lys Asp Glu Lys Val Thr Pro Glu Gln Gln Ile Leu Leu
 185 190 195

 cgc cgc atc cag gga att ttg cac gcg cag aac ttc ctc atg ctg gat 739
 Arg Arg Ile Gln Gly Ile Leu His Ala Gln Asn Phe Leu Met Leu Asp
 200 205 210

 tac aac gtc gac cgc gac aac ctg gac gct gcc act gca gta acc cca 787
 Tyr Asn Val Asp Arg Asp Asn Leu Asp Ala Ala Thr Ala Val Thr Pro
 215 220 225

 ggc tta tcc ggc cca acg gta tcc cca ctg gca cgc gac aac tgg gtt 835
 Gly Leu Ser Gly Pro Thr Val Ser Pro Leu Ala Arg Asp Asn Trp Val
 230 235 240 245

 gct gta cgc gcc atg gtg cca cgc agg tca gct aac gcc atc atg gat 883
 Ala Val Arg Ala Met Val Pro Arg Arg Ser Ala Asn Ala Ile Met Asp
 250 255 260

 aag ctt gct gga ctc ggc gct gaa gcc atc ctg gct tct gaa atc cgc 931
 Lys Leu Ala Gly Leu Gly Ala Glu Ala Ile Leu Ala Ser Glu Ile Arg
 265 270 275

 atc gcc cgc atc tagttttaac taccctcgaa aat 966
 Ile Ala Arg Ile
 280

<210> 376

<211> 281

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 376

Met Leu Lys Ile Ala Val Pro Asn Lys Gly Ser Leu Ser Glu Arg Ala
 1 5 10 15

Met Glu Ile Leu Ala Glu Ala Gly Tyr Ala Gly Arg Gly Asp Ser Lys
 20 25 30

Ser Leu Asn Val Phe Asp Glu Ala Asn Asn Val Glu Phe Phe Phe Leu
 35 40 45

Arg Pro Lys Asp Ile Ala Ile Tyr Val Ala Gly Gly Gln Leu Asp Leu
 50 55 60

Gly Ile Thr Gly Arg Asp Leu Ala Arg Asp Ser Gln Ala Asp Val His
 65 70 75 80

Glu Val Leu Ser Leu Gly Phe Gly Ser Ser Thr Phe Arg Tyr Ala Ala
 85 90 95

Pro Ala Asp Glu Glu Trp Ser Ile Glu Lys Leu Asp Gly Lys Arg Ile
 100 105 110
 Ala Thr Ser Tyr Pro Asn Leu Val Arg Asp Asp Leu Ala Ala Arg Gly
 115 120 125
 Leu Ser Ala Glu Val Leu Arg Leu Asp Gly Ala Val Glu Val Ser Ile
 130 135 140
 Lys Leu Gly Val Ala Asp Ala Ile Ala Asp Val Val Ser Thr Gly Arg
 145 150 155 160
 Thr Leu Arg Gln Gln Gly Leu Ala Pro Phe Gly Glu Val Leu Cys Thr
 165 170 175
 Ser Glu Ala Val Ile Val Gly Arg Lys Asp Glu Lys Val Thr Pro Glu
 180 185 190
 Gln Gln Ile Leu Leu Arg Arg Ile Gln Gly Ile Leu His Ala Gln Asn
 195 200 205
 Phe Leu Met Leu Asp Tyr Asn Val Asp Arg Asp Asn Leu Asp Ala Ala
 210 215 220
 Thr Ala Val Thr Pro Gly Leu Ser Gly Pro Thr Val Ser Pro Leu Ala
 225 230 235 240
 Arg Asp Asn Trp Val Ala Val Arg Ala Met Val Pro Arg Arg Ser Ala
 245 250 255
 Asn Ala Ile Met Asp Lys Leu Ala Gly Leu Gly Ala Glu Ala Ile Leu
 260 265 270
 Ala Ser Glu Ile Arg Ile Ala Arg Ile
 275 280

<210> 377

<211> 393

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(370)

<223> RXA02195

<400> 377

tcgagccggc aggtgtcgca aaataaaacc aggtggggga gtgaaattat tcgactaata 60

tcctccccca aacacacatt gataactgtt gtgtggaaga atg tac cga gtg aag 115
 Met Tyr Arg Val Lys
 1 5

aca ttt gac tcg ctg tac gaa gaa ctt ctt aac cgt gct cag acc cgc 163
 Thr Phe Asp Ser Leu Tyr Glu Glu Leu Leu Asn Arg Ala Gln Thr Arg
 10 15 20

cct gaa ggg tct gga acc gtg gcc gcc ttg gat aaa ggc atc cat cat 211
 Pro Glu Gly Ser Gly Thr Val Ala Ala Leu Asp Lys Gly Ile His His

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                25                30                35
cta ggt aag aag gtc atc gaa gaa gcc gga gag gtc tgg att gca gcc 259
Leu Gly Lys Lys Val Ile Glu Glu Ala Gly Glu Val Trp Ile Ala Ala
      40                45                50

gag tat gag acc gat gaa gag cta gcc gga gaa atc tcc cag ctc att 307
Glu Tyr Glu Thr Asp Glu Glu Leu Ala Gly Glu Ile Ser Gln Leu Ile
      55                60                65

tat tgg acc cag gtc atc atg gtt gct cgc ggc ctg aag cca gaa gat 355
Tyr Trp Thr Gln Val Ile Met Val Ala Arg Gly Leu Lys Pro Glu Asp
      70                75                80                85

atc tac aag aac ctg taggagtttt aaagcaatca tgt 393
Ile Tyr Lys Asn Leu
      90

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<210> 378
 <211> 90
 <212> PRT
 <213> Corynebacterium glutamicum

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<400> 378
Met Tyr Arg Val Lys Thr Phe Asp Ser Leu Tyr Glu Glu Leu Leu Asn
  1                5                10                15

Arg Ala Gln Thr Arg Pro Glu Gly Ser Gly Thr Val Ala Ala Leu Asp
      20                25                30

Lys Gly Ile His His Leu Gly Lys Lys Val Ile Glu Glu Ala Gly Glu
      35                40                45

Val Trp Ile Ala Ala Glu Tyr Glu Thr Asp Glu Glu Leu Ala Gly Glu
      50                55                60

Ile Ser Gln Leu Ile Tyr Trp Thr Gln Val Ile Met Val Ala Arg Gly
      65                70                75                80

Leu Lys Pro Glu Asp Ile Tyr Lys Asn Leu
      85                90

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<210> 379
 <211> 477
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(454)
 <223> RXA01097

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<400> 379
gcgccaacgc agtgcttgcc gcgaccattt tccacttccg cgaagtaacc atcgccgaag 60

taaagggagc cattaaagat gcaggatttg aggtgcggaa atg agt gac aat cca 115
      Met Ser Asp Asn Pro
      1                5

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caa gag tat gag ctg gat tgg gac gtc gaa aag cga tta aag ctt aac 163
 Gln Glu Tyr Glu Leu Asp Trp Asp Val Glu Lys Arg Leu Lys Leu Asn
 10 15 20

gac gcc ggc ctg gtg ccg gca atc gtc cag gcc gac ggg acc aac gag 211
 Asp Ala Gly Leu Val Pro Ala Ile Val Gln Ala Asp Gly Thr Asn Glu
 25 30 35

gtc ctc atg atg gcc tgg atg gat acc cac gcg cta gcc tat act ttg 259
 Val Leu Met Met Ala Trp Met Asp Thr His Ala Leu Ala Tyr Thr Leu
 40 45 50

gcg acc cgc cgt gga acc tat ttt tct agg tcc cgc aac gag tac tgg 307
 Ala Thr Arg Arg Gly Thr Tyr Phe Ser Arg Ser Arg Asn Glu Tyr Trp
 55 60 65

atc aag ggc ctg acc tct gga aac gtc caa gaa gtc acc gga ctt gcc 355
 Ile Lys Gly Leu Thr Ser Gly Asn Val Gln Glu Val Thr Gly Leu Ala
 70 75 80 85

ctc gac tgc gac ggc gac acc gtc ctt ctg acc gtg aaa caa acc ggc 403
 Leu Asp Cys Asp Gly Asp Thr Val Leu Leu Thr Val Lys Gln Thr Gly
 90 95 100

ggt gcg tgc cac act ggt gcc cac aca tgt ttc gac aat gac gtt ttg 451
 Gly Ala Cys His Thr Gly Ala His Thr Cys Phe Asp Asn Asp Val Leu
 105 110 115

ctg taaaagcaac aacgattaag gaa 477
 Leu

<210> 380

<211> 118

<212> PRT

<213> Corynebacterium glutamicum

<400> 380

Met Ser Asp Asn Pro Gln Glu Tyr Glu Leu Asp Trp Asp Val Glu Lys
 1 5 10 15

Arg Leu Lys Leu Asn Asp Ala Gly Leu Val Pro Ala Ile Val Gln Ala
 20 25 30

Asp Gly Thr Asn Glu Val Leu Met Met Ala Trp Met Asp Thr His Ala
 35 40 45

Leu Ala Tyr Thr Leu Ala Thr Arg Arg Gly Thr Tyr Phe Ser Arg Ser
 50 55 60

Arg Asn Glu Tyr Trp Ile Lys Gly Leu Thr Ser Gly Asn Val Gln Glu
 65 70 75 80

Val Thr Gly Leu Ala Leu Asp Cys Asp Gly Asp Thr Val Leu Leu Thr
 85 90 95

Val Lys Gln Thr Gly Gly Ala Cys His Thr Gly Ala His Thr Cys Phe
 100 105 110

Asp Asn Asp Val Leu Leu


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<210> 381
<211> 861
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(838)  
<223> RXA01100
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570

Phe Val Val Thr Asp Val Ser Lys Asp Gly Thr Leu Ser Gly Pro Asn
 170 175 180
 gtt gag ctg ctg cgt gag gtt gct gca gct aca gac gca cct atc gtg 691
 Val Glu Leu Leu Arg Glu Val Ala Ala Ala Thr Asp Ala Pro Ile Val
 185 190 195
 gca tct ggt gga att tct gtt ttg gaa gat gtt ttg gaa cta gcc aag 739
 Ala Ser Gly Gly Ile Ser Val Leu Glu Asp Val Leu Glu Leu Ala Lys
 200 205 210
 tac cag gat gag ggc att gat tcc gtc atc att ggc aag gca ctt tat 787
 Tyr Gln Asp Glu Gly Ile Asp Ser Val Ile Ile Gly Lys Ala Leu Tyr
 215 220 225
 gag cac aag ttc acc ctc gaa gag gct ttg gct gca gta gaa aag ctc 835
 Glu His Lys Phe Thr Leu Glu Glu Ala Leu Ala Ala Val Glu Lys Leu
 230 235 240 245
 ggt taatacatgg atgctcgtgg gat 861
 Gly

<210> 382

<211> 246

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 382

Met Thr Phe Thr Ile Leu Pro Ala Val Asp Val Val Asn Gly Gln Ala
 1 5 10 15
 Val Arg Leu Asp Gln Gly Glu Ala Gly Thr Glu Lys Ser Tyr Gly Thr
 20 25 30
 Pro Leu Glu Ser Ala Leu Lys Trp Gln Glu Gln Gly Ala Lys Trp Leu
 35 40 45
 His Phe Val Asp Leu Asp Ala Ala Phe Asn Arg Gly Ser Asn His Glu
 50 55 60
 Met Met Ala Glu Ile Val Gly Lys Leu Asp Val Asp Val Glu Leu Thr
 65 70 75 80
 Gly Gly Ile Arg Asp Asp Glu Ser Leu Glu Arg Ala Leu Ala Thr Gly
 85 90 95
 Ala Arg Arg Val Asn Ile Gly Thr Ala Ala Leu Glu Lys Pro Glu Trp
 100 105 110
 Ile Ala Ser Ala Ile Gln Arg Tyr Gly Glu Lys Ile Ala Val Asp Ile
 115 120 125
 Ala Val Arg Leu Glu Asp Gly Glu Trp Arg Thr Arg Gly Asn Gly Trp
 130 135 140
 Val Ser Asp Gly Gly Asp Leu Trp Glu Val Leu Glu Arg Leu Asp Ser
 145 150 155 160
 Gln Gly Cys Ala Arg Phe Val Val Thr Asp Val Ser Lys Asp Gly Thr

165										170					175				
Leu	Ser	Gly	Pro	Asn	Val	Glu	Leu	Leu	Arg	Glu	Val	Ala	Ala	Ala	Thr				
			180					185					190						
Asp	Ala	Pro	Ile	Val	Ala	Ser	Gly	Gly	Ile	Ser	Val	Leu	Glu	Asp	Val				
		195					200					205							
Leu	Glu	Leu	Ala	Lys	Tyr	Gln	Asp	Glu	Gly	Ile	Asp	Ser	Val	Ile	Ile				
	210					215					220								
Gly	Lys	Ala	Leu	Tyr	Glu	His	Lys	Phe	Thr	Leu	Glu	Glu	Ala	Leu	Ala				
225					230					235					240				
Ala	Val	Glu	Lys	Leu	Gly														
				245															

<210> 383

<211> 756

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(733)

<223> RXA01101

<400> 383

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atcgagccta ggccagtgtg gtggatataa aacccttttg gggagaaaga aactcgactg 60
cggttcttga tcctgaaagc acgtgacata aactatcggc atg acc aaa act gtc 115
Met Thr Lys Thr Val
1 5

gcc ctt ctc gac tac gga tct gga aac ctt cgt tct gct caa cgc gca 163
Ala Leu Leu Asp Tyr Gly Ser Gly Asn Leu Arg Ser Ala Gln Arg Ala
10 15 20

cta gag cgt gcc ggt gca gaa gtt atc gtg agc tcc gat cca gaa gtt 211
Leu Glu Arg Ala Gly Ala Glu Val Ile Val Ser Ser Asp Pro Glu Val
25 30 35

tgc acc aac gct gat ggc ctc cta gtt cct gga gtg ggc gca ttt gat 259
Cys Thr Asn Ala Asp Gly Leu Leu Val Pro Gly Val Gly Ala Phe Asp
40 45 50

gcc tgc atg aag ggt ttg aaa aac gtc ttc gga cat cgc att atc gga 307
Ala Cys Met Lys Gly Leu Lys Asn Val Phe Gly His Arg Ile Ile Gly
55 60 65

cag cgt ctt gct ggt gga cgt cca gtg atg ggt att tgt gtg ggc atg 355
Gln Arg Leu Ala Gly Gly Arg Pro Val Met Gly Ile Cys Val Gly Met
70 75 80 85

cag atc ctg ttc gat gaa ggc gat gag cac ggc att aag tca gct ggt 403
Gln Ile Leu Phe Asp Glu Gly Asp Glu His Gly Ile Lys Ser Ala Gly
90 95 100

tgc ggc gag tgg cct ggc aaa gtg gaa cgc ctc caa gcg gag atc ctg 451
Cys Gly Glu Trp Pro Gly Lys Val Glu Arg Leu Gln Ala Glu Ile Leu

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105	110	115	
cct cac atg ggg tgg aac aca ctt gaa atg cct acc aac tca cca atg			499
Pro His Met Gly Trp Asn Thr Leu Glu Met Pro Thr Asn Ser Pro Met			
120	125	130	
ttt gag gga att tca cct gat gag cgt ttc tac ttc gtg cac tcc tat			547
Phe Glu Gly Ile Ser Pro Asp Glu Arg Phe Tyr Phe Val His Ser Tyr			
135	140	145	
ggt gtg cgc aag tgg acg ttg gaa acc gac gat ctg acc acg cct cca			595
Gly Val Arg Lys Trp Thr Leu Glu Thr Asp Asp Leu Thr Thr Pro Pro			
150	155	160	165
gag gtt gtg tgg gcg aag cac gaa aat gat cgt ttt gtg gca gct gtg			643
Glu Val Val Trp Ala Lys His Glu Asn Asp Arg Phe Val Ala Ala Val			
170	175		180
gaa aac ggc acg ctg tgg gct act caa ttc cac cca gaa aaa tca ggt			691
Glu Asn Gly Thr Leu Trp Ala Thr Gln Phe His Pro Glu Lys Ser Gly			
185	190		195
gac gca ggc gca cag cta ctg cga aac tgg atc aac tac atc			733
Asp Ala Gly Ala Gln Leu Leu Arg Asn Trp Ile Asn Tyr Ile			
200	205	210	
taacagatag gatcaatatt cat			756

<210> 384

<211> 211

<212> PRT

<213> Corynebacterium glutamicum

<400> 384

Met Thr Lys Thr Val Ala Leu Leu Asp Tyr Gly Ser Gly Asn Leu Arg
1 5 10 15

Ser Ala Gln Arg Ala Leu Glu Arg Ala Gly Ala Glu Val Ile Val Ser
20 25 30

Ser Asp Pro Glu Val Cys Thr Asn Ala Asp Gly Leu Leu Val Pro Gly
35 40 45

Val Gly Ala Phe Asp Ala Cys Met Lys Gly Leu Lys Asn Val Phe Gly
50 55 60

His Arg Ile Ile Gly Gln Arg Leu Ala Gly Gly Arg Pro Val Met Gly
65 70 75 80

Ile Cys Val Gly Met Gln Ile Leu Phe Asp Glu Gly Asp Glu His Gly
85 90 95

Ile Lys Ser Ala Gly Cys Gly Glu Trp Pro Gly Lys Val Glu Arg Leu
100 105 110

Gln Ala Glu Ile Leu Pro His Met Gly Trp Asn Thr Leu Glu Met Pro
115 120 125

Thr Asn Ser Pro Met Phe Glu Gly Ile Ser Pro Asp Glu Arg Phe Tyr
130 135 140

Phe Val His Ser Tyr Gly Val Arg Lys Trp Thr Leu Glu Thr Asp Asp
145 150 155 160

Leu Thr Thr Pro Pro Glu Val Val Trp Ala Lys His Glu Asn Asp Arg
165 170 175

Phe Val Ala Ala Val Glu Asn Gly Thr Leu Trp Ala Thr Gln Phe His
180 185 190

Pro Glu Lys Ser Gly Asp Ala Gly Ala Gln Leu Leu Arg Asn Trp Ile
195 200 205

Asn Tyr Ile
210

<210> 385

<211> 723

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(700)

<223> RXN01657

<400> 385

cctccgcatc tgccgacgta tcccgcggcc tgggtgaagc catggtgggc atcaacgtat 60

ccgacgttcc agcaccacac cgactcgccg agcgcggctg gtg atc gtt gga gtt 115
Val Ile Val Gly Val
1 5

tta gct ctc cag ggc ggg gtg gaa gaa cac ctc acc gcc ttg gaa gct 163
Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu Thr Ala Leu Glu Ala
10 15 20

ctc gga gcg acg acc cga aaa gta cgt gtg cca aag gac ctt gat ggt 211
Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro Lys Asp Leu Asp Gly
25 30 35

ctc gaa ggc atc gtc atc ccc ggc ggg gaa tcc acc gtg ttg gac aaa 259
Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser Thr Val Leu Asp Lys
40 45 50

ctg gct cgg aca ttc gac gtg gta gaa cct cta gcg aat ctc att cgc 307
Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu Ala Asn Leu Ile Arg
55 60 65

gac ggc cta ccc gtt ttc gct acc tgc gct ggc ctg atc tat ctg gcg 355
Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly Leu Ile Tyr Leu Ala
70 75 80 85

aaa cac ctc gac aac cca gca agg gga caa caa acc ttg gcg gta gtg 403
Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln Thr Leu Ala Val Val
90 95 100

gac gtg gtg gtg cgt cga aac gca ttt ggc gcc caa cgc gaa tcc ttc 451
Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala Gln Arg Glu Ser Phe
105 110 115

gac acc acc gtg gat gtt tcc ttc gac ggt gca aca ttc ccc gga gtg 499
 Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala Thr Phe Pro Gly Val
 120 125 130
 cag gcc tcg ttt atc cga gct ccc atc gtc act gct ttt ggt cct acg 547
 Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr Ala Phe Gly Pro Thr
 135 140 145
 gta gaa gcg atc gct gct ctc aac ggt ggg gag gtg gtt ggt gta cgc 595
 Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu Val Val Gly Val Arg
 150 155 160 165
 caa ggc aac atc atc gcg ctg tct ttc cat ccc gaa gaa acc ggc gat 643
 Gln Gly Asn Ile Ile Ala Leu Ser Phe His Pro Glu Glu Thr Gly Asp
 170 175 180
 tac cgc atc cac caa gcc tgg ctg gac ctg gtg aga aaa cac gct gaa 691
 Tyr Arg Ile His Gln Ala Trp Leu Asp Leu Val Arg Lys His Ala Glu
 185 190 195
 ctg gcg att tgatgttttc ggtagcgctc tgt 723
 Leu Ala Ile
 200

<210> 386

<211> 200

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 386

Val Ile Val Gly Val Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu
 1 5 10 15
 Thr Ala Leu Glu Ala Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro
 20 25 30
 Lys Asp Leu Asp Gly Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser
 35 40 45
 Thr Val Leu Asp Lys Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu
 50 55 60
 Ala Asn Leu Ile Arg Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly
 65 70 75 80
 Leu Ile Tyr Leu Ala Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln
 85 90 95
 Thr Leu Ala Val Val Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala
 100 105 110
 Gln Arg Glu Ser Phe Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala
 115 120 125
 Thr Phe Pro Gly Val Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr
 130 135 140
 Ala Phe Gly Pro Thr Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu
 145 150 155 160

Val Val Gly Val Arg Gln Gly Asn Ile Ile Ala Leu Ser Phe His Pro
165 170 175

Glu Glu Thr Gly Asp Tyr Arg Ile His Gln Ala Trp Leu Asp Leu Val
180 185 190

Arg Lys His Ala Glu Leu Ala Ile
195 200

<210> 387

<211> 601

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(601)

<223> FRXA01657

<400> 387

cctccgctcat tgccgacgta tcccgcggcc tgggtgaagc catggtgggc atcaacgtat 60

ccgacgttcc agcaccacac cgactcgccg agcgcggctg gtg atc gtt gga gtt 115
Val Ile Val Gly Val
1 5

tta gct ctc cag ggc ggg gtg gaa gaa cac ctc acc gcc ttg gaa gct 163
Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu Thr Ala Leu Glu Ala
10 15 20

ctc gga gcg acg acc cga aaa gta cgt gtg cca aag gac ctt gat ggt 211
Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro Lys Asp Leu Asp Gly
25 30 35

ctc gaa ggc atc gtc atc ccc ggc ggg gaa tcc acc gtg ttg gac aaa 259
Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser Thr Val Leu Asp Lys
40 45 50

ctg gct cgg aca ttc gac gtg gta gaa cct cta gcg aat ctc att cgc 307
Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu Ala Asn Leu Ile Arg
55 60 65

gac ggc cta ccc gtt ttc gct acc tgc gct ggc ctg atc tat ctg gcg 355
Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly Leu Ile Tyr Leu Ala
70 75 80 85

aaa cac ctc gac aac cca gca agg gga caa caa acc ttg gcg gta gtg 403
Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln Thr Leu Ala Val Val
90 95 100

gac gtg gtg gtg cgt cga aac gca ttt ggc gcc caa cgc gaa tcc ttc 451
Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala Gln Arg Glu Ser Phe
105 110 115

gac acc acc gtg gat gtt tcc ttc gac ggt gca aca ttc ccc gga gtg 499
Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala Thr Phe Pro Gly Val
120 125 130

cag gcc tcg ttt atc cga gct ccc atc gtc act gct ttt ggt cct acg 547

Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr Ala Phe Gly Pro Thr
 135 140 145

gta gaa gcg atc gct gct ctc aac ggt ggg gag gtg gtt ggt gta cgc 595
 Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu Val Val Gly Val Arg
 150 155 160 165

caa ggc 601
 Gln Gly

<210> 388
 <211> 167
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 388
 Val Ile Val Gly Val Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu
 1 5 10 15

Thr Ala Leu Glu Ala Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro
 20 25 30

Lys Asp Leu Asp Gly Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser
 35 40 45

Thr Val Leu Asp Lys Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu
 50 55 60

Ala Asn Leu Ile Arg Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly
 65 70 75 80

Leu Ile Tyr Leu Ala Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln
 85 90 95

Thr Leu Ala Val Val Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala
 100 105 110

Gln Arg Glu Ser Phe Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala
 115 120 125

Thr Phe Pro Gly Val Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr
 130 135 140

Ala Phe Gly Pro Thr Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu
 145 150 155 160

Val Val Gly Val Arg Gln Gly
 165

<210> 389
 <211> 897
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(874)
 <223> RXA01098

<400> 389

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aaaagggtc acgatgtgct gttaagtaag attgaaaaag ttcggttgat gcatgcagat 60
gcaggtaatg accagtcgtt aaatgaggag tacaagtaaa atg ggc gtg gca att 115
                                     Met Gly Val Ala Ile
                                     1 5
cga gtt att cct tgc ctg gac gtg gac aac ggc cgg gtt gtt aaa ggc 163
Arg Val Ile Pro Cys Leu Asp Val Asp Asn Gly Arg Val Val Lys Gly
                                     10 15 20
gtg aac ttt gaa aac ctc cgc gat gct ggc gat cct gtg gag ttg gca 211
Val Asn Phe Glu Asn Leu Arg Asp Ala Gly Asp Pro Val Glu Leu Ala
                                     25 30 35
aag cgc tat gac gag gaa ggg gca gat gag ctg acc ttc ctg gat gtc 259
Lys Arg Tyr Asp Glu Glu Gly Ala Asp Glu Leu Thr Phe Leu Asp Val
                                     40 45 50
acc gcc tcg aag cat ggt cgc ggc acc atg ctg gat gtt gtt cga cgc 307
Thr Ala Ser Lys His Gly Arg Gly Thr Met Leu Asp Val Val Arg Arg
                                     55 60 65
acc gct gat cag gtg ttc atc cct ctg act gtc ggt ggc ggc gtg cgc 355
Thr Ala Asp Gln Val Phe Ile Pro Leu Thr Val Gly Gly Gly Val Arg
                                     70 75 80 85
agc gaa gaa gat gtt gat caa ttg ctg cgc gct ggc gcc gac aag gtt 403
Ser Glu Glu Asp Val Asp Gln Leu Leu Arg Ala Gly Ala Asp Lys Val
                                     90 95 100
tcg gtg aac acg tct gcg att gcc cgt cca gaa ctg ctg tca gag ctg 451
Ser Val Asn Thr Ser Ala Ile Ala Arg Pro Glu Leu Leu Ser Glu Leu
                                     105 110 115
tcc aag cgt ttt ggt gct cag tgc atc gtg ttg tct gtg gat gcc agg 499
Ser Lys Arg Phe Gly Ala Gln Cys Ile Val Leu Ser Val Asp Ala Arg
                                     120 125 130
cgc gtt cct gaa ggt gga act cct cag cca tct ggt ttt gaa gtc acc 547
Arg Val Pro Glu Gly Gly Thr Pro Gln Pro Ser Gly Phe Glu Val Thr
                                     135 140 145
acc cac ggc ggt tcc aag tcc gca gaa ctt gat gca atc gag tgg gca 595
Thr His Gly Gly Ser Lys Ser Ala Glu Leu Asp Ala Ile Glu Trp Ala
                                     150 155 160 165
aag cgc ggc gaa gag ctg ggc gtt ggc gaa att ctg ctc aac tcc atg 643
Lys Arg Gly Glu Glu Leu Gly Val Gly Glu Ile Leu Leu Asn Ser Met
                                     170 175 180
gac ggc gac ggc acc aaa aac ggc ttt gac cta gag ctg ctg gaa aaa 691
Asp Gly Asp Gly Thr Lys Asn Gly Phe Asp Leu Glu Leu Leu Glu Lys
                                     185 190 195
gtt cgc gca gcc gta tcc att cct gta atc gcc tcc ggc ggc gct ggc 739
Val Arg Ala Ala Val Ser Ile Pro Val Ile Ala Ser Gly Gly Ala Gly
                                     200 205 210
aag gcg gag cat ttc cca cca gct gtt gca gct ggc gcc aac gca gtg 787

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Lys Ala Glu His Phe Pro Pro Ala Val Ala Ala Gly Ala Asn Ala Val
 215 220 225

ctt gcc gcg acc att ttc cac ttc cgc gaa gta acc atc gcc gaa gta 835
 Leu Ala Ala Thr Ile Phe His Phe Arg Glu Val Thr Ile Ala Glu Val
 230 235 240 245

aag gga gcc att aaa gat gca gga ttt gag gtg cgg aaa tgagtgacaa 884
 Lys Gly Ala Ile Lys Asp Ala Gly Phe Glu Val Arg Lys
 250 255

tccacaagag tat 897

<210> 390
 <211> 258
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 390
 Met Gly Val Ala Ile Arg Val Ile Pro Cys Leu Asp Val Asp Asn Gly
 1 5 10 15

Arg Val Val Lys Gly Val Asn Phe Glu Asn Leu Arg Asp Ala Gly Asp
 20 25 30

Pro Val Glu Leu Ala Lys Arg Tyr Asp Glu Glu Gly Ala Asp Glu Leu
 35 40 45

Thr Phe Leu Asp Val Thr Ala Ser Lys His Gly Arg Gly Thr Met Leu
 50 55 60

Asp Val Val Arg Arg Thr Ala Asp Gln Val Phe Ile Pro Leu Thr Val
 65 70 75 80

Gly Gly Gly Val Arg Ser Glu Glu Asp Val Asp Gln Leu Leu Arg Ala
 85 90 95

Gly Ala Asp Lys Val Ser Val Asn Thr Ser Ala Ile Ala Arg Pro Glu
 100 105 110

Leu Leu Ser Glu Leu Ser Lys Arg Phe Gly Ala Gln Cys Ile Val Leu
 115 120 125

Ser Val Asp Ala Arg Arg Val Pro Glu Gly Gly Thr Pro Gln Pro Ser
 130 135 140

Gly Phe Glu Val Thr Thr His Gly Gly Ser Lys Ser Ala Glu Leu Asp
 145 150 155 160

Ala Ile Glu Trp Ala Lys Arg Gly Glu Glu Leu Gly Val Gly Glu Ile
 165 170 175

Leu Leu Asn Ser Met Asp Gly Asp Gly Thr Lys Asn Gly Phe Asp Leu
 180 185 190

Glu Leu Leu Glu Lys Val Arg Ala Ala Val Ser Ile Pro Val Ile Ala
 195 200 205

Ser Gly Gly Ala Gly Lys Ala Glu His Phe Pro Pro Ala Val Ala Ala
 210 215 220

Gly Ala Asn Ala Val Leu Ala Ala Thr Ile Phe His Phe Arg Glu Val
 225 230 235 240

Thr Ile Ala Glu Val Lys Gly Ala Ile Lys Asp Ala Gly Phe Glu Val
 245 250 255

Arg Lys

<210> 391

<211> 729

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(706)

<223> RXN01104

<400> 391

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gagatcatca agctgaacct gtaagagaga agaatttttc atg act gtc gca cca 115
 Met Thr Val Ala Pro
 1 5

aga att ggt acc gca acc cgc acc acc agc gaa tcc gac atc acc gtc 163
 Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu Ser Asp Ile Thr Val
 10 15 20

gag atc aac ctg gac ggc acc ggc aaa gta gat atc gat acc ggc ctg 211
 Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp Ile Asp Thr Gly Leu
 25 30 35

cca ttt ttc gac cac atg ctc act gca ttc ggc gtg cac ggc agt ttt 259
 Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly Val His Gly Ser Phe
 40 45 50

gat ctg aaa gtc cat gcc aag ggc gac atc gag atc gac gca cac cac 307
 Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu Ile Asp Ala His His
 55 60 65

acc gtg gaa gat acc gcc atc gtg ctc ggc caa gca ctc ctt gac gct 355
 Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln Ala Leu Leu Asp Ala
 70 75 80 85

att ggc gac aag aaa ggc atc cgc cgt ttc gca tcc tgc cag ctg ccc 403
 Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala Ser Cys Gln Leu Pro
 90 95 100

atg gat gag gca tta gtg gag tcc gtg gtg gat atc tcc ggt cgc cca 451
 Met Asp Glu Ala Leu Val Glu Ser Val Val Asp Ile Ser Gly Arg Pro
 105 110 115

tac ttc gtg atc tcc ggc gaa cca gac cac atg atc acc tcc gtg atc 499
 Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met Ile Thr Ser Val Ile
 120 125 130

ggg gga cac tac gca acc gtg atc aac gag cac ttc ttt gaa acc ctc 547

Gly Gly His Tyr Ala Thr Val Ile Asn Glu His Phe Phe Glu Thr Leu
 135 140 145

gcg ctc aac tcc cga atc acc ctc cac gtg atc tgc cac tac ggc cgc 595
 Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile Cys His Tyr Gly Arg
 150 155 160 165

gac cct cac cac atc acc gaa gca gag tac aag gct gtt gcc cgt gcg 643
 Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys Ala Val Ala Arg Ala
 170 175 180

ctg cgc ggt gcc gta gag atg gat cct cgt caa aca gga atc cca tcc 691
 Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln Thr Gly Ile Pro Ser
 185 190 195

act aag gga gcg ctc tagacatgaa ctcttctccc atc 729
 Thr Lys Gly Ala Leu
 200

<210> 392

<211> 202

<212> PRT

<213> Corynebacterium glutamicum

<400> 392

Met Thr Val Ala Pro Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu
 1 5 10 15

Ser Asp Ile Thr Val Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp
 20 25 30

Ile Asp Thr Gly Leu Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly
 35 40 45

Val His Gly Ser Phe Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu
 50 55 60

Ile Asp Ala His His Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln
 65 70 75 80

Ala Leu Leu Asp Ala Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala
 85 90 95

Ser Cys Gln Leu Pro Met Asp Glu Ala Leu Val Glu Ser Val Val Asp
 100 105 110

Ile Ser Gly Arg Pro Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met
 115 120 125

Ile Thr Ser Val Ile Gly Gly His Tyr Ala Thr Val Ile Asn Glu His
 130 135 140

Phe Phe Glu Thr Leu Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile
 145 150 155 160

Cys His Tyr Gly Arg Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys
 165 170 175

Ala Val Ala Arg Ala Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln
 180 185 190

Thr Gly Ile Pro Ser Thr Lys Gly Ala Leu
 195 200

<210> 393

<211> 729

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(706)

<223> FRXA01104

<400> 393

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cacttgcgca ctaccattgg tgtgcctgag gaaaatgatg cgtttttgga cgcagctgca 60
gagatcatca agctgaacct gtaagagaga agaatttttc atg act gtc gca cca 115
Met Thr Val Ala Pro
1 5
aga att ggt acc gca acc cgc acc acc agc gaa tcc gac atc acc gtc 163
Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu Ser Asp Ile Thr Val
10 15 20
gag atc aac ctg gac ggc acc ggc aaa gta gat atc gat acc ggc ctg 211
Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp Ile Asp Thr Gly Leu
25 30 35
cca ttt ttc gac cac atg ctc act gca ttc ggc gtg cac ggc agt ttt 259
Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly Val His Gly Ser Phe
40 45 50
gat ctg aaa gtc cat gcc aag ggc gac atc gag atc gac gca cac cac 307
Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu Ile Asp Ala His His
55 60 65
acc gtg gaa gat acc gcc atc gtg ctc ggc caa gca ctc ctt gac gct 355
Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln Ala Leu Leu Asp Ala
70 75 80 85
att ggc gac aag aaa ggc atc cgc cgt ttc gca tcc tgc cag ctg ccc 403
Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala Ser Cys Gln Leu Pro
90 95 100
atg gat gag gca tta gtg gag tcc gtg gtg gat atc tcc ggt cgc cca 451
Met Asp Glu Ala Leu Val Glu Ser Val Val Asp Ile Ser Gly Arg Pro
105 110 115
tac ttc gtg atc tcc ggc gaa cca gac cac atg atc acc tcc gtg atc 499
Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met Ile Thr Ser Val Ile
120 125 130
ggt gga cac tac gca acc gtg atc aac gag cac ttc ttt gaa acc ctc 547
Gly Gly His Tyr Ala Thr Val Ile Asn Glu His Phe Phe Glu Thr Leu
135 140 145
gcg ctc aac tcc cga atc acc ctc cac gtg atc tgc cac tac ggc cgc 595
Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile Cys His Tyr Gly Arg
150 155 160 165

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gac cct cac cac atc acc gaa gca gag tac aag gct gtt gcc cgt gcg 643
 Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys Ala Val Ala Arg Ala
 170 175 180

ctg cgc ggt gcc gta gag atg gat cct cgt caa aca gga atc cca tcc 691
 Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln Thr Gly Ile Pro Ser
 185 190 195

act aag gga gcg ctc tagacatgaa ctcttctccc atc 729
 Thr Lys Gly Ala Leu
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<210> 394

<211> 202

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 394

Met Thr Val Ala Pro Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu
 1 5 10 15

Ser Asp Ile Thr Val Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp
 20 25 30

Ile Asp Thr Gly Leu Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly
 35 40 45

Val His Gly Ser Phe Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu
 50 55 60

Ile Asp Ala His His Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln
 65 70 75 80

Ala Leu Leu Asp Ala Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala
 85 90 95

Ser Cys Gln Leu Pro Met Asp Glu Ala Leu Val Glu Ser Val Val Asp
 100 105 110

Ile Ser Gly Arg Pro Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met
 115 120 125

Ile Thr Ser Val Ile Gly Gly His Tyr Ala Thr Val Ile Asn Glu His
 130 135 140

Phe Phe Glu Thr Leu Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile
 145 150 155 160

Cys His Tyr Gly Arg Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys
 165 170 175

Ala Val Ala Arg Ala Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln
 180 185 190

Thr Gly Ile Pro Ser Thr Lys Gly Ala Leu
 195 200

<210> 395

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<220>  
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<222> (101)..(964)  
<223> RXN00446
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ctc cgt gag gct ctt gca gag cat tta gag gtt gag ttt gac cag gtc 163
Leu Arg Glu Ala Leu Ala Glu His Leu Glu Val Glu Phe Asp Gln Val
10 15 20

acg tgc gct cag ggc gat gag gtc att ttt cca tgg cgc agc ttt gag 259
Thr Cys Ala Gln Gly Asp Glu Val Ile Phe Pro Trp Arg Ser Phe Glu
40 45 50

cgc	ctg	act	gct	gat	cag	aat	cat	gat	ctt	gat	gcg	atg	gca	gcc	gcg	355
Pro	Leu	Thr	Ala	Asp	Gln	Asn	His	Asp	Leu	Asp	Ala	Met	Ala	Ala	Ala	
70					75					80					85	

atc act gat aag acc cgc ctc att ttc atc tgc aac ccc aac aat cct 403
Ile Thr Asp Lys Thr Arg Leu Ile Phe Ile Cys Asn Pro Asn Asn Pro
90 95 100

tcg ggc acc acc atc acc cag gcg cag ttt gat aat ttc atg gaa aag 451
Ser Gly Thr Thr Ile Thr Gln Ala Gln Phe Asp Asn Phe Met Glu Lys
105 110 115

gtt cca aac gat gtc gtt gtt ggg ctg gat gag gct tat ttt gag ttc 499
Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr Phe Glu Phe
120 125 130

aac cgc gcg gac gac acc cca gtt gcc act gag gaa atc cac cgc cac 547
 Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile His Arg His
 135 140 145

gac aac gtg att ggt ttg cgc acg ttc tcc aag gcg tat ggc ctg gcg 595
Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr Gly Leu Ala
150 155 160 165

ggc ttg cgt gtt ggt tac gcc ttc gga aac gca gag atc atc gca gcg 643
Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile Ile Ala Ala
170 175 180

atg aat aag gtg gct att cct ttc gcg gtg aat tca gca gct cag gcg 691

Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala Ala Gln Ala
 185 190 195

gca gcg ctt gcg agt ttg aat tct gcc gat gag ttg atg gaa cgg gtg 739
 Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met Glu Arg Val
 200 205 210

gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg ctt ggt gct 787
 Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala Leu Gly Ala
 215 220 225

gcg ccg acg cag gcc aat ttc gtc tgg ctg ccg ggc gag ggc gcc gct 835
 Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu Gly Ala Ala
 230 235 240 245

gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att cgc gcg ttc 883
 Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile Arg Ala Phe
 250 255 260

ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa act gac aag 931
 Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu Thr Asp Lys
 265 270 275

ctg ctg cgc gcg tgg gag gcc atc aat gct ggg tagtctttgg cgttttgcgg 984
 Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
 280 285

tgc 987

<210> 396

<211> 288

<212> PRT

<213> Corynebacterium glutamicum

<400> 396

Met Gly Ala Val Glu Leu Arg Glu Ala Leu Ala Glu His Leu Glu Val
 1 5 10 15

Glu Phe Asp Gln Val Thr Val Gly Cys Gly Ser Ser Ala Leu Cys Gln
 20 25 30

Gln Leu Val Gln Ala Thr Cys Ala Gln Gly Asp Glu Val Ile Phe Pro
 35 40 45

Trp Arg Ser Phe Glu Ala Tyr Pro Ile Phe Ala Gln Val Ala Gly Ala
 50 55 60

Thr Pro Val Ala Ile Pro Leu Thr Ala Asp Gln Asn His Asp Leu Asp
 65 70 75 80

Ala Met Ala Ala Ala Ile Thr Asp Lys Thr Arg Leu Ile Phe Ile Cys
 85 90 95

Asn Pro Asn Asn Pro Ser Gly Thr Thr Ile Thr Gln Ala Gln Phe Asp
 100 105 110

Asn Phe Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu
 115 120 125

Ala Tyr Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu

130	135	140
Glu Ile His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys		
145	150	155 160
Ala Tyr Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala		
	165	170 175
Glu Ile Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn		
	180	185 190
Ser Ala Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu		
	195	200 205
Leu Met Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val		
	210	215 220
Ser Ala Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro		
	225	230 235 240
Gly Glu Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile		
	245	250 255
Val Ile Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala		
	260	265 270
Glu Glu Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly		
	275	280 285

<210> 397
 <211> 545
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1)..(522)
 <223> FRXA00446

<400> 397	
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Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr	
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ttt gag ttc aac cgc gcg gac gac acc cca gtt gcc act gag gaa atc	96
Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile	
20 25 30	
cac cgc cac gac aac gtg att ggt ttg cgc acg ttc tcc aag gcg tat	144
His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr	
35 40 45	
ggc ctg gcg ggc ttg cgt gtt ggt tac gcc ttc gga aac gca gag atc	192
Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile	
50 55 60	
atc gca gcg atg aat aag gtg gct att cct ttc gcg gtg aat tca gca	240

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Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala
 65              70              75              80

gct cag gcg gca gcg ctt gcg agt ttg aat tct gcc gat gag ttg atg 288
Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met
              85              90              95

gaa cgg gtg gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg 336
Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala
              100              105              110

ctt ggt gct gcg ccg acg cag gcc aat ttc gtc tgg ctg ccg ggc gag 384
Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu
              115              120              125

ggc gcc gct gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att 432
Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile
              130              135              140

cgc gcg ttc ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa 480
Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu
              145              150              155              160

act gac aag ctg ctg cgc gcg tgg gag gcc atc aat gct ggg 522
Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
              165              170

tagtcctttgg cgttttgcgg tgc 545

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<210> 398

<211> 174

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 398

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Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr
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Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile
              20              25              30

His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr
              35              40              45

Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile
              50              55              60

Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala
 65              70              75              80

Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met
              85              90              95

Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala
              100              105              110

Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu
              115              120              125

Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile

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130	135	140	
Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu			
145	150	155	160
Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly			
	165	170	

<210> 399
 <211> 1221
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(1198)
 <223> RXA01105

 <400> 399
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 gctttgaaaa cctccccacc accgacgagg cctaagaaaa atg acc aaa att act 115
 Met Thr Lys Ile Thr 5

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 ttg agc gat ttg cca ttg cgt gaa gaa ctg cgc ggt gag cac gct tac 163
 Leu Ser Asp Leu Pro Leu Arg Glu Glu Leu Arg Gly Glu His Ala Tyr 20
 10 15

 ggc gca ccc cag ctc aac gtt gat att cgc ctc aac acc aac gaa aac 211
 Gly Ala Pro Gln Leu Asn Val Asp Ile Arg Leu Asn Thr Asn Glu Asn 35
 25 30

 cct tac cca ccg tca gag gca ttg gtc gct gac ttg gtt gcc acc gtg 259
 Pro Tyr Pro Pro Ser Glu Ala Leu Val Ala Asp Leu Val Ala Thr Val 50
 40 45

 gat aag atc gcc acc gag ctg aac cgc tac cca gag cgc gat gct gtg 307
 Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro Glu Arg Asp Ala Val 65
 55 60

 gaa ctg cgt gat gag ttg gct gcg tac atc acc aag caa acc ggc gtg 355
 Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr Lys Gln Thr Gly Val 85
 70 75 80

 gct gtc acc agg gat aac ctg tgg gct gcc aat ggt tcc aat gaa att 403
 Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn Gly Ser Asn Glu Ile 100
 90 95

 ctg cag cag ctg ctg cag gct ttt ggt gga cct gga cgc acc gcg ttg 451
 Leu Gln Gln Leu Leu Gln Ala Phe Gly Gly Pro Gly Arg Thr Ala Leu 115
 105 110

 gga ttc caa ccc agc tat tcc atg cac cca att ttg gct aaa ggc acc 499
 Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile Leu Ala Lys Gly Thr 130
 120 125

 cac act gaa ttc att gcg gtg tcc cga ggt gct gat ttc cgc atc gat 547
 His Thr Glu Phe Ile Ala Val Ser Arg Gly Ala Asp Phe Arg Ile Asp 145
 135 140

atg gat gtg gcg ctg gaa gaa att cgt gca aag cag cct gac att gtt	595
Met Asp Val Ala Leu Glu Glu Ile Arg Ala Lys Gln Pro Asp Ile Val	
150 155 160 165	
ttt gtc acc acc ccg aac aac ccg acc ggt gat gtg acc tcg ctg gac	643
Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp Val Thr Ser Leu Asp	
170 175 180	
gat gtt gag cgc atc atc aac gtt gcc cca ggc atc gtg atc gtg gat	691
Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly Ile Val Ile Val Asp	
185 190 195	
gaa gct tat gcg gaa ttc tcc cca tca cct tca gca acc act ctt ctg	739
Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser Ala Thr Thr Leu Leu	
200 205 210	
gag aag tac cca acc aag ctg gtg gtg tcc cgc acc atg agt aag gct	787
Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg Thr Met Ser Lys Ala	
215 220 225	
ttt gat ttc gca ggt gga cgc ctc ggc tac ttc gtg gcc aac cca gcg	835
Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe Val Ala Asn Pro Ala	
230 235 240 245	
ttt atc gac gcc gtg atg cta gtc cgc ctt ccg tat cat ctt tca gcg	883
Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro Tyr His Leu Ser Ala	
250 255 260	
ctg agc caa gca gcc gca atc gta gcg ctg cgt cac tcc gct gac acg	931
Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg His Ser Ala Asp Thr	
265 270 275	
ctg gga acc gtc gaa aag ctc tct gta gag cgt gtt cgc gtg gca gca	979
Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg Val Arg Val Ala Ala	
280 285 290	
cgc ttg gag gaa ctg ggc tac gct gtg gtt cca agt gag tcc aac ttt	
1027	
Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro Ser Glu Ser Asn Phe	
295 300 305	
gtg ttc ttt gga gat ttc tcc gat cag cac gcg gca tgg cag gca ttt	
1075	
Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala Ala Trp Gln Ala Phe	
310 315 320 325	
ttg gat agg gga gtg ctc atc cgc gat gtg gga atc gct ggg cac ttg	
1123	
Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly Ile Ala Gly His Leu	
330 335 340	
cgc act acc att ggt gtg cct gag gaa aat gat gcg ttt ttg gac gca	
1171	
Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp Ala Phe Leu Asp Ala	
345 350 355	
gct gca gag atc atc aag ctg aac ctg taagagagaa gaatttttca	
1218	
Ala Ala Glu Ile Ile Lys Leu Asn Leu	
360 365	

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<210> 400
<211> 366
<212> PRT
<213> Corynebacterium glutamicum
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Gly	Glu	His	Ala 20	Tyr	Gly	Ala	Pro	Gln 25	Leu	Asn	Val	Asp	Ile 30	Arg	Leu
Asn	Thr	Asn 35	Glu	Asn	Pro	Tyr	Pro 40	Pro	Ser	Glu	Ala	Leu 45	Val	Ala	Asp
Leu	Val 50	Ala	Thr	Val	Asp	Lys 55	Ile	Ala	Thr	Glu	Leu 60	Asn	Arg	Tyr	Pro
Glu 65	Arg	Asp	Ala	Val	Glu 70	Leu	Arg	Asp	Glu	Leu 75	Ala	Ala	Tyr	Ile	Thr 80
Lys	Gln	Thr	Gly 85	Val	Ala	Val	Thr	Arg	Asp 90	Asn	Leu	Trp	Ala 95	Ala	Asn
Gly	Ser	Asn	Glu 100	Ile	Leu	Gln	Gln	Leu 105	Leu	Gln	Ala	Phe	Gly 110	Gly	Pro
Gly	Arg	Thr 115	Ala	Leu	Gly	Phe	Gln 120	Pro	Ser	Tyr	Ser	Met 125	His	Pro	Ile
Leu 130	Ala	Lys	Gly	Thr	His	Thr 135	Glu	Phe	Ile	Ala	Val 140	Ser	Arg	Gly	Ala
Asp 145	Phe	Arg	Ile	Asp	Met 150	Asp	Val	Ala	Leu	Glu 155	Glu	Ile	Arg	Ala	Lys 160
Gln	Pro	Asp	Ile 165	Val	Phe	Val	Thr	Thr 170	Pro	Asn	Asn	Pro	Thr	Gly 175	Asp
Val	Thr	Ser	Leu 180	Asp	Asp	Val	Glu	Arg 185	Ile	Ile	Asn	Val	Ala 190	Pro	Gly
Ile	Val	Ile 195	Val	Asp	Glu	Ala	Tyr 200	Ala	Glu	Phe	Ser	Pro 205	Ser	Pro	Ser
Ala 210	Thr	Thr	Leu	Leu	Glu	Lys 215	Tyr	Pro	Thr	Lys	Leu 220	Val	Val	Ser	Arg
Thr 225	Met	Ser	Lys	Ala	Phe 230	Asp	Phe	Ala	Gly	Gly 235	Arg	Leu	Gly	Tyr	Phe 240
Val	Ala	Asn	Pro	Ala 245	Phe	Ile	Asp	Ala	Val 250	Met	Leu	Val	Arg	Leu 255	Pro
Tyr	His	Leu	Ser 260	Ala	Leu	Ser	Gln	Ala 265	Ala	Ala	Ile	Val	Ala 270	Leu	Arg

His Ser Ala Asp Thr Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg
 275 280 285
 Val Arg Val Ala Ala Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro
 290 295 300
 Ser Glu Ser Asn Phe Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala
 305 310 315 320
 Ala Trp Gln Ala Phe Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly
 325 330 335
 Ile Ala Gly His Leu Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp
 340 345 350
 Ala Phe Leu Asp Ala Ala Ala Glu Ile Ile Lys Leu Asn Leu
 355 360 365

<210> 401

<211> 1449

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1426)

<223> RXA01106

<400> 401

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aagaatttcg attcaacctt ttaagggaga acttttcgcc atg ttg aat gtc act 115
 Met Leu Asn Val Thr 5

gac ctg cga ggt caa aca cca tcc aag agc gac atc cga cgt gct ttg 163
 Asp Leu Arg Gly Gln Thr Pro Ser Lys Ser Asp Ile Arg Arg Ala Leu 20

cca cgt ggt ggc act gac gtg tgg tct gtg ctt ccc ata gtg cag cct 211
 Pro Arg Gly Gly Thr Asp Val Trp Ser Val Leu Pro Ile Val Gln Pro 35

gtt gta gaa gat gtc caa aac cgc ggc gct gaa gct gct ttg gat tac 259
 Val Val Glu Asp Val Gln Asn Arg Gly Ala Glu Ala Ala Leu Asp Tyr 40 45 50

ggc gag aag ttc gac cat att cgc ccc gcc tcg gtg cgg gtg cca gct 307
 Gly Glu Lys Phe Asp His Ile Arg Pro Ala Ser Val Arg Val Pro Ala 55 60 65

gag gtt att gct gca gca gaa aac acc tta gat ccg ttg gtg cgt gaa 355
 Glu Val Ile Ala Ala Ala Glu Asn Thr Leu Asp Pro Leu Val Arg Glu 70 75 80 85

tcg att gaa gag tcg att cgt cgc gtc cgc aag gtt cac gct gag caa 403
 Ser Ile Glu Glu Ser Ile Arg Arg Val Arg Lys Val His Ala Glu Gln 90 95 100

aag cca tcc gag cac acc act gaa ctt tca cca ggt ggc acc gtc act 451
Lys Pro Ser Glu His Thr Thr Glu Leu Ser Pro Gly Gly Thr Val Thr
105 110 115

gag cgt ttc atg ccg att gat cgc gtg gga ctg tac gtt cca ggc ggc 499
Glu Arg Phe Met Pro Ile Asp Arg Val Gly Leu Tyr Val Pro Gly Gly
120 125 130

aat gcg gtg tac cca tca agc gtg att atg aat act gtc cca gct caa 547
Asn Ala Val Tyr Pro Ser Ser Val Ile Met Asn Thr Val Pro Ala Gln
135 140 145

gag gct ggt gtg aac tcc ctt gtg gtt gcg tcg cct cct cag gct gag 595
Glu Ala Gly Val Asn Ser Leu Val Val Ala Ser Pro Pro Gln Ala Glu
150 155 160 165

cac ggt ggc tgg cct cac ccc acc att ttg gcg gcg tgt tcc atc ttg 643
His Gly Gly Trp Pro His Pro Thr Ile Leu Ala Ala Cys Ser Ile Leu
170 175 180

ggg gtt gat gag gtg tgg gct gtc ggc ggc ggt cag gcc gtg gcg ttg 691
Gly Val Asp Glu Val Trp Ala Val Gly Gly Gly Gln Ala Val Ala Leu
185 190 195

ctg gct tat ggt gat gac gct gca ggt ctc gag cct gtg gat atg atc 739
Leu Ala Tyr Gly Asp Asp Ala Ala Gly Leu Glu Pro Val Asp Met Ile
200 205 210

act gga cct ggc aat atc ttt gtc acc gct gcg aag cgc ctg gtc agg 787
Thr Gly Pro Gly Asn Ile Phe Val Thr Ala Ala Lys Arg Leu Val Arg
215 220 225

gga gtg gta ggt act gat tct gag gct ggc cct aca gaa atc gct gtg 835
Gly Val Val Gly Thr Asp Ser Glu Ala Gly Pro Thr Glu Ile Ala Val
230 235 240 245

ctt gct gat gcc tct gcc aac gcc gtc aac gtt gcc tac gat ctg atc 883
Leu Ala Asp Ala Ser Ala Asn Ala Val Asn Val Ala Tyr Asp Leu Ile
250 255 260

agc caa gca gaa cac gat gtc atg gct gcg tcc gtg ctc atc act gac 931
Ser Gln Ala Glu His Asp Val Met Ala Ala Ser Val Leu Ile Thr Asp
265 270 275

tcc gag cag ctt gcc aag gac gta aac agg gaa atc gag gcg cgt tac 979
Ser Glu Gln Leu Ala Lys Asp Val Asn Arg Glu Ile Glu Ala Arg Tyr
280 285 290

tca atc acg cgc aac gcc gag cgc gtc gca gaa gct ttg cgc ggg gcc
1027
Ser Ile Thr Arg Asn Ala Glu Arg Val Ala Glu Ala Leu Arg Gly Ala
295 300 305

cag agt ggc atc gtg ctt gtc gac gac att tcc gtg ggt atc caa gta
1075
Gln Ser Gly Ile Val Leu Val Asp Asp Ile Ser Val Gly Ile Gln Val
310 315 320 325

gcc gat caa tac gca gcg gaa cac ctg gaa atc cac act gag aac gcg
1123
Ala Asp Gln Tyr Ala Ala Glu His Leu Glu Ile His Thr Glu Asn Ala

330 335 340
 cgc gcc gta gca gag cag atc acc aac gcg ggt gcg atc ttc gtg ggc
 1171
 Arg Ala Val Ala Glu Gln Ile Thr Asn Ala Gly Ala Ile Phe Val Gly
 345 350 355
 gat ttc tca cca gta cca ctg ggt gat tac tcc gca gga tcc aac cac
 1219
 Asp Phe Ser Pro Val Pro Leu Gly Asp Tyr Ser Ala Gly Ser Asn His
 360 365 370
 gtg ctg cca acc tct gga tcc gct cgt ttc tcc gca ggt cta tcc acg
 1267
 Val Leu Pro Thr Ser Gly Ser Ala Arg Phe Ser Ala Gly Leu Ser Thr
 375 380 385
 cac acg ttc ctt cgc cca gtc aac ctc att gaa tac gat gag gct gct
 1315
 His Thr Phe Leu Arg Pro Val Asn Leu Ile Glu Tyr Asp Glu Ala Ala
 390 395 400 405
 ctg aag gac gtc tcg cag gtt gtc atc aac ttt gcc aac gcc gaa gat
 1363
 Leu Lys Asp Val Ser Gln Val Val Ile Asn Phe Ala Asn Ala Glu Asp
 410 415 420
 ctt cca gcg cac ggc gaa gca atc cgt gca cgc ttt gaa aac ctc ccc
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 Thr Thr Asp Glu Ala
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 <211> 442
 <212> PRT
 <213> *Corynebacterium glutamicum*
 <400> 402
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 20 25 30
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 35 40 45
 Ala Ala Leu Asp Tyr Gly Glu Lys Phe Asp His Ile Arg Pro Ala Ser
 50 55 60
 Val Arg Val Pro Ala Glu Val Ile Ala Ala Ala Glu Asn Thr Leu Asp
 65 70 75 80
 Pro Leu Val Arg Glu Ser Ile Glu Glu Ser Ile Arg Arg Val Arg Lys
 85 90 95

Val His Ala Glu Gln Lys Pro Ser Glu His Thr Thr Glu Leu Ser Pro
 100 105 110
 Gly Gly Thr Val Thr Glu Arg Phe Met Pro Ile Asp Arg Val Gly Leu
 115 120 125
 Tyr Val Pro Gly Gly Asn Ala Val Tyr Pro Ser Ser Val Ile Met Asn
 130 135 140
 Thr Val Pro Ala Gln Glu Ala Gly Val Asn Ser Leu Val Val Ala Ser
 145 150 155 160
 Pro Pro Gln Ala Glu His Gly Gly Trp Pro His Pro Thr Ile Leu Ala
 165 170 175
 Ala Cys Ser Ile Leu Gly Val Asp Glu Val Trp Ala Val Gly Gly Gly
 180 185 190
 Gln Ala Val Ala Leu Leu Ala Tyr Gly Asp Asp Ala Ala Gly Leu Glu
 195 200 205
 Pro Val Asp Met Ile Thr Gly Pro Gly Asn Ile Phe Val Thr Ala Ala
 210 215 220
 Lys Arg Leu Val Arg Gly Val Val Gly Thr Asp Ser Glu Ala Gly Pro
 225 230 235 240
 Thr Glu Ile Ala Val Leu Ala Asp Ala Ser Ala Asn Ala Val Asn Val
 245 250 255
 Ala Tyr Asp Leu Ile Ser Gln Ala Glu His Asp Val Met Ala Ala Ser
 260 265 270
 Val Leu Ile Thr Asp Ser Glu Gln Leu Ala Lys Asp Val Asn Arg Glu
 275 280 285
 Ile Glu Ala Arg Tyr Ser Ile Thr Arg Asn Ala Glu Arg Val Ala Glu
 290 295 300
 Ala Leu Arg Gly Ala Gln Ser Gly Ile Val Leu Val Asp Asp Ile Ser
 305 310 315 320
 Val Gly Ile Gln Val Ala Asp Gln Tyr Ala Ala Glu His Leu Glu Ile
 325 330 335
 His Thr Glu Asn Ala Arg Ala Val Ala Glu Gln Ile Thr Asn Ala Gly
 340 345 350
 Ala Ile Phe Val Gly Asp Phe Ser Pro Val Pro Leu Gly Asp Tyr Ser
 355 360 365
 Ala Gly Ser Asn His Val Leu Pro Thr Ser Gly Ser Ala Arg Phe Ser
 370 375 380
 Ala Gly Leu Ser Thr His Thr Phe Leu Arg Pro Val Asn Leu Ile Glu
 385 390 395 400
 Tyr Asp Glu Ala Ala Leu Lys Asp Val Ser Gln Val Val Ile Asn Phe
 405 410 415

Ala Asn Ala Glu Asp Leu Pro Ala His Gly Glu Ala Ile Arg Ala Arg
 420 425 430

Phe Glu Asn Leu Pro Thr Thr Asp Glu Ala
 435 440

<210> 403
 <211> 876
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(853)
 <223> RXC00930

<400> 403
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 ttccggtgga tgatggaagc tagacgacga aagggagcat atg tct ggc cac tca 115
 Met Ser Gly His Ser
 1 5
 aaa tgg gcg act acc aag cac aag aag gct gct aac gac gcc aag cga 163
 Lys Trp Ala Thr Thr Lys His Lys Lys Ala Ala Asn Asp Ala Lys Arg
 10 15 20
 ggc aag gaa ttt gcc aag ctg atc aag aac atc gaa gtt gcg gca cgt 211
 Gly Lys Glu Phe Ala Lys Leu Ile Lys Asn Ile Glu Val Ala Ala Arg
 25 30 35
 aca ggc ggt gga gat ccg tct gcg aac cca acg ctt gat gac atg atc 259
 Thr Gly Gly Gly Asp Pro Ser Ala Asn Pro Thr Leu Asp Asp Met Ile
 40 45 50
 aag aaa gcc aag aag gct tct gtg ccg aac gat aac atc gaa cgt gca 307
 Lys Lys Ala Lys Lys Ala Ser Val Pro Asn Asp Asn Ile Glu Arg Ala
 55 60 65
 cgc aag cgt ggc tcc ggc gaa gaa gct ggt ggc gct gac tgg atg aac 355
 Arg Lys Arg Gly Ser Gly Glu Glu Ala Gly Gly Ala Asp Trp Met Asn
 70 75 80 85
 atc atg tac gag gga tac ggc ccc aac ggc gtt gcc atg ctt atc gag 403
 Ile Met Tyr Glu Gly Tyr Gly Pro Asn Gly Val Ala Met Leu Ile Glu
 90 95 100
 tgt ctg acc gac aac cgt aac cgc gca gct acc gaa gtt cgc acc gca 451
 Cys Leu Thr Asp Asn Arg Asn Arg Ala Ala Thr Glu Val Arg Thr Ala
 105 110 115
 atg acc aaa aac ggt ggc aac ttg ggc gag tcc ggt tcc gtg tcc tac 499
 Met Thr Lys Asn Gly Gly Asn Leu Gly Glu Ser Gly Ser Val Ser Tyr
 120 125 130
 atg ttc acc cgc acc ggt gtc gtc acc gta caa aag ggc gat ctt agt 547
 Met Phe Thr Arg Thr Gly Val Val Thr Val Gln Lys Gly Asp Leu Ser
 135 140 145
 gaa gat gac gtg ctc atg gct gtt ctt gaa gct ggt gct gaa gaa gtc 595

Glu Asp Asp Val Leu Met Ala Val Leu Glu Ala Gly Ala Glu Glu Val
 150 155 160 165
 aac gac aac ggc gat ctg ttc gag gtt acc tgc gca cca act gac att 643
 Asn Asp Asn Gly Asp Leu Phe Glu Val Thr Cys Ala Pro Thr Asp Ile
 170 175 180
 cag gct gtt cgc gac gca ctc gtg gaa gct ggc att gaa gta gaa gat 691
 Gln Ala Val Arg Asp Ala Leu Val Glu Ala Gly Ile Glu Val Glu Asp
 185 190 195
 tct gaa tca gac ttc cgg gca tct gtt cag gtc ccc ctg gac gct gac 739
 Ser Glu Ser Asp Phe Arg Ala Ser Val Gln Val Pro Leu Asp Ala Asp
 200 205 210
 ggt gca cgc aag atc ttc aag ctt gtg gac gcg ttg gaa gat tcc gac 787
 Gly Ala Arg Lys Ile Phe Lys Leu Val Asp Ala Leu Glu Asp Ser Asp
 215 220 225
 gat gtg caa aac gtc tac acc aac atc gac ttg agc gat gag gtt ttg 835
 Asp Val Gln Asn Val Tyr Thr Asn Ile Asp Leu Ser Asp Glu Val Leu
 230 235 240 245
 aca gag ctg gaa aac gac tagttcgtat tttccgcact ccg 876
 Thr Glu Leu Glu Asn Asp
 250

<210> 404

<211> 251

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 404

Met Ser Gly His Ser Lys Trp Ala Thr Thr Lys His Lys Lys Ala Ala
 1 5 10 15
 Asn Asp Ala Lys Arg Gly Lys Glu Phe Ala Lys Leu Ile Lys Asn Ile
 20 25 30
 Glu Val Ala Ala Arg Thr Gly Gly Gly Asp Pro Ser Ala Asn Pro Thr
 35 40 45
 Leu Asp Asp Met Ile Lys Lys Ala Lys Lys Ala Ser Val Pro Asn Asp
 50 55 60
 Asn Ile Glu Arg Ala Arg Lys Arg Gly Ser Gly Glu Glu Ala Gly Gly
 65 70 75 80
 Ala Asp Trp Met Asn Ile Met Tyr Glu Gly Tyr Gly Pro Asn Gly Val
 85 90 95
 Ala Met Leu Ile Glu Cys Leu Thr Asp Asn Arg Asn Arg Ala Ala Thr
 100 105 110
 Glu Val Arg Thr Ala Met Thr Lys Asn Gly Gly Asn Leu Gly Glu Ser
 115 120 125
 Gly Ser Val Ser Tyr Met Phe Thr Arg Thr Gly Val Val Thr Val Gln
 130 135 140

Lys Gly Asp Leu Ser Glu Asp Asp Val Leu Met Ala Val Leu Glu Ala
145 150 155 160

Gly Ala Glu Glu Val Asn Asp Asn Gly Asp Leu Phe Glu Val Thr Cys
165 170 175

Ala Pro Thr Asp Ile Gln Ala Val Arg Asp Ala Leu Val Glu Ala Gly
180 185 190

Ile Glu Val Glu Asp Ser Glu Ser Asp Phe Arg Ala Ser Val Gln Val
195 200 205

Pro Leu Asp Ala Asp Gly Ala Arg Lys Ile Phe Lys Leu Val Asp Ala
210 215 220

Leu Glu Asp Ser Asp Asp Val Gln Asn Val Tyr Thr Asn Ile Asp Leu
225 230 235 240

Ser Asp Glu Val Leu Thr Glu Leu Glu Asn Asp
245 250

<210> 405

<211> 547

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(547)

<223> RXC01096

<400> 405

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gttttgctgt aaaagcaaca acgattaagg aagaaatctt atg aag cca cgc gtg 115
Met Lys Pro Arg Val
1 5

ctg tca gca tta ggc att gga gct ggc gcc ctg gtt gtc tgg atc agc 163
Leu Ser Ala Leu Gly Ile Gly Ala Gly Ala Leu Val Val Trp Ile Ser
10 15 20

tca cgc atg aac tgg gta acc atc gag gct ttc gac gat aaa tca ggt 211
Ser Arg Met Asn Trp Val Thr Ile Glu Ala Phe Asp Asp Lys Ser Gly
25 30 35

agt gtc acc caa tct att gtg ggt gca acc tgg tct aca gaa atc atg 259
Ser Val Thr Gln Ser Ile Val Gly Ala Thr Trp Ser Thr Glu Ile Met
40 45 50

gcg ctt gca ctt gct ttg ctc gct gcc ttc gcc gcc gcg ttg gtg ctc 307
Ala Leu Ala Leu Ala Leu Leu Ala Ala Phe Ala Ala Ala Leu Val Leu
55 60 65

aag cgc atg ggt cgg cgc atc att ggt ggt att tcg gcg ctg atc gcg 355
Lys Arg Met Gly Arg Arg Ile Ile Gly Gly Ile Ser Ala Leu Ile Ala
70 75 80 85

gtg ggt gcc agc ctg tct cca ctc gcg ctt ctc acc caa gac cca gac 403
Val Gly Ala Ser Leu Ser Pro Leu Ala Leu Leu Thr Gln Asp Pro Asp

	90	95	100	
gca gaa cgg gcc cga acc ctg ctg acc tcc ggt gtg gcc tca cag aag				451
Ala Glu Arg Ala Arg Thr Leu Leu Thr Ser Gly Val Ala Ser Gln Lys				
	105	110	115	
gct aat tcc gga acc ctg ctg tct gat tgg gcg gag atc atc aat acc				499
Ala Asn Ser Gly Thr Leu Leu Ser Asp Trp Ala Glu Ile Ile Asn Thr				
	120	125	130	
acc acc cat cca ctg gcg gca gtg gta gcc atg att ggc tgc gcg cta				547
Thr Thr His Pro Leu Ala Ala Val Val Ala Met Ile Gly Cys Ala Leu				
	135	140	145	

<210> 406

<211> 149

<212> PRT

<213> Corynebacterium glutamicum

<400> 406

Met Lys Pro Arg Val Leu Ser Ala Leu Gly Ile Gly Ala Gly Ala Leu				
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Val Val Trp Ile Ser Ser Arg Met Asn Trp Val Thr Ile Glu Ala Phe				
	20	25	30	
Asp Asp Lys Ser Gly Ser Val Thr Gln Ser Ile Val Gly Ala Thr Trp				
	35	40	45	
Ser Thr Glu Ile Met Ala Leu Ala Leu Ala Leu Ala Ala Phe Ala				
	50	55	60	
Ala Ala Leu Val Leu Lys Arg Met Gly Arg Arg Ile Ile Gly Gly Ile				
	65	70	75	80
Ser Ala Leu Ile Ala Val Gly Ala Ser Leu Ser Pro Leu Ala Leu Leu				
	85	90	95	
Thr Gln Asp Pro Asp Ala Glu Arg Ala Arg Thr Leu Leu Thr Ser Gly				
	100	105	110	
Val Ala Ser Gln Lys Ala Asn Ser Gly Thr Leu Leu Ser Asp Trp Ala				
	115	120	125	
Glu Ile Ile Asn Thr Thr Thr His Pro Leu Ala Ala Val Val Ala Met				
	130	135	140	
Ile Gly Cys Ala Leu				
145				

<210> 407

<211> 1020

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) .. (997)

<223> RXC01656

<400> 407

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atctaccgct agtccacttt gtggcggttg atcatctgtc atg acc gaa act caa 115
Met Thr Glu Thr Gln
1 5

gaa act tac caa gca acc act cgt gtg aag cgc ggc ctt gcc gac atg 163
Glu Thr Tyr Gln Ala Thr Thr Arg Val Lys Arg Gly Leu Ala Asp Met
10 15 20

ctc aag ggt ggt gtg atc atg gat gtg gtc acc cct gaa caa gcg cgc 211
Leu Lys Gly Gly Val Ile Met Asp Val Val Thr Pro Glu Gln Ala Arg
25 30 35

atc gcc gaa gat gca ggt gcc agc gca gtt atg gca ctc gag cgc gtt 259
Ile Ala Glu Asp Ala Gly Ala Ser Ala Val Met Ala Leu Glu Arg Val
40 45 50

ccc gcc gat atc cgt tct cag ggc ggc gtt gct cgc atg agt gat cct 307
Pro Ala Asp Ile Arg Ser Gln Gly Gly Val Ala Arg Met Ser Asp Pro
55 60 65

gac ctg atc gaa gga atc gtc aat gcg gtc tcc atc ccg gtc atg gcg 355
Asp Leu Ile Glu Gly Ile Val Asn Ala Val Ser Ile Pro Val Met Ala
70 75 80 85

aaa gct cgc atc ggt cac ttc gtg gaa gct cag gtt ctg gaa gct ctc 403
Lys Ala Arg Ile Gly His Phe Val Glu Ala Gln Val Leu Glu Ala Leu
90 95 100

ggt gtt gat ttc atc gac gag tcc gaa gtt ctc agc cct gcc gac tac 451
Gly Val Asp Phe Ile Asp Glu Ser Glu Val Leu Ser Pro Ala Asp Tyr
105 110 115

acg cac cac atc aac aag tgg aag ttc gac gtt cct ttc gtc tgt ggc 499
Thr His His Ile Asn Lys Trp Lys Phe Asp Val Pro Phe Val Cys Gly
120 125 130

gcg acc aac ctc ggc gaa gct ttg cga cgc atc acc gaa ggc gct gca 547
Ala Thr Asn Leu Gly Glu Ala Leu Arg Arg Ile Thr Glu Gly Ala Ala
135 140 145

atg atc cgt tcc aag ggc gaa gcc ggc acc ggc gat gtc tct gaa gct 595
Met Ile Arg Ser Lys Gly Glu Ala Gly Thr Gly Asp Val Ser Glu Ala
150 155 160 165

gtc cgt cac ctg cgc acc atc cgc ggc gac atc aat cgc ctg cgc tcc 643
Val Arg His Leu Arg Thr Ile Arg Gly Asp Ile Asn Arg Leu Arg Ser
170 175 180

ctg gat gag gat gaa ctc ttc gtc gcc gcc aag gaa ttc cag gca cca 691
Leu Asp Glu Asp Glu Leu Phe Val Ala Ala Lys Glu Phe Gln Ala Pro
185 190 195

tac gac ctg gtc cgc gaa gtc gcc tcc acc ggc aag ctc cct gtg gtc 739
Tyr Asp Leu Val Arg Glu Val Ala Ser Thr Gly Lys Leu Pro Val Val
200 205 210

acc ttc gtt gca ggt ggc gtc gca acc cca gcc gac gct gca ctc gtg 787

Thr Phe Val Ala Gly Gly Val Ala Thr Pro Ala Asp Ala Ala Leu Val
 215 220 225
 cgc caa atg ggc gcc gaa ggc gtc ttt gtc ggc tcc ggc atc ttc aaa 835
 Arg Gln Met Gly Ala Glu Gly Val Phe Val Gly Ser Gly Ile Phe Lys
 230 235 240 245
 tcc ggc aat cca gcc gcc cgc gcc gca gcg atc gtc aag gct gca acg 883
 Ser Gly Asn Pro Ala Ala Arg Ala Ala Ile Val Lys Ala Ala Thr
 250 255 260
 ctt ttc gac gac ccc tcc gtc att gcc gac gta tcc cgc ggc ctg ggt 931
 Leu Phe Asp Asp Pro Ser Val Ile Ala Asp Val Ser Arg Gly Leu Gly
 265 270 275
 gaa gcc atg gtg ggc atc aac gta tcc gac gtt cca gca cca cac cga 979
 Glu Ala Met Val Gly Ile Asn Val Ser Asp Val Pro Ala Pro His Arg
 280 285 290
 ctc gcc gag cgc ggc tgg tgatcggttg agtttttagct ctc
 1020
 Leu Ala Glu Arg Gly Trp
 295

<210> 408

<211> 299

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 408

Met Thr Glu Thr Gln Glu Thr Tyr Gln Ala Thr Thr Arg Val Lys Arg
 1 5 10 15
 Gly Leu Ala Asp Met Leu Lys Gly Gly Val Ile Met Asp Val Val Thr
 20 25 30
 Pro Glu Gln Ala Arg Ile Ala Glu Asp Ala Gly Ala Ser Ala Val Met
 35 40 45
 Ala Leu Glu Arg Val Pro Ala Asp Ile Arg Ser Gln Gly Gly Val Ala
 50 55 60
 Arg Met Ser Asp Pro Asp Leu Ile Glu Gly Ile Val Asn Ala Val Ser
 65 70 75 80
 Ile Pro Val Met Ala Lys Ala Arg Ile Gly His Phe Val Glu Ala Gln
 85 90 95
 Val Leu Glu Ala Leu Gly Val Asp Phe Ile Asp Glu Ser Glu Val Leu
 100 105 110
 Ser Pro Ala Asp Tyr Thr His His Ile Asn Lys Trp Lys Phe Asp Val
 115 120 125
 Pro Phe Val Cys Gly Ala Thr Asn Leu Gly Glu Ala Leu Arg Arg Ile
 130 135 140
 Thr Glu Gly Ala Ala Met Ile Arg Ser Lys Gly Glu Ala Gly Thr Gly
 145 150 155 160

ctc gca acc ggc ccg ttt gat	cca ttc atg ctt cgc ctt aaa gta gcg	355
Leu Ala Thr Gly Pro Phe Asp	Pro Phe Met Leu Arg Leu Lys Val Ala	
70	80	85
gcg ttg gtg ggt atg gtt ctt	ggc tca ccc gtg tgg ctg agc cag ctg	403
Ala Leu Val Gly Met Val Leu	Gly Ser Pro Val Trp Leu Ser Gln Leu	
90	95	100
tgg ggc ttt atc acc cca ggt	ttg atg aag aat gag cgc cgt tac acc	451
Trp Gly Phe Ile Thr Pro Gly	Leu Met Lys Asn Glu Arg Arg Tyr Thr	
105	110	115
gca atc ttc gtc acg att gct	ggt ttg atg aag aat gag cgc cgt tac acc	499
Ala Ile Phe Val Thr Ile Ala	Val Val Leu Phe Val Gly Gly Ala Val	
120	125	130
ctt gcg tac ttc gtc gtt gca	tat ggt ttg gag ttc ctc ctt acc att	547
Leu Ala Tyr Phe Val Val Ala	Tyr Gly Leu Glu Phe Leu Leu Thr Ile	
135	140	145
ggt gga gac acc cag gca gcg gcc	ctg act ggt gat aag tac ttc gga	595
Gly Gly Asp Thr Gln Ala Ala	Ala Leu Thr Gly Asp Lys Tyr Phe Gly	
150	155	160
ttc ttg ctc gcg ttg ttg gcg	att ttc ggc gtg agc ttc gaa gtt cca	643
Phe Leu Leu Ala Leu Leu Ala	Ile Phe Gly Val Ser Phe Glu Val Pro	
170	175	180
ctg gtg atc ggc atg ctc aac	att gtg ggt atc ttg cct tac gat gcc	691
Leu Val Ile Gly Met Leu Asn	Ile Val Gly Ile Leu Pro Tyr Asp Ala	
185	190	195
att aaa gat aag cga cgc atg	atc atc atg att ttg ttc gtg ttc gct	739
Ile Lys Asp Lys Arg Arg Met	Ile Ile Met Ile Leu Phe Val Phe Ala	
200	205	210
gct ttc atg aca ccc ggc cag	gat cct ttc acc atg ttg gtg ttg gcg	787
Ala Phe Met Thr Pro Gly Gln	Asp Pro Phe Thr Met Leu Val Leu Ala	
215	220	225
ctt tca ctc acc gtt ctg gta	gag ctt gcc ctg cag ttc tgt cgc ttc	835
Leu Ser Leu Thr Val Leu Val	Glu Leu Ala Leu Gln Phe Cys Arg Phe	
230	235	240
aac gac aaa cgc cgg gac aag	aag cgc cca gaa tgg ctt gat ggc gat	883
Asn Asp Lys Arg Arg Asp Lys	Lys Arg Pro Glu Trp Leu Asp Gly Asp	
250	255	260
gac ctc tct gca tca cca ctg	gat act tct gct ggt gga gaa gat gct	931
Asp Leu Ser Ala Ser Pro Leu	Asp Thr Ser Ala Gly Gly Glu Asp Ala	
265	270	275
cca agc cca gtc gaa acc cca	gag gcg gtg gag cct tcg cgg atg ctg	979
Pro Ser Pro Val Glu Thr Pro	Glu Ala Val Glu Pro Ser Arg Met Leu	
280	285	290
aac cca agt ggg gag gcg tcg	ata agc tat aaa ccc ggg cgc gcc gac	1027
Asn Pro Ser Gly Glu Ala Ser	Ile Ser Tyr Lys Pro Gly Arg Ala Asp	
295	300	305

ttc ggt gac gtg ctc tagggcctag ccaggtaccc tta
 1065
 Phe Gly Asp Val Leu
 310

<210> 410

<211> 314

<212> PRT

<213> Corynebacterium glutamicum

<400> 410

Met Ser Ile Val Glu His Ile Lys Glu Phe Arg Arg Arg Leu Leu Ile
 1 5 10 15

Ala Leu Ala Gly Ile Leu Val Gly Thr Ile Ile Gly Phe Ile Trp Tyr
 20 25 30

Asp Phe Ser Phe Trp Gln Ile Pro Thr Leu Gly Glu Leu Leu Arg Asp
 35 40 45

Pro Tyr Cys Ser Leu Pro Ala Glu Ser Arg Trp Ala Met Ser Asp Ser
 50 55 60

Glu Glu Cys Arg Leu Leu Ala Thr Gly Pro Phe Asp Pro Phe Met Leu
 65 70 75 80

Arg Leu Lys Val Ala Ala Leu Val Gly Met Val Leu Gly Ser Pro Val
 85 90 95

Trp Leu Ser Gln Leu Trp Gly Phe Ile Thr Pro Gly Leu Met Lys Asn
 100 105 110

Glu Arg Arg Tyr Thr Ala Ile Phe Val Thr Ile Ala Val Val Leu Phe
 115 120 125

Val Gly Gly Ala Val Leu Ala Tyr Phe Val Val Ala Tyr Gly Leu Glu
 130 135 140

Phe Leu Leu Thr Ile Gly Gly Asp Thr Gln Ala Ala Ala Leu Thr Gly
 145 150 155 160

Asp Lys Tyr Phe Gly Phe Leu Leu Ala Leu Leu Ala Ile Phe Gly Val
 165 170 175

Ser Phe Glu Val Pro Leu Val Ile Gly Met Leu Asn Ile Val Gly Ile
 180 185 190

Leu Pro Tyr Asp Ala Ile Lys Asp Lys Arg Arg Met Ile Ile Met Ile
 195 200 205

Leu Phe Val Phe Ala Ala Phe Met Thr Pro Gly Gln Asp Pro Phe Thr
 210 215 220

Met Leu Val Leu Ala Leu Ser Leu Thr Val Leu Val Glu Leu Ala Leu
 225 230 235 240

Gln Phe Cys Arg Phe Asn Asp Lys Arg Arg Asp Lys Lys Arg Pro Glu
 245 250 255

Trp Leu Asp Gly Asp Asp Leu Ser Ala Ser Pro Leu Asp Thr Ser Ala

260	265	270
Gly Gly Glu Asp Ala Pro Ser Pro Val Glu Thr Pro Glu Ala Val Glu		
275	280	285
Pro Ser Arg Met Leu Asn Pro Ser Gly Glu Ala Ser Ile Ser Tyr Lys		
290	295	300
Pro Gly Arg Ala Asp Phe Gly Asp Val Leu		
305	310	

<210> 411
 <211> 1413
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1390)
 <223> RXA02458

<400> 411
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 ggtggtgaac aaaacaaatc ttccacacat aacatctatt atg gtc ttt gtg tct 115
 Met Val Phe Val Ser 5
 gat tcg tct atc tct ttg ccc att tgg gat gct ccg cgc gct cgc ggc 163
 Asp Ser Ser Ile Ser Leu Pro Ile Trp Asp Ala Pro Arg Ala Arg Gly 20
 10 15
 ccc ata gtc tcg gac ctg gct atc cct ggt tcc aag tcg atc acc aac 211
 Pro Ile Val Ser Asp Leu Ala Ile Pro Gly Ser Lys Ser Ile Thr Asn 35
 25 30
 cgc gcc ctc atc ttg gct gcg ctc gca tca act cca tcc acc atc att 259
 Arg Ala Leu Ile Leu Ala Ala Leu Ala Ser Thr Pro Ser Thr Ile Ile 50
 40 45
 gat gtc ctt cgt agt cgt gat acc gat ctc atg act gat ggt cta cgc 307
 Asp Val Leu Arg Ser Arg Asp Thr Asp Leu Met Thr Asp Gly Leu Arg 65
 55 60
 agc ctc gga atc acc att act gaa gag gca gtc gat cgc tac cgc gtt 355
 Ser Leu Gly Ile Thr Ile Thr Glu Glu Ala Val Asp Arg Tyr Arg Val 85
 70 75 80
 gag ccc gga cag ttg tct gct ggc tcc gtt gag tgt ggt ctt gct ggt 403
 Glu Pro Gly Gln Leu Ser Ala Gly Ser Val Glu Cys Gly Leu Ala Gly 100
 90 95
 acg gtc atg cgc ttt ttg cct cct gtt gct gct ttc gct gat ggt cct 451
 Thr Val Met Arg Phe Leu Pro Pro Val Ala Ala Phe Ala Asp Gly Pro 115
 105 110
 gtt cat ttt gat ggc gat cct caa gct cgt gtt cgt ccg atg acc agc 499
 Val His Phe Asp Gly Asp Pro Gln Ala Arg Val Arg Pro Met Thr Ser 130
 120 125 130

att ttg gat gcg ctg cgt tcg ctt ggt gtg gag gta gac aac aac aat	547
Ile Leu Asp Ala Leu Arg Ser Leu Gly Val Glu Val Asp Asn Asn Asn	
135 140 145	
ctg cct ttc act gtt aat gct ggt gag gtc cct gag ggt ggc gtg gtt	595
Leu Pro Phe Thr Val Asn Ala Gly Glu Val Pro Glu Gly Gly Val Val	
150 155 160 165	
gag att gat gct tcc ggc tca tct cag ttt gtt tct ggt ctt ttg ctt	643
Glu Ile Asp Ala Ser Gly Ser Ser Gln Phe Val Ser Gly Leu Leu Leu	
170 175 180	
tca gcg cct cgt ttt aaa aat ggc gtc acc gtt aag cac gtc ggt ggt	691
Ser Ala Pro Arg Phe Lys Asn Gly Val Thr Val Lys His Val Gly Gly	
185 190 195	
cgt ctg ccg agc atg ccg cat att gag atg acc gtc gat atg ctt cgt	739
Arg Leu Pro Ser Met Pro His Ile Glu Met Thr Val Asp Met Leu Arg	
200 205 210	
tcc gca ggc att gag atc gaa gag tca gaa aat cag tgg gtt gtt cat	787
Ser Ala Gly Ile Glu Ile Glu Glu Ser Glu Asn Gln Trp Val Val His	
215 220 225	
cct ggt gag atc ttg ggt cgg acc tgg cgc att gag ccg gat ctt tct	835
Pro Gly Glu Ile Leu Gly Arg Thr Trp Arg Ile Glu Pro Asp Leu Ser	
230 235 240 245	
aat gcg act ccg ttc cta gct gcc gct gcg gtc act ggt gga acc atc	883
Asn Ala Thr Pro Phe Leu Ala Ala Ala Val Thr Gly Gly Thr Ile	
250 255 260	
aag att aac cac tgg cca atc aaa act act cag cct ggc gat gct att	931
Lys Ile Asn His Trp Pro Ile Lys Thr Thr Gln Pro Gly Asp Ala Ile	
265 270 275	
cgt tcg att ctt gag cgc atg ggc tgc gaa gtt gag ctg gtt gct cag	979
Arg Ser Ile Leu Glu Arg Met Gly Cys Glu Val Glu Leu Val Ala Gln	
280 285 290	
ggt gaa ggt tac gat ctg tcg gtg act ggt ccg gtt gct ctc aag ggc	
1027	
Gly Glu Gly Tyr Asp Leu Ser Val Thr Gly Pro Val Ala Leu Lys Gly	
295 300 305	
att gag atc gat atg tcc gat atc ggt gag ttg acc cct acc gtg gcg	
1075	
Ile Glu Ile Asp Met Ser Asp Ile Gly Glu Leu Thr Pro Thr Val Ala	
310 315 320 325	
gcg ttg gct gcg ttg gcg tcg aca gag tct cgt ttg acc ggt att gct	
1123	
Ala Leu Ala Ala Leu Ala Ser Thr Glu Ser Arg Leu Thr Gly Ile Ala	
330 335 340	
cat ctt cgt ggc cat gag acg gat cgt ttg gct gcg ttg act gcg gag	
1171	
His Leu Arg Gly His Glu Thr Asp Arg Leu Ala Ala Leu Thr Ala Glu	
345 350 355	

atc aac aaa ctt ggt gga aag tgc act gag ctt aag gat ggt ctg ttg
 1219
 Ile Asn Lys Leu Gly Gly Lys Cys Thr Glu Leu Lys Asp Gly Leu Leu
 360 365 370

att gag cct gcg tcg ctg cac ggt ggt gtg tgg cat tca tat gct gat
 1267
 Ile Glu Pro Ala Ser Leu His Gly Gly Val Trp His Ser Tyr Ala Asp
 375 380 385

cac cgt atg gct act gct ggt gcg atc att ggc ctc gcg gtt gat ggc
 1315
 His Arg Met Ala Thr Ala Gly Ala Ile Ile Gly Leu Ala Val Asp Gly
 390 395 400 405

gtt cag gtt gaa gac att aag acc act tcc aaa act ttc cct ggt ttt
 1363
 Val Gln Val Glu Asp Ile Lys Thr Thr Ser Lys Thr Phe Pro Gly Phe
 410 415 420

gaa aat gtt tgg gag gag atg gtt ggc tagacgcagc tatgacgaat
 1410
 Glu Asn Val Trp Glu Glu Met Val Gly
 425 430

ccg
 1413

<210> 412
 <211> 430
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 412
 Met Val Phe Val Ser Asp Ser Ser Ile Ser Leu Pro Ile Trp Asp Ala
 1 5 10 15

Pro Arg Ala Arg Gly Pro Ile Val Ser Asp Leu Ala Ile Pro Gly Ser
 20 25 30

Lys Ser Ile Thr Asn Arg Ala Leu Ile Leu Ala Ala Leu Ala Ser Thr
 35 40 45

Pro Ser Thr Ile Ile Asp Val Leu Arg Ser Arg Asp Thr Asp Leu Met
 50 55 60

Thr Asp Gly Leu Arg Ser Leu Gly Ile Thr Ile Thr Glu Glu Ala Val
 65 70 75 80

Asp Arg Tyr Arg Val Glu Pro Gly Gln Leu Ser Ala Gly Ser Val Glu
 85 90 95

Cys Gly Leu Ala Gly Thr Val Met Arg Phe Leu Pro Pro Val Ala Ala
 100 105 110

Phe Ala Asp Gly Pro Val His Phe Asp Gly Asp Pro Gln Ala Arg Val
 115 120 125

Arg Pro Met Thr Ser Ile Leu Asp Ala Leu Arg Ser Leu Gly Val Glu
 130 135 140

Val Asp Asn Asn Asn Leu Pro Phe Thr Val Asn Ala Gly Glu Val Pro
 145 150 155 160
 Glu Gly Gly Val Val Glu Ile Asp Ala Ser Gly Ser Ser Gln Phe Val
 165 170 175
 Ser Gly Leu Leu Leu Ser Ala Pro Arg Phe Lys Asn Gly Val Thr Val
 180 185 190
 Lys His Val Gly Gly Arg Leu Pro Ser Met Pro His Ile Glu Met Thr
 195 200 205
 Val Asp Met Leu Arg Ser Ala Gly Ile Glu Ile Glu Glu Ser Glu Asn
 210 215 220
 Gln Trp Val Val His Pro Gly Glu Ile Leu Gly Arg Thr Trp Arg Ile
 225 230 235 240
 Glu Pro Asp Leu Ser Asn Ala Thr Pro Phe Leu Ala Ala Ala Ala Val
 245 250 255
 Thr Gly Gly Thr Ile Lys Ile Asn His Trp Pro Ile Lys Thr Thr Gln
 260 265 270
 Pro Gly Asp Ala Ile Arg Ser Ile Leu Glu Arg Met Gly Cys Glu Val
 275 280 285
 Glu Leu Val Ala Gln Gly Glu Gly Tyr Asp Leu Ser Val Thr Gly Pro
 290 295 300
 Val Ala Leu Lys Gly Ile Glu Ile Asp Met Ser Asp Ile Gly Glu Leu
 305 310 315 320
 Thr Pro Thr Val Ala Ala Leu Ala Ala Leu Ala Ser Thr Glu Ser Arg
 325 330 335
 Leu Thr Gly Ile Ala His Leu Arg Gly His Glu Thr Asp Arg Leu Ala
 340 345 350
 Ala Leu Thr Ala Glu Ile Asn Lys Leu Gly Gly Lys Cys Thr Glu Leu
 355 360 365
 Lys Asp Gly Leu Leu Ile Glu Pro Ala Ser Leu His Gly Gly Val Trp
 370 375 380
 His Ser Tyr Ala Asp His Arg Met Ala Thr Ala Gly Ala Ile Ile Gly
 385 390 395 400
 Leu Ala Val Asp Gly Val Gln Val Glu Asp Ile Lys Thr Thr Ser Lys
 405 410 415
 Thr Phe Pro Gly Phe Glu Asn Val Trp Glu Glu Met Val Gly
 420 425 430

<210> 413

<211> 1266

<212> DNA

<213> *Corynebacterium glutamicum*

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agggaaattt cccaggatga accaaatccg aaaccgcgcg atg gag ccc gtc tac																115
Met Glu Pro Val Tyr																5
1																
gta aag cgc cgc caa cgg ttt att gcc gtg acg atc gct tca ctc atc																163
Val Lys Arg Arg Gln Arg Phe Ile Ala Val Thr Ile Ala Ser Leu Ile																20
10 15																
ctc att atc ggt gcc atc atc tat atc ggt gta gcc acc tca aac cgg																211
Leu Ile Ile Ile Gly Ala Ile Ile Tyr Ile Gly Val Ala Thr Ser Asn Arg																25 30 35
25																
acg cca cat gac tat gaa ggc tcc gga aac ggt gtg gtt cag ctg gtc																259
Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly Val Val Gln Leu Val																40 45 50
40																
gaa atc cct gaa ggt tcc tcc ata tca gag ctc ggc cca gag ttg gaa																307
Glu Ile Pro Glu Gly Ser Ser Ile Ser Glu Leu Gly Pro Glu Leu Glu																55 60 65
55 60 65																
gaa cga gat atc gtg gcc acc aac tca gcg ttc caa aca gcg gcc agc																355
Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe Gln Thr Ala Ala Ser																70 75 80 85
70 75 80 85																
aac aac ccc aac gcg ggt agt gta cag cca ggt ttc tac cgt ctg cag																403
Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly Phe Tyr Arg Leu Gln																90 95 100
90 95 100																
gaa caa atg aac gca gca gct gca gtg tcg gct ctg ctt gat cca gac																451
Glu Gln Met Asn Ala Ala Ala Ala Val Ser Ala Leu Leu Asp Pro Asp																105 110 115
105 110 115																
aac cag gtt gat ctc ctc gac att cac ggc ggc gcc acc ttg atg gac																499
Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly Ala Thr Leu Met Asp																120 125 130
120 125 130																
gtc act gtt gtc ggc gga aac acc cgc gcg gga atc tac tcc cag atc																547
Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly Ile Tyr Ser Gln Ile																135 140 145
135 140 145																
gca gcc gtg acc tgc acc gaa ggc tcc gcc aac tgc atc acc gct gag																595
Ala Ala Val Thr Cys Thr Glu Gly Ser Ala Asn Cys Ile Thr Ala Glu																150 155 160 165
150 155 160 165																
gat ttg cag cag gtt gcc tcc acc gtg tcg cct gca gaa ttg ggt gtc																643
Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro Ala Glu Leu Gly Val																170 175 180
170 175 180																
cca gat tgg gca atc gct gct gtg gaa gct cgc gga act gat cca aag																691
Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg Gly Thr Asp Pro Lys																185 190 195
185 190 195																
cgc ctc gaa ggc ctg atc atg cct ggc caa tac gtg gtg gat cca tcc																739

Arg Leu Glu Gly Leu Ile Met Pro Gly Gln Tyr Val Val Asp Pro Ser
 200 205 210
 aac gac gcc cag gga atc ctc acc gat ctg atc acg cga tca gca aac 787
 Asn Asp Ala Gln Gly Ile Leu Thr Asp Leu Ile Thr Arg Ser Ala Asn
 215 220 225
 cat ttc caa gaa acc gac atc acg ggc cgt gca gat gcc atc gga ctt 835
 His Phe Gln Glu Thr Asp Ile Thr Gly Arg Ala Asp Ala Ile Gly Leu
 230 235 240 245
 act cca tat gag ctg gtc acc gca gca tct tta atc gag cgc gaa gca 883
 Thr Pro Tyr Glu Leu Val Thr Ala Ala Ser Leu Ile Glu Arg Glu Ala
 250 255 260
 cca gca gga gat ttt gat aag gtc gcc cgc gtc atc ttg aac cgt ctc 931
 Pro Ala Gly Asp Phe Asp Lys Val Ala Arg Val Ile Leu Asn Arg Leu
 265 270 275
 gcc gag cca atg cag ctg caa ttc gac tcc acc gtc aac tac ggt ctg 979
 Ala Glu Pro Met Gln Leu Gln Phe Asp Ser Thr Val Asn Tyr Gly Leu
 280 285 290
 tct gaa caa gaa gta gca acc acc gac gaa gac cgt cag acc gtc acc
 1027
 Ser Glu Gln Glu Val Ala Thr Thr Asp Glu Asp Arg Gln Thr Val Thr
 295 300 305
 cca tgg aac act tac gcc atg gac ggc ctg cca caa acc ccc atc gcc
 1075
 Pro Trp Asn Thr Tyr Ala Met Asp Gly Leu Pro Gln Thr Pro Ile Ala
 310 315 320 325
 gca gta tcc acc gaa gca ctc caa gcc atg gaa aac cct gca gaa gga
 1123
 Ala Val Ser Thr Glu Ala Leu Gln Ala Met Glu Asn Pro Ala Glu Gly
 330 335 340
 aac tgg ctg tac ttt gtc acc atc gac acc gat gga acc acc gtg ttc
 1171
 Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp Gly Thr Thr Val Phe
 345 350 355
 aac gac acc ttc gaa gag cac gaa gcc gac att gag caa gct ttg aac
 1219
 Asn Asp Thr Phe Glu Glu His Glu Ala Asp Ile Glu Gln Ala Leu Asn
 360 365 370
 agt ggc gtt cta gac agc aac cga taaggatcag cgaataaaaat tgg
 1266
 Ser Gly Val Leu Asp Ser Asn Arg
 375 380

<210> 414

<211> 381

<212> PRT

<213> Corynebacterium glutamicum

<400> 414

Met Glu Pro Val Tyr Val Lys Arg Arg Gln Arg Phe Ile Ala Val Thr

1	5	10	15
Ile Ala Ser Leu Ile Leu Ile Ile Gly Ala Ile Ile Tyr Ile Gly Val	20	25	30
Ala Thr Ser Asn Arg Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly	35	40	45
Val Val Gln Leu Val Glu Ile Pro Glu Gly Ser Ser Ile Ser Glu Leu	50	55	60
Gly Pro Glu Leu Glu Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe	65	70	75
Gln Thr Ala Ala Ser Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly	85	90	95
Phe Tyr Arg Leu Gln Glu Gln Met Asn Ala Ala Ala Ala Val Ser Ala	100	105	110
Leu Leu Asp Pro Asp Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly	115	120	125
Ala Thr Leu Met Asp Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly	130	135	140
Ile Tyr Ser Gln Ile Ala Ala Val Thr Cys Thr Glu Gly Ser Ala Asn	145	150	155
Cys Ile Thr Ala Glu Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro	165	170	175
Ala Glu Leu Gly Val Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg	180	185	190
Gly Thr Asp Pro Lys Arg Leu Glu Gly Leu Ile Met Pro Gly Gln Tyr	195	200	205
Val Val Asp Pro Ser Asn Asp Ala Gln Gly Ile Leu Thr Asp Leu Ile	210	215	220
Thr Arg Ser Ala Asn His Phe Gln Glu Thr Asp Ile Thr Gly Arg Ala	225	230	235
Asp Ala Ile Gly Leu Thr Pro Tyr Glu Leu Val Thr Ala Ala Ser Leu	245	250	255
Ile Glu Arg Glu Ala Pro Ala Gly Asp Phe Asp Lys Val Ala Arg Val	260	265	270
Ile Leu Asn Arg Leu Ala Glu Pro Met Gln Leu Gln Phe Asp Ser Thr	275	280	285
Val Asn Tyr Gly Leu Ser Glu Gln Glu Val Ala Thr Thr Asp Glu Asp	290	295	300
Arg Gln Thr Val Thr Pro Trp Asn Thr Tyr Ala Met Asp Gly Leu Pro	305	310	315
Gln Thr Pro Ile Ala Ala Val Ser Thr Glu Ala Leu Gln Ala Met Glu	325	330	335

Asn Pro Ala Glu Gly Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp
340 345 350

Gly Thr Thr Val Phe Asn Asp Thr Phe Glu Glu His Glu Ala Asp Ile
355 360 365

Glu Gln Ala Leu Asn Ser Gly Val Leu Asp Ser Asn Arg
370 375 380

<210> 415

<211> 644

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(621)

<223> RXN00954

<400> 415

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Ala Val Lys Trp Phe Glu Ala Ser Asn Phe Thr Phe Leu Phe Ala Pro
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gcg tac aac cct gcg att gcg cat gtg cag ccg gtt cgc cag gcg ctg 96
Ala Tyr Asn Pro Ala Ile Ala His Val Gln Pro Val Arg Gln Ala Leu
20 25 30

aaa ttc ccc acc atc ttc aac acg ctt gga cca ttg ctg tcc ccg gcg 144
Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro Leu Leu Ser Pro Ala
35 40 45

cgc ccg gag cgt cag atc atg ggc gtg gcc aat gcc aat cat gga cag 192
Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn Ala Asn His Gly Gln
50 55 60

ctc atc gcc gag gtc ttc cgc gag ttg ggc cgt aca cgc gcg ctt gtt 240
Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg Thr Arg Ala Leu Val
65 70 75 80

gtg cat ggc gca ggc acc gat gag atc gca gtc cac ggc acc acc ttg 288
Val His Gly Ala Gly Thr Asp Glu Ile Ala Val His Gly Thr Thr Leu
85 90 95

gtg tgg gag ctt aaa gaa gac ggc acc atc gag cat tac acc atc gag 336
Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu His Tyr Thr Ile Glu
100 105 110

cct gag gac ctt ggc ctt ggc cgc tac acc ctt gag gat ctc gta ggt 384
Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu Glu Asp Leu Val Gly
115 120 125

ggc ctc ggc act gag aac gcc gaa gct atg cgc gct act ttc gcg ggc 432
Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg Ala Thr Phe Ala Gly
130 135 140

acc ggc cct gat gca cac cgt gat gcg ttg gct gcg tcc gca ggt gcg 480
Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala Ala Ser Ala Gly Ala
145 150 155 160

atg ttc tac ctc aac ggc gat gtc gac tcc ttg aaa gat ggt gca caa 528
 Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu Lys Asp Gly Ala Gln
 165 170 175

aag gcg ctt tcc ttg ctt gcc gac ggc acc acc cag gca tgg ttg gcc 576
 Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr Gln Ala Trp Leu Ala
 180 185 190

aag cac gaa gag atc gat tac tca gaa aag gag tct tcc aat gac 621
 Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu Ser Ser Asn Asp
 195 200 205

tagtaataat ctgcccacag tgt 644

<210> 416
 <211> 207
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 416
 Ala Val Lys Trp Phe Glu Ala Ser Asn Phe Thr Phe Leu Phe Ala Pro
 1 5 10 15

Ala Tyr Asn Pro Ala Ile Ala His Val Gln Pro Val Arg Gln Ala Leu
 20 25 30

Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro Leu Leu Ser Pro Ala
 35 40 45

Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn Ala Asn His Gly Gln
 50 55 60

Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg Thr Arg Ala Leu Val
 65 70 75 80

Val His Gly Ala Gly Thr Asp Glu Ile Ala Val His Gly Thr Thr Leu
 85 90 95

Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu His Tyr Thr Ile Glu
 100 105 110

Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu Glu Asp Leu Val Gly
 115 120 125

Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg Ala Thr Phe Ala Gly
 130 135 140

Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala Ala Ser Ala Gly Ala
 145 150 155 160

Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu Lys Asp Gly Ala Gln
 165 170 175

Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr Gln Ala Trp Leu Ala
 180 185 190

Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu Ser Ser Asn Asp
 195 200 205

<210> 417
 <211> 611
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(588)
 <223> FRXA00954

<400> 417
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 Phe Leu Phe Ala Pro Ala Tyr Asn Pro Ala Ile Ala His Val Gln Pro
 1 5 10 15
 gtt cgc cag gcg ctg aaa ttc ccc acc atc ttc aac acg ctt gga cca 96
 Val Arg Gln Ala Leu Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro
 20 25 30
 ttg ctg tcc ccg gcg cgc ccg gag cgt cag atc atg ggc gtg gcc aat 144
 Leu Leu Ser Pro Ala Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn
 35 40 45
 gcc aat cat gga cag ctc atc gcc gag gtc ttc cgc gag ttg ggc cgt 192
 Ala Asn His Gly Gln Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg
 50 55 60
 aca cgc gcg ctt gtt gtg cat ggc gca ggc acc gat gag atc gca gtc 240
 Thr Arg Ala Leu Val Val His Gly Ala Gly Thr Asp Glu Ile Ala Val
 65 70 75 80
 cac ggc acc acc ttg gtg tgg gag ctt aaa gaa gac ggc acc atc gag 288
 His Gly Thr Thr Leu Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu
 85 90 95
 cat tac acc atc gag cct gag gac ctt ggc ctt ggc cgc tac acc ctt 336
 His Tyr Thr Ile Glu Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu
 100 105 110
 gag gat ctc gta ggt ggc ctc ggc act gag aac gcc gaa gct atg cgc 384
 Glu Asp Leu Val Gly Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg
 115 120 125
 gct act ttc gcg ggc acc ggc cct gat gca cac cgt gat gcg ttg gct 432
 Ala Thr Phe Ala Gly Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala
 130 135 140 -
 gcg tcc gca ggt gcg atg ttc tac ctc aac ggc gat gtc gac tcc ttg 480
 Ala Ser Ala Gly Ala Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu
 145 150 155 160
 aaa gat ggt gca caa aag gcg ctt tcc ttg ctt gcc gac ggc acc acc 528
 Lys Asp Gly Ala Gln Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr
 165 170 175
 cag gca tgg ttg gcc aag cac gaa gag atc gat tac tca gaa aag gag 576
 Gln Ala Trp Leu Ala Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu
 180 185 190
 tct tcc aat gac tagtaataat ctgccacag tgt 611

Ser Ser Asn Asp
195

<210> 418
<211> 196
<212> PRT
<213> Corynebacterium glutamicum

<400> 418
Phe Leu Phe Ala Pro Ala Tyr Asn Pro Ala Ile Ala His Val Gln Pro
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Val Arg Gln Ala Leu Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro
20 25 30
Leu Leu Ser Pro Ala Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn
35 40 45
Ala Asn His Gly Gln Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg
50 55 60
Thr Arg Ala Leu Val Val His Gly Ala Gly Thr Asp Glu Ile Ala Val
65 70 75 80
His Gly Thr Thr Leu Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu
85 90 95
His Tyr Thr Ile Glu Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu
100 105 110
Glu Asp Leu Val Gly Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg
115 120 125
Ala Thr Phe Ala Gly Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala
130 135 140
Ala Ser Ala Gly Ala Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu
145 150 155 160
Lys Asp Gly Ala Gln Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr
165 170 175
Gln Ala Trp Leu Ala Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu
180 185 190

Ser Ser Asn Asp
195

<210> 419
<211> 1677
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1654)
<223> RXN00957

<400> 419

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aaggcttcag ccccaacaatg atttcctcgg taggtgcccc atg agc acg aat ccc 115
Met Ser Thr Asn Pro
1 5
cat gtt ttc tcc cta gat gtc cgc tat cac gag gat gct tct gca ttg 163
His Val Phe Ser Leu Asp Val Arg Tyr His Glu Asp Ala Ser Ala Leu
10 15 20
ttt gcc cac ttg ggt ggc aca acc gca gat gat gca gcc ctg ttg gaa 211
Phe Ala His Leu Gly Gly Thr Thr Ala Asp Asp Ala Ala Leu Leu Glu
25 30 35
agc gct gat atc acc acc aag aat ggt att tct tcc ctc gcg gtg ttg 259
Ser Ala Asp Ile Thr Thr Lys Asn Gly Ile Ser Ser Leu Ala Val Leu
40 45 50
aag agt tcg gtg cgc att acg tgc acg ggc aac acg gtg gta acg cag 307
Lys Ser Ser Val Arg Ile Thr Cys Thr Gly Asn Thr Val Val Thr Gln
55 60 65
ccg ctg acg gac tcg ggt agg gca gtg gtt gcg cgc cta acg cag cag 355
Pro Leu Thr Asp Ser Gly Arg Ala Val Val Ala Arg Leu Thr Gln Gln
70 75 80 85
ctt ggc cag tac aac acc gca gag aac acc ttt agc ttc ccc gcc tca 403
Leu Gly Gln Tyr Asn Thr Ala Glu Asn Thr Phe Ser Phe Pro Ala Ser
90 95 100
gat gcg gtt gat gag cgc gag cgc ctc acc gca cca agc acc atc gaa 451
Asp Ala Val Asp Glu Arg Glu Arg Leu Thr Ala Pro Ser Thr Ile Glu
105 110 115
gtg ctg cgc aag ttg cag ttc gag tcc ggt tac agc gac gcg tcc ctg 499
Val Leu Arg Lys Leu Gln Phe Glu Ser Gly Tyr Ser Asp Ala Ser Leu
120 125 130
cca ctg ctc atg ggc ggt ttc gcg ttt gat ttc tta gaa acc ttt gaa 547
Pro Leu Leu Met Gly Gly Phe Ala Phe Asp Phe Leu Glu Thr Phe Glu
135 140 145
acg ctc ccc gct gtc gag gag agc gtc aac act tac ccc gat tac cag 595
Thr Leu Pro Ala Val Glu Glu Ser Val Asn Thr Tyr Pro Asp Tyr Gln
150 155 160 165
ttc gtc ctc gcg gaa atc gtc ctg gac atc aat cac cag gac cag acc 643
Phe Val Leu Ala Glu Ile Val Leu Asp Ile Asn His Gln Asp Gln Thr
170 175 180
gcc aaa ctc gcc ggc gtc tcc aac gcc cca ggc gag ctc gag gcc gag 691
Ala Lys Leu Ala Gly Val Ser Asn Ala Pro Gly Glu Leu Glu Ala Glu
185 190 195
ctc aac aag ctt tca ttg ctt atc gac gcc gcc ctc ccc gca acc gaa 739
Leu Asn Lys Leu Ser Leu Leu Ile Asp Ala Ala Leu Pro Ala Thr Glu
200 205 210
cac gcc tac caa acc acc cct cac gac ggc gac act ctt cgc gtt gtg 787
His Ala Tyr Gln Thr Thr Pro His Asp Gly Asp Thr Leu Arg Val Val
215 220 225

gct gat att ccc gat gct cag ttc cgc acc cag atc aat gag ctg aaa 835
 Ala Asp Ile Pro Asp Ala Gln Phe Arg Thr Gln Ile Asn Glu Leu Lys
 230 235 240 245

gaa aac att tac aac ggt gac atc tac caa gtt gtc ccg gcg cgc act 883
 Glu Asn Ile Tyr Asn Gly Asp Ile Tyr Gln Val Val Pro Ala Arg Thr
 250 255 260

ttc acc gca cca tgt cct gat gca ttc gct gct tat ctg cag ctg cgt 931
 Phe Thr Ala Pro Cys Pro Asp Ala Phe Ala Ala Tyr Leu Gln Leu Arg
 265 270 275

gcc acc aac ccg tcg ccg tac atg ttc tat atc cgt ggc ctc aac gaa 979
 Ala Thr Asn Pro Ser Pro Tyr Met Phe Tyr Ile Arg Gly Leu Asn Glu
 280 285 290

ggc cgc tcc tat gaa ctt ttt ggc gca tcc cct gag tcc aac ctc aag
 1027
 Gly Arg Ser Tyr Glu Leu Phe Gly Ala Ser Pro Glu Ser Asn Leu Lys
 295 300 305

ttc acc gct gct aac cgt gag ctg cag ctg tac cca atc gca ggt acc
 1075
 Phe Thr Ala Ala Asn Arg Glu Leu Gln Leu Tyr Pro Ile Ala Gly Thr
 310 315 320 325

cgc ccc cgt gga ctc aac cca gat ggc tcc atc aac gat gag cta gat
 1123
 Arg Pro Arg Gly Leu Asn Pro Asp Gly Ser Ile Asn Asp Glu Leu Asp
 330 335 340

atc cgc aat gag ttg gat atg cgc act gat gcc aaa gag atc gcg gag
 1171
 Ile Arg Asn Glu Leu Asp Met Arg Thr Asp Ala Lys Glu Ile Ala Glu
 345 350 355

cac acc atg ctt gtc gat ctc gcc cgc aac gac ctg gcc cgc gtc tcg
 1219
 His Thr Met Leu Val Asp Leu Ala Arg Asn Asp Leu Ala Arg Val Ser
 360 365 370

gtc cca gcg tcg cgc cgg gtt gcg gat ctt ttg cag gtg gat cgc tat
 1267
 Val Pro Ala Ser Arg Arg Val Ala Asp Leu Leu Gln Val Asp Arg Tyr
 375 380 385

tcc cgc gtg atg cac ttg gtg tcc cgt gtg acg gcg acg ttg gac cca
 1315
 Ser Arg Val Met His Leu Val Ser Arg Val Thr Ala Thr Leu Asp Pro
 390 395 400 405

gag ctt gat gct ttg gac gcc tat cgg gcg tgc atg aat atg ggc acg
 1363
 Glu Leu Asp Ala Leu Asp Ala Tyr Arg Ala Cys Met Asn Met Gly Thr
 410 415 420

ttg acc ggc gct ccg aag ttg cgc gct atg gag ctg ttg cgc ggc gtc
 1411
 Leu Thr Gly Ala Pro Lys Leu Arg Ala Met Glu Leu Leu Arg Gly Val
 425 430 435

gaa aag cgc agg cgt ggt tct tat ggt ggg gca gtg ggg tac ctg cgc
 1459
 Glu Lys Arg Arg Arg Gly Ser Tyr Gly Gly Ala Val Gly Tyr Leu Arg
 440 445 450

ggc aat ggc gat atg gat aat tgc att gtt att cgt tcg gcg ttt gtc
 1507
 Gly Asn Gly Asp Met Asp Asn Cys Ile Val Ile Arg Ser Ala Phe Val
 455 460 465

cag gat ggt gtg gct gct gtg cag gct ggt gct ggt gtg gtc cgc gat
 1555
 Gln Asp Gly Val Ala Ala Val Gln Ala Gly Ala Gly Val Val Arg Asp
 470 475 480 485

tct aat cct caa tct gaa gcc gat gag acg ttg cac aag gcg tat gcc
 1603
 Ser Asn Pro Gln Ser Glu Ala Asp Glu Thr Leu His Lys Ala Tyr Ala
 490 495 500

gtg ttg aat gcc att gcg ctt gct gct ggt tcc act ttg gag gtc atc
 1651
 Val Leu Asn Ala Ile Ala Leu Ala Ala Gly Ser Thr Leu Glu Val Ile
 505 510 515

cga tgacacacgt tgttctcatt gat
 1677
 Arg

<210> 420
 <211> 518
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 420
 Met Ser Thr Asn Pro His Val Phe Ser Leu Asp Val Arg Tyr His Glu
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 Asp Ala Ser Ala Leu Phe Ala His Leu Gly Gly Thr Thr Ala Asp Asp
 20 25 30
 Ala Ala Leu Leu Glu Ser Ala Asp Ile Thr Thr Lys Asn Gly Ile Ser
 35 40 45
 Ser Leu Ala Val Leu Lys Ser Ser Val Arg Ile Thr Cys Thr Gly Asn
 50 55 60
 Thr Val Val Thr Gln Pro Leu Thr Asp Ser Gly Arg Ala Val Val Ala
 65 70 75 80
 Arg Leu Thr Gln Gln Leu Gly Gln Tyr Asn Thr Ala Glu Asn Thr Phe
 85 90 95
 Ser Phe Pro Ala Ser Asp Ala Val Asp Glu Arg Glu Arg Leu Thr Ala
 100 105 110
 Pro Ser Thr Ile Glu Val Leu Arg Lys Leu Gln Phe Glu Ser Gly Tyr
 115 120 125

Ser Asp Ala Ser Leu Pro Leu Leu Met Gly Gly Phe Ala Phe Asp Phe
 130 135 140
 Leu Glu Thr Phe Glu Thr Leu Pro Ala Val Glu Glu Ser Val Asn Thr
 145 150 155 160
 Tyr Pro Asp Tyr Gln Phe Val Leu Ala Glu Ile Val Leu Asp Ile Asn
 165 170 175
 His Gln Asp Gln Thr Ala Lys Leu Ala Gly Val Ser Asn Ala Pro Gly
 180 185 190
 Glu Leu Glu Ala Glu Leu Asn Lys Leu Ser Leu Leu Ile Asp Ala Ala
 195 200 205
 Leu Pro Ala Thr Glu His Ala Tyr Gln Thr Thr Pro His Asp Gly Asp
 210 215 220
 Thr Leu Arg Val Val Ala Asp Ile Pro Asp Ala Gln Phe Arg Thr Gln
 225 230 235 240
 Ile Asn Glu Leu Lys Glu Asn Ile Tyr Asn Gly Asp Ile Tyr Gln Val
 245 250 255
 Val Pro Ala Arg Thr Phe Thr Ala Pro Cys Pro Asp Ala Phe Ala Ala
 260 265 270
 Tyr Leu Gln Leu Arg Ala Thr Asn Pro Ser Pro Tyr Met Phe Tyr Ile
 275 280 285
 Arg Gly Leu Asn Glu Gly Arg Ser Tyr Glu Leu Phe Gly Ala Ser Pro
 290 295 300
 Glu Ser Asn Leu Lys Phe Thr Ala Ala Asn Arg Glu Leu Gln Leu Tyr
 305 310 315 320
 Pro Ile Ala Gly Thr Arg Pro Arg Gly Leu Asn Pro Asp Gly Ser Ile
 325 330 335
 Asn Asp Glu Leu Asp Ile Arg Asn Glu Leu Asp Met Arg Thr Asp Ala
 340 345 350
 Lys Glu Ile Ala Glu His Thr Met Leu Val Asp Leu Ala Arg Asn Asp
 355 360 365
 Leu Ala Arg Val Ser Val Pro Ala Ser Arg Arg Val Ala Asp Leu Leu
 370 375 380
 Gln Val Asp Arg Tyr Ser Arg Val Met His Leu Val Ser Arg Val Thr
 385 390 395 400
 Ala Thr Leu Asp Pro Glu Leu Asp Ala Leu Asp Ala Tyr Arg Ala Cys
 405 410 415
 Met Asn Met Gly Thr Leu Thr Gly Ala Pro Lys Leu Arg Ala Met Glu
 420 425 430
 Leu Leu Arg Gly Val Glu Lys Arg Arg Arg Gly Ser Tyr Gly Gly Ala
 435 440 445

Val Gly Tyr Leu Arg Gly Asn Gly Asp Met Asp Asn Cys Ile Val Ile
 450 455 460

Arg Ser Ala Phe Val Gln Asp Gly Val Ala Ala Val Gln Ala Gly Ala
 465 470 475 480

Gly Val Val Arg Asp Ser Asn Pro Gln Ser Glu Ala Asp Glu Thr Leu
 485 490 495

His Lys Ala Tyr Ala Val Leu Asn Ala Ile Ala Leu Ala Ala Gly Ser
 500 505 510

Thr Leu Glu Val Ile Arg
 515

<210> 421
 <211> 1151
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1128)
 <223> FRXA00957

<400> 421
 gat ttc tta gaa acc ttt gaa acg ctc ccc gct gtc gag gag agc gtc 48
 Asp Phe Leu Glu Thr Phe Glu Thr Leu Pro Ala Val Glu Glu Ser Val
 1 5 10 15

aac act tac ccc gat tac cag ttc gtc ctc gcg gaa atc gtc ctg gac 96
 Asn Thr Tyr Pro Asp Tyr Gln Phe Val Leu Ala Glu Ile Val Leu Asp
 20 25 30

atc aat cac cag gac cag acc gcc aaa ctc gcc ggc gtc tcc aac gcc 144
 Ile Asn His Gln Asp Gln Thr Ala Lys Leu Ala Gly Val Ser Asn Ala
 35 40 45

cca ggc gag ctc gag gcc gag ctc aac aag ctt tca ttg ctt atc gac 192
 Pro Gly Glu Leu Glu Ala Glu Leu Asn Lys Leu Ser Leu Leu Ile Asp
 50 55 60

gcc gcc ctc ccc gca acc gaa cac gcc tac caa acc acc cct cac gac 240
 Ala Ala Leu Pro Ala Thr Glu His Ala Tyr Gln Thr Thr Pro His Asp
 65 70 75 80

ggc gac act ctt cgc gtt gtg gct gat att ccc gat gct cag ttc cgc 288
 Gly Asp Thr Leu Arg Val Val Ala Asp Ile Pro Asp Ala Gln Phe Arg
 85 90 95

acc cag atc aat gag ctg aaa gaa aac att tac aac ggt gac atc tac 336
 Thr Gln Ile Asn Glu Leu Lys Glu Asn Ile Tyr Asn Gly Asp Ile Tyr
 100 105 110

caa gtt gtc ccg gcg cgc act ttc acc gca cca tgt cct gat gca ttc 384
 Gln Val Val Pro Ala Arg Thr Phe Thr Ala Pro Cys Pro Asp Ala Phe
 115 120 125

gct gct tat ctg cag ctg cgt gcc acc aac ccg tcg ccg tac atg ttc 432
 Ala Ala Tyr Leu Gln Leu Arg Ala Thr Asn Pro Ser Pro Tyr Met Phe

130	135	140	
tat atc cgt ggc ctc aac gaa ggc cgc tcc tat gaa ctt ttt ggc gca			480
Tyr Ile Arg Gly Leu Asn Glu Gly Arg Ser Tyr Glu Leu Phe Gly Ala			
145	150	155	160
tcc cct gag tcc aac ctc aag ttc acc gct gct aac cgt gag ctg cag			528
Ser Pro Glu Ser Asn Leu Lys Phe Thr Ala Asn Arg Glu Leu Gln			
	165	170	175
ctg tac cca atc gca ggt acc cgc ccc cgt gga ctc aac cca gat ggc			576
Leu Tyr Pro Ile Ala Gly Thr Arg Pro Arg Gly Leu Asn Pro Asp Gly			
	180	185	190
tcc atc aac gat gag cta gat atc cgc aat gag ttg gat atg cgc act			624
Ser Ile Asn Asp Glu Leu Asp Ile Arg Asn Glu Leu Asp Met Arg Thr			
	195	200	205
gat gcc aaa gag atc gcg gag cac acc atg ctt gtc gat ctc gcc cgc			672
Asp Ala Lys Glu Ile Ala Glu His Thr Met Leu Val Asp Leu Ala Arg			
	210	215	220
aac gac ctg gcc cgc gtc tcg gtc cca gcg tcg cgc cgg gtt gcg gat			720
Asn Asp Leu Ala Arg Val Ser Val Pro Ala Ser Arg Arg Val Ala Asp			
	225	230	240
ctt ttg cag gtg gat cgc tat tcc cgc gtg atg cac ttg gtg tcc cgt			768
Leu Leu Gln Val Asp Arg Tyr Ser Arg Val Met His Leu Val Ser Arg			
	245	250	255
gtg acg gcg acg ttg gac cca gag ctt gat gct ttg gac gcc tat cgg			816
Val Thr Ala Thr Leu Asp Pro Glu Leu Asp Ala Leu Asp Ala Tyr Arg			
	260	265	270
gcg tgc atg aat atg ggc acg ttg acc ggc gct ccg aag ttg cgc gct			864
Ala Cys Met Asn Met Gly Thr Leu Thr Gly Ala Pro Lys Leu Arg Ala			
	275	280	285
atg gag ctg ttg cgc ggc gtc gaa aag cgc agg cgt ggt tct tat ggt			912
Met Glu Leu Leu Arg Gly Val Glu Lys Arg Arg Arg Gly Ser Tyr Gly			
	290	295	300
ggg gca gtg ggg tac ctg cgc ggc aat ggc gat atg gat aat tgc att			960
Gly Ala Val Gly Tyr Leu Arg Gly Asn Gly Asp Met Asp Asn Cys Ile			
	305	310	315
ggt att cgt tcg gcg ttt gtc cag gat ggt gtg gct gct gtg cag gct			
1008			
Val Ile Arg Ser Ala Phe Val Gln Asp Gly Val Ala Ala Val Gln Ala			
	325	330	335
ggt gct ggt gtg gtc cgc gat tct aat cct caa tct gaa gcc gat gag			
1056			
Gly Ala Gly Val Val Arg Asp Ser Asn Pro Gln Ser Glu Ala Asp Glu			
	340	345	350
acg ttg cac aag gcg tat gcc gtg ttg aat gcc att gcg ctt gct gct			
1104			
Thr Leu His Lys Ala Tyr Ala Val Leu Asn Ala Ile Ala Leu Ala Ala			
	355	360	365

ggt tcc act ttg gag gtc atc cga tgacacacgt tgttctcatt gat
 1151
 Gly Ser Thr Leu Glu Val Ile Arg
 370 375

<210> 422

<211> 376

<212> PRT

<213> Corynebacterium glutamicum

<400> 422

Asp	Phe	Leu	Glu	Thr	Phe	Glu	Thr	Leu	Pro	Ala	Val	Glu	Glu	Ser	Val
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Asn	Thr	Tyr	Pro	Asp	Tyr	Gln	Phe	Val	Leu	Ala	Glu	Ile	Val	Leu	Asp
			20					25					30		
Ile	Asn	His	Gln	Asp	Gln	Thr	Ala	Lys	Leu	Ala	Gly	Val	Ser	Asn	Ala
		35					40					45			
Pro	Gly	Glu	Leu	Glu	Ala	Glu	Leu	Asn	Lys	Leu	Ser	Leu	Leu	Ile	Asp
	50					55					60				
Ala	Ala	Leu	Pro	Ala	Thr	Glu	His	Ala	Tyr	Gln	Thr	Thr	Pro	His	Asp
	65				70					75					80
Gly	Asp	Thr	Leu	Arg	Val	Val	Ala	Asp	Ile	Pro	Asp	Ala	Gln	Phe	Arg
				85					90					95	
Thr	Gln	Ile	Asn	Glu	Leu	Lys	Glu	Asn	Ile	Tyr	Asn	Gly	Asp	Ile	Tyr
			100					105					110		
Gln	Val	Val	Pro	Ala	Arg	Thr	Phe	Thr	Ala	Pro	Cys	Pro	Asp	Ala	Phe
		115					120					125			
Ala	Ala	Tyr	Leu	Gln	Leu	Arg	Ala	Thr	Asn	Pro	Ser	Pro	Tyr	Met	Phe
		130				135					140				
Tyr	Ile	Arg	Gly	Leu	Asn	Glu	Gly	Arg	Ser	Tyr	Glu	Leu	Phe	Gly	Ala
	145				150					155					160
Ser	Pro	Glu	Ser	Asn	Leu	Lys	Phe	Thr	Ala	Ala	Asn	Arg	Glu	Leu	Gln
				165					170					175	
Leu	Tyr	Pro	Ile	Ala	Gly	Thr	Arg	Pro	Arg	Gly	Leu	Asn	Pro	Asp	Gly
			180					185					190		
Ser	Ile	Asn	Asp	Glu	Leu	Asp	Ile	Arg	Asn	Glu	Leu	Asp	Met	Arg	Thr
		195					200					205			
Asp	Ala	Lys	Glu	Ile	Ala	Glu	His	Thr	Met	Leu	Val	Asp	Leu	Ala	Arg
	210					215					220				
Asn	Asp	Leu	Ala	Arg	Val	Ser	Val	Pro	Ala	Ser	Arg	Arg	Val	Ala	Asp
	225				230					235					240
Leu	Leu	Gln	Val	Asp	Arg	Tyr	Ser	Arg	Val	Met	His	Leu	Val	Ser	Arg
			245						250					255	
Val	Thr	Ala	Thr	Leu	Asp	Pro	Glu	Leu	Asp	Ala	Leu	Asp	Ala	Tyr	Arg

260	265	270
Ala Cys Met Asn Met Gly Thr Leu Thr Gly Ala Pro Lys Leu Arg Ala		
275	280	285
Met Glu Leu Leu Arg Gly Val Glu Lys Arg Arg Arg Gly Ser Tyr Gly		
290	295	300
Gly Ala Val Gly Tyr Leu Arg Gly Asn Gly Asp Met Asp Asn Cys Ile		
305	310	315
Val Ile Arg Ser Ala Phe Val Gln Asp Gly Val Ala Ala Val Gln Ala		
325	330	335
Gly Ala Gly Val Val Arg Asp Ser Asn Pro Gln Ser Glu Ala Asp Glu		
340	345	350
Thr Leu His Lys Ala Tyr Ala Val Leu Asn Ala Ile Ala Leu Ala Ala		
355	360	365
Gly Ser Thr Leu Glu Val Ile Arg		
370	375	

<210> 423

<211> 1068

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1045)

<223> RXA02687

<400> 423

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tggacaccca ccttagttcg gcggggtaag ctgtgtaacc	atg agc gac gca cca	115
	Met Ser Asp Ala Pro	
	1 5	

act gtt gtg gcc tat ttg ggg cct gcc gga acc ttc acc gaa gaa gcc	163
Thr Val Val Ala Tyr Leu Gly Pro Ala Gly Thr Phe Thr Glu Glu Ala	
10 15 20	

ctc tac aaa ttt gcc gac gcc ggc gta ttc ggc gac ggt gag atc gag	211
Leu Tyr Lys Phe Ala Asp Ala Gly Val Phe Gly Asp Gly Glu Ile Glu	
25 30 35	

cag cta cca gcc aaa tcg cca caa gaa gct gtc gac gcc gtc cgc cac	259
Gln Leu Pro Ala Lys Ser Pro Gln Glu Ala Val Asp Ala Val Arg His	
40 45 50	

ggc acc gcc cag ttc gcg gtg gtc gcc atc gaa aac ttc gtc gac ggc	307
Gly Thr Ala Gln Phe Ala Val Val Ala Ile Glu Asn Phe Val Asp Gly	
55 60 65	

ccc gtc acc ccc acc ttc gac gcc ctt gac cag ggc tcc aac gtg caa	355
Pro Val Thr Pro Thr Phe Asp Ala Leu Asp Gln Gly Ser Asn Val Gln	
70 75 80 85	

atc atc gcc gaa gaa gaa ctc gac atc gcc ttt tcc atc atg gtc cgg 403
 Ile Ile Ala Glu Glu Glu Leu Asp Ile Ala Phe Ser Ile Met Val Arg
 90 95 100

cca ggg act tcg ctt gcc gac gtc aaa acc ctc gcc acc cac ccg gtt 451
 Pro Gly Thr Ser Leu Ala Asp Val Lys Thr Leu Ala Thr His Pro Val
 105 110 115

ggg tac caa caa gtg aaa aac tgg atg gca acc acc att ccg gac gcc 499
 Gly Tyr Gln Gln Val Lys Asn Trp Met Ala Thr Thr Ile Pro Asp Ala
 120 125 130

atg tat ctt tca gca agc tcc aac ggc gcc ggc gca caa atg gtt gcc 547
 Met Tyr Leu Ser Ala Ser Ser Asn Gly Ala Gly Ala Gln Met Val Ala
 135 140 145

gaa gga acc gcc gac gca gcc gca gcg ccc tcc cgc gca gcc gaa ctc 595
 Glu Gly Thr Ala Asp Ala Ala Ala Pro Ser Arg Ala Ala Glu Leu
 150 155 160 165

ttc gga ctg gaa cgc ctt gtt gat gat gtc gcc gac gtc cgt ggc gcc 643
 Phe Gly Leu Glu Arg Leu Val Asp Asp Val Ala Asp Val Arg Gly Ala
 170 175 180

cgc acc cgc ttc gtt gct gtc caa gcc caa gca gcc gtt tcc gaa ccg 691
 Arg Thr Arg Phe Val Ala Val Gln Ala Gln Ala Ala Val Ser Glu Pro
 185 190 195

acc ggc cac gac cgc acc tcc gtc att ttc tcc cta ccg aat gtg cca 739
 Thr Gly His Asp Arg Thr Ser Val Ile Phe Ser Leu Pro Asn Val Pro
 200 205 210

ggc agc ctc gtg cgc gcc ctc aac gaa ttc gcc atc cgc ggc gtt gac 787
 Gly Ser Leu Val Arg Ala Leu Asn Glu Phe Ala Ile Arg Gly Val Asp
 215 220 225

ctc acc cgc atc gaa tcc cgc ccc acc cgc aaa gtc ttc gga acc tac 835
 Leu Thr Arg Ile Glu Ser Arg Pro Thr Arg Lys Val Phe Gly Thr Tyr
 230 235 240 245

cgc ttc cac ctg gac ata tcc gga cat atc cgc gat atc ccc gtc gcc 883
 Arg Phe His Leu Asp Ile Ser Gly His Ile Arg Asp Ile Pro Val Ala
 250 255 260

gaa gcc ctc cgc gca ctc cac ctc caa gcc gaa gaa ctc gtc ttc gtc 931
 Glu Ala Leu Arg Ala Leu His Leu Gln Ala Glu Glu Leu Val Phe Val
 265 270 275

ggc tcc tgg ccc tcc aac cgt gcg gaa gac agc acg ccc caa acc gac 979
 Gly Ser Trp Pro Ser Asn Arg Ala Glu Asp Ser Thr Pro Gln Thr Asp
 280 285 290

caa cta gct aag cta cac aag gcg gac gaa tgg gtt cgc gca gca agc
 1027
 Gln Leu Ala Lys Leu His Lys Ala Asp Glu Trp Val Arg Ala Ala Ser
 295 300 305

gaa gga agg aaa ctt aac tagccatggc cggccggatt att
 1068
 Glu Gly Arg Lys Leu Asn
 310 315

<210> 424

<211> 315

<212> PRT

<213> Corynebacterium glutamicum

<400> 424

Met Ser Asp Ala Pro Thr Val Val Ala Tyr Leu Gly Pro Ala Gly Thr
 1 5 10 15

Phe Thr Glu Glu Ala Leu Tyr Lys Phe Ala Asp Ala Gly Val Phe Gly
 20 25 30

Asp Gly Glu Ile Glu Gln Leu Pro Ala Lys Ser Pro Gln Glu Ala Val
 35 40 45

Asp Ala Val Arg His Gly Thr Ala Gln Phe Ala Val Val Ala Ile Glu
 50 55 60

Asn Phe Val Asp Gly Pro Val Thr Pro Thr Phe Asp Ala Leu Asp Gln
 65 70 75 80

Gly Ser Asn Val Gln Ile Ile Ala Glu Glu Glu Leu Asp Ile Ala Phe
 85 90 95

Ser Ile Met Val Arg Pro Gly Thr Ser Leu Ala Asp Val Lys Thr Leu
 100 105 110

Ala Thr His Pro Val Gly Tyr Gln Gln Val Lys Asn Trp Met Ala Thr
 115 120 125

Thr Ile Pro Asp Ala Met Tyr Leu Ser Ala Ser Ser Asn Gly Ala Gly
 130 135 140

Ala Gln Met Val Ala Glu Gly Thr Ala Asp Ala Ala Ala Ala Pro Ser
 145 150 155 160

Arg Ala Ala Glu Leu Phe Gly Leu Glu Arg Leu Val Asp Asp Val Ala
 165 170 175

Asp Val Arg Gly Ala Arg Thr Arg Phe Val Ala Val Gln Ala Gln Ala
 180 185 190

Ala Val Ser Glu Pro Thr Gly His Asp Arg Thr Ser Val Ile Phe Ser
 195 200 205

Leu Pro Asn Val Pro Gly Ser Leu Val Arg Ala Leu Asn Glu Phe Ala
 210 215 220

Ile Arg Gly Val Asp Leu Thr Arg Ile Glu Ser Arg Pro Thr Arg Lys
 225 230 235 240

Val Phe Gly Thr Tyr Arg Phe His Leu Asp Ile Ser Gly His Ile Arg
 245 250 255

Asp Ile Pro Val Ala Glu Ala Leu Arg Ala Leu His Leu Gln Ala Glu
 260 265 270

Glu Leu Val Phe Val Gly Ser Trp Pro Ser Asn Arg Ala Glu Asp Ser
 275 280 285

Thr Pro Gln Thr Asp Gln Leu Ala Lys Leu His Lys Ala Asp Glu Trp
 290 295 300

Val Arg Ala Ala Ser Glu Gly Arg Lys Leu Asn
 305 310 315

<210> 425

<211> 1353

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1330)

<223> RXN01698

<400> 425

cgctagtgcc tgcagttatg tcgctttttg acgtcgaaaa gcaatttttaa aaagcccttg 60

gggtgggctg gatacgtctt ctgcggcctt tcgtgcgata atg cta ggc atg ctt 115
 Met Leu Gly Met Leu
 1 5

cga tgg act aca gca ggt gaa tcc cac ggc cag gcg ctt atc gcc acg 163
 Arg Trp Thr Thr Ala Gly Glu Ser His Gly Gln Ala Leu Ile Ala Thr
 10 15 20

gtt gaa cac atg cca gca ggc gtg ccc gtg act aaa gat gag gtc tcg 211
 Val Glu His Met Pro Ala Gly Val Pro Val Thr Lys Asp Glu Val Ser
 25 30 35

tat caa ttg gcg cgc cga cgc ctt gga tat ggt cgc ggc gct cgc atg 259
 Tyr Gln Leu Ala Arg Arg Arg Leu Gly Tyr Gly Arg Gly Ala Arg Met
 40 45 50

aag ttt gag caa gac gcg ttg acc ttc ctc acc ggc atc cgc cac ggc 307
 Lys Phe Glu Gln Asp Ala Leu Thr Phe Leu Thr Gly Ile Arg His Gly
 55 60 65

ctc act ttg ggt agc ccc atc tca atc atg atc ggc aac act gag tgg 355
 Leu Thr Leu Gly Ser Pro Ile Ser Ile Met Ile Gly Asn Thr Glu Trp
 70 75 80 85

gat aag tgg acc acc atc atg tcc tct gac gct ttg gac atg gaa gac 403
 Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala Leu Asp Met Glu Asp
 90 95 100

cca gat aac gtt gcg gcg atg tct tcg ggt cgg ggc gca aaa ctg act 451
 Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg Gly Ala Lys Leu Thr
 105 110 115

cgt ccg cgt cca ggc cac gct gat tac gca ggc atg ctc aag tac gga 499
 Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly Met Leu Lys Tyr Gly
 120 125 130

ttc gat gat gcc cgc aac gtg ctg gag cgt tct tca gcc cgt gag acg 547
 Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser Ser Ala Arg Glu Thr
 135 140 145

gca gca cgc gtg gca gca gca acc gtt gcg cgt tcc ttc ctg cgt gaa 595
 Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg Ser Phe Leu Arg Glu
 150 155 160 165

acc ttg ggc gtg gaa gtg ctt tcc cac gta att tcc att ggt gcg tcc 643
 Thr Leu Gly Val Glu Val Leu Ser His Val Ile Ser Ile Gly Ala Ser
 170 175 180

gag cct tac act ggc gcg gag cca acc ttt gca gat att caa gca atc 691
 Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala Asp Ile Gln Ala Ile
 185 190 195

gat gat tcc cca gtt cgt gca ttc ggt aaa gac gct gaa gaa tcc atg 739
 Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp Ala Glu Glu Ser Met
 200 205 210

atc gcg gaa atc gag gcc gca aag aaa gcc ggc gat acc ctc ggt ggc 787
 Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly Asp Thr Leu Gly Gly
 215 220 225

atc gtg gaa gtg att gtt gaa ggc ctg ccc atc ggt ttg ggc tca cac 835
 Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile Gly Leu Gly Ser His
 230 235 240 245

att tct ggc gaa gat cgc ctc gat gcg cag atc gca gct gca ctc atg 883
 Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile Ala Ala Ala Leu Met
 250 255 260

ggc att cag gcc atc aag ggc gtg gaa atc ggt gac ggt ttc gaa gaa 931
 Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly Asp Gly Phe Glu Glu
 265 270 275

gct cgt cga cgt ggc tcc gaa gcc cac gat gaa gtg ttc ctg gat gac 979
 Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu Val Phe Leu Asp Asp
 280 285 290

aac ggc gta tac cgc aac acc aac cgt gca ggt ggc ctc gaa ggc ggc
 1027
 Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly Gly Leu Glu Gly Gly
 295 300 305

atg acc aac ggt gaa acc ctg cgc gtt cgt gct ggc atg aag cca att
 1075
 Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala Gly Met Lys Pro Ile
 310 315 320 325

tct act gtg cct cgc gcc ctg aaa acc att gat atg gaa aac ggc aag
 1123
 Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp Met Glu Asn Gly Lys
 330 335 340

gca gca acc gga atc cac cag cgt tcc gac gtg tgc gct gtt cca gcc
 1171
 Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val Cys Ala Val Pro Ala
 345 350 355

gcc ggt gtc gtt gca gaa gca atg gtc acc ctg gtt ctc gcc cgc gca
 1219
 Ala Gly Val Val Ala Glu Ala Met Val Thr Leu Val Leu Ala Arg Ala
 360 365 370

gtc ctg cag aaa ttc ggc ggt gac tcc ctg agc gaa acc aag agc aac
 1267
 Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser Glu Thr Lys Ser Asn
 375 380 385

att gac acc tac ctc aaa aac att gag gaa cga atg aaa ttc gaa ggt
 1315
 Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg Met Lys Phe Glu Gly
 390 395 400 405

tta gag gat gga gcg taatgaagtg aatgatcaaa ttc
 1353
 Leu Glu Asp Gly Ala
 410

<210> 426
 <211> 410
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 426
 Met Leu Gly Met Leu Arg Trp Thr Thr Ala Gly Glu Ser His Gly Gln
 1 5 10 15

Ala Leu Ile Ala Thr Val Glu His Met Pro Ala Gly Val Pro Val Thr
 20 25 30

Lys Asp Glu Val Ser Tyr Gln Leu Ala Arg Arg Arg Leu Gly Tyr Gly
 35 40 45

Arg Gly Ala Arg Met Lys Phe Glu Gln Asp Ala Leu Thr Phe Leu Thr
 50 55 60

Gly Ile Arg His Gly Leu Thr Leu Gly Ser Pro Ile Ser Ile Met Ile
 65 70 75 80

Gly Asn Thr Glu Trp Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala
 85 90 95

Leu Asp Met Glu Asp Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg
 100 105 110

Gly Ala Lys Leu Thr Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly
 115 120 125

Met Leu Lys Tyr Gly Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser
 130 135 140

Ser Ala Arg Glu Thr Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg
 145 150 155 160

Ser Phe Leu Arg Glu Thr Leu Gly Val Glu Val Leu Ser His Val Ile
 165 170 175

Ser Ile Gly Ala Ser Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala
 180 185 190

Asp Ile Gln Ala Ile Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp
 195 200 205

Ala Glu Glu Ser Met Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly
 210 215 220

Asp Thr Leu Gly Gly Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile
 225 230 235 240

Gly Leu Gly Ser His Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile
 245 250 255

Ala Ala Ala Leu Met Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly
 260 265 270

Asp Gly Phe Glu Glu Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu
 275 280 285

Val Phe Leu Asp Asp Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly
 290 295 300

Gly Leu Glu Gly Gly Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala
 305 310 315 320

Gly Met Lys Pro Ile Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp
 325 330 335

Met Glu Asn Gly Lys Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val
 340 345 350

Cys Ala Val Pro Ala Ala Gly Val Val Ala Glu Ala Met Val Thr Leu
 355 360 365

Val Leu Ala Arg Ala Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser
 370 375 380

Glu Thr Lys Ser Asn Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg
 385 390 395 400

Met Lys Phe Glu Gly Leu Glu Asp Gly Ala
 405 410

<210> 427

<211> 1013

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(990)

<223> FRXA01698

<400> 427

ggc aac act gag tgg gat aag tgg acc acc atc atg tcc tct gac gct 48
 Gly Asn Thr Glu Trp Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala
 1 5 10 15

ttg gac atg gaa gac cca gat aac gtt gcg gcg atg tct tcg ggt cgg 96
 Leu Asp Met Glu Asp Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg
 20 25 30

ggc gca aaa ctg act cgt ccg cgt cca ggc cac gct gat tac gca ggc 144
 Gly Ala Lys Leu Thr Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly

35					40					45						
atg	ctc	aag	tac	gga	ttc	gat	gat	gcc	cgc	aac	gtg	ctg	gag	cgt	tct	192
Met	Leu	Lys	Tyr	Gly	Phe	Asp	Asp	Ala	Arg	Asn	Val	Leu	Glu	Arg	Ser	
	50					55					60					
tca	gcc	cgt	gag	acg	gca	gca	cgc	gtg	gca	gca	gca	acc	gtt	gcg	cgt	240
Ser	Ala	Arg	Glu	Thr	Ala	Ala	Arg	Val	Ala	Ala	Ala	Thr	Val	Ala	Arg	
	65				70					75					80	
tcc	ttc	ctg	cgt	gaa	acc	ttg	ggc	gtg	gaa	gtg	ctt	tcc	cac	gta	att	288
Ser	Phe	Leu	Arg	Glu	Thr	Leu	Gly	Val	Glu	Val	Leu	Ser	His	Val	Ile	
				85					90					95		
tcc	att	ggg	gcg	tcc	gag	cct	tac	act	ggc	gcg	gag	cca	acc	ttt	gca	336
Ser	Ile	Gly	Ala	Ser	Glu	Pro	Tyr	Thr	Gly	Ala	Glu	Pro	Thr	Phe	Ala	
			100					105					110			
gat	att	caa	gca	atc	gat	gat	tcc	cca	gtt	cgt	gca	ttc	ggg	aaa	gac	384
Asp	Ile	Gln	Ala	Ile	Asp	Asp	Ser	Pro	Val	Arg	Ala	Phe	Gly	Lys	Asp	
		115					120					125				
gct	gaa	gaa	tcc	atg	atc	gcg	gaa	atc	gag	gcc	gca	aag	aaa	gcc	ggc	432
Ala	Glu	Glu	Ser	Met	Ile	Ala	Glu	Ile	Glu	Ala	Ala	Lys	Lys	Ala	Gly	
	130					135					140					
gat	acc	ctc	ggg	ggc	atc	gtg	gaa	gtg	att	gtt	gaa	ggc	ctg	ccc	atc	480
Asp	Thr	Leu	Gly	Gly	Ile	Val	Glu	Val	Ile	Val	Glu	Gly	Leu	Pro	Ile	
	145				150					155					160	
ggg	ttg	ggc	tca	cac	att	tct	ggc	gaa	gat	cgc	ctc	gat	gcg	cag	atc	528
Gly	Leu	Gly	Ser	His	Ile	Ser	Gly	Glu	Asp	Arg	Leu	Asp	Ala	Gln	Ile	
				165					170					175		
gca	gct	gca	ctc	atg	ggc	att	cag	gcc	atc	aag	ggc	gtg	gaa	atc	ggg	576
Ala	Ala	Ala	Leu	Met	Gly	Ile	Gln	Ala	Ile	Lys	Gly	Val	Glu	Ile	Gly	
			180					185					190			
gac	ggg	ttc	gaa	gaa	gct	cgt	cga	cgt	ggc	tcc	gaa	gcc	cac	gat	gaa	624
Asp	Gly	Phe	Glu	Glu	Ala	Arg	Arg	Arg	Gly	Ser	Glu	Ala	His	Asp	Glu	
		195					200					205				
gtg	ttc	ctg	gat	gac	aac	ggc	gta	tac	cgc	aac	acc	aac	cgt	gca	ggg	672
Val	Phe	Leu	Asp	Asp	Asn	Gly	Val	Tyr	Arg	Asn	Thr	Asn	Arg	Ala	Gly	
	210					215					220					
ggc	ctc	gaa	ggc	ggc	atg	acc	aac	ggg	gaa	acc	ctg	cgc	gtt	cgt	gct	720
Gly	Leu	Glu	Gly	Gly	Met	Thr	Asn	Gly	Glu	Thr	Leu	Arg	Val	Arg	Ala	
	225				230					235					240	
ggc	atg	aag	cca	att	tct	act	gtg	cct	cgc	gcc	ctg	aaa	acc	att	gat	768
Gly	Met	Lys	Pro	Ile	Ser	Thr	Val	Pro	Arg	Ala	Leu	Lys	Thr	Ile	Asp	
				245					250					255		
atg	gaa	aac	ggc	aag	gca	gca	acc	gga	atc	cac	cag	cgt	tcc	gac	gtg	816
Met	Glu	Asn	Gly	Lys	Ala	Ala	Thr	Gly	Ile	His	Gln	Arg	Ser	Asp	Val	
			260					265					270			
tgc	gct	gtt	cca	gcc	gcc	ggg	gtc	gtt	gca	gaa	gca	atg	gtc	acc	ctg	864
Cys	Ala	Val	Pro	Ala	Ala	Gly	Val	Val	Ala	Glu	Ala	Met	Val	Thr	Leu	
		275					280					285				

gtt ctc gcc cgc gca gtc ctg cag aaa ttc ggc ggt gac tcc ctg agc 912
 Val Leu Ala Arg Ala Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser
 290 295 300

gaa acc aag agc aac att gac acc tac ctc aaa aac att gag gaa cga 960
 Glu Thr Lys Ser Asn Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg
 305 310 315 320

atg aaa ttc gaa ggt tta gag gat gga gcg taatgaagtg aatgatcaaa
 1010
 Met Lys Phe Glu Gly Leu Glu Asp Gly Ala
 325 330

ttc
 1013

<210> 428
 <211> 330
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 428
 Gly Asn Thr Glu Trp Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala
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Leu Asp Met Glu Asp Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg
 20 25 30

Gly Ala Lys Leu Thr Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly
 35 40 45

Met Leu Lys Tyr Gly Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser
 50 55 60

Ser Ala Arg Glu Thr Ala Ala Arg Val Ala Ala Thr Val Ala Arg
 65 70 75 80

Ser Phe Leu Arg Glu Thr Leu Gly Val Glu Val Leu Ser His Val Ile
 85 90 95

Ser Ile Gly Ala Ser Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala
 100 105 110

Asp Ile Gln Ala Ile Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp
 115 120 125

Ala Glu Glu Ser Met Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly
 130 135 140

Asp Thr Leu Gly Gly Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile
 145 150 155 160

Gly Leu Gly Ser His Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile
 165 170 175

Ala Ala Ala Leu Met Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly
 180 185 190

Asp Gly Phe Glu Glu Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu

195					200					205					
Val	Phe	Leu	Asp	Asp	Asn	Gly	Val	Tyr	Arg	Asn	Thr	Asn	Arg	Ala	Gly
210						215					220				
Gly	Leu	Glu	Gly	Gly	Met	Thr	Asn	Gly	Glu	Thr	Leu	Arg	Val	Arg	Ala
225					230					235					240
Gly	Met	Lys	Pro	Ile	Ser	Thr	Val	Pro	Arg	Ala	Leu	Lys	Thr	Ile	Asp
				245					250					255	
Met	Glu	Asn	Gly	Lys	Ala	Ala	Thr	Gly	Ile	His	Gln	Arg	Ser	Asp	Val
			260					265					270		
Cys	Ala	Val	Pro	Ala	Ala	Gly	Val	Val	Ala	Glu	Ala	Met	Val	Thr	Leu
		275					280					285			
Val	Leu	Ala	Arg	Ala	Val	Leu	Gln	Lys	Phe	Gly	Gly	Asp	Ser	Leu	Ser
	290					295					300				
Glu	Thr	Lys	Ser	Asn	Ile	Asp	Thr	Tyr	Leu	Lys	Asn	Ile	Glu	Glu	Arg
305					310					315					320
Met	Lys	Phe	Glu	Gly	Leu	Glu	Asp	Gly	Ala						
				325					330						

<210> 429

<211> 906

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(883)

<223> RXA01095

<400> 429

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ataaccttaa acacagcatt ggttggaagg aggttggggc atg gtt gca aca gag 115
                                     Met Val Ala Thr Glu
                                     1 5
aac cgc atg ttg atg gaa atc gct gcg gaa ata tcg gct cgg gaa gca 163
Asn Arg Met Leu Met Glu Ile Ala Ala Glu Ile Ser Ala Arg Glu Ala
                                     10 15 20
acg ctt ggt ttt caa gaa gtc aaa act aaa tct cga tca gca ggt ctc 211
Thr Leu Gly Phe Gln Glu Val Lys Thr Lys Ser Arg Ser Ala Gly Leu
                                     25 30 35
acg gcg gct ttc gat att gct tca gtc ttt ttt tcg tct gga tgt aat 259
Thr Ala Ala Phe Asp Ile Ala Ser Val Phe Phe Ser Ser Gly Cys Asn
                                     40 45 50
gtc gta gtc gcc ttt gat cgt ttt gca tcc aat tgg tct gat cat tcg 307
Val Val Val Ala Phe Asp Arg Phe Ala Ser Asn Trp Ser Asp His Ser
                                     55 60 65
gat cat gtg gac tac gct gca cag gtt gcg ggt ttt ggc gca tca atg 355

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Asp His Val Asp Tyr Ala Ala Gln Val Ala Gly Phe Gly Ala Ser Met
 70 75 80 85
 ctt gca tat acg gtg cgc agg gga cag ttt gat acc gca gta cgc gat 403
 Leu Ala Tyr Thr Val Arg Arg Gly Gln Phe Asp Thr Ala Val Arg Asp
 90 95 100
 atc agg gac atc aaa tct gaa gta gac att ccc att ctg ctt cat gat 451
 Ile Arg Asp Ile Lys Ser Glu Val Asp Ile Pro Ile Leu Leu His Asp
 105 110 115
 ccc atc atc gat ccg tat caa atc cac gaa gcc cgc gtc atg ggc atc 499
 Pro Ile Ile Asp Pro Tyr Gln Ile His Glu Ala Arg Val Met Gly Ile
 120 125 130
 gac gct ctt caa ttc ccc gta tgg gcg atg gaa caa gct cga ctg gaa 547
 Asp Ala Leu Gln Phe Pro Val Trp Ala Met Glu Gln Ala Arg Leu Glu
 135 140 145
 tct ttg gtg gac cgc acc gaa tca ttg ggc atg aca gcc atc gtg tct 595
 Ser Leu Val Asp Arg Thr Glu Ser Leu Gly Met Thr Ala Ile Val Ser
 150 155 160 165
 gtg cga aac cac gaa gaa gcg cat cgt gca gtg gac gca gga gcg aca 643
 Val Arg Asn His Glu Glu Ala His Arg Ala Val Asp Ala Gly Ala Thr
 170 175 180
 gtg gta gca att gat att act ggt tat acc ggc tca ctc act ttg cct 691
 Val Val Ala Ile Asp Ile Thr Gly Tyr Thr Gly Ser Leu Thr Leu Pro
 185 190 195
 gaa gcg ttt tcg ggt atc acc caa ttc atg ccc aaa gag gta gcc cgc 739
 Glu Ala Phe Ser Gly Ile Thr Gln Phe Met Pro Lys Glu Val Ala Arg
 200 205 210
 att gtg ctc gga ggt tgc agc agc cct aaa gaa ctc atg cgg ttt gca 787
 Ile Val Leu Gly Gly Cys Ser Ser Pro Lys Glu Leu Met Arg Phe Ala
 215 220 225
 cga cat tct gca gac gcc atc ttt gtt cca cat gca gac ctc gcc acc 835
 Arg His Ser Ala Asp Ala Ile Phe Val Pro His Ala Asp Leu Ala Thr
 230 235 240 245
 aca aaa tct ctt gtg aca gca ggt atg cat cca gcg tgc cca tcg cgt 883
 Thr Lys Ser Leu Val Thr Ala Gly Met His Pro Ala Cys Pro Ser Arg
 250 255 260
 tgaagaggtg ctctgtggtc agc 906

<210> 430

<211> 261

<212> PRT

<213> Corynebacterium glutamicum

<400> 430

Met Val Ala Thr Glu Asn Arg Met Leu Met Glu Ile Ala Ala Glu Ile
 1 5 10 15

Ser Ala Arg Glu Ala Thr Leu Gly Phe Gln Glu Val Lys Thr Lys Ser
 20 25 30

Arg Ser Ala Gly Leu Thr Ala Ala Phe Asp Ile Ala Ser Val Phe Phe
 35 40 45
 Ser Ser Gly Cys Asn Val Val Val Ala Phe Asp Arg Phe Ala Ser Asn
 50 55 60
 Trp Ser Asp His Ser Asp His Val Asp Tyr Ala Ala Gln Val Ala Gly
 65 70 75 80
 Phe Gly Ala Ser Met Leu Ala Tyr Thr Val Arg Arg Gly Gln Phe Asp
 85 90 95
 Thr Ala Val Arg Asp Ile Arg Asp Ile Lys Ser Glu Val Asp Ile Pro
 100 105 110
 Ile Leu Leu His Asp Pro Ile Ile Asp Pro Tyr Gln Ile His Glu Ala
 115 120 125
 Arg Val Met Gly Ile Asp Ala Leu Gln Phe Pro Val Trp Ala Met Glu
 130 135 140
 Gln Ala Arg Leu Glu Ser Leu Val Asp Arg Thr Glu Ser Leu Gly Met
 145 150 155 160
 Thr Ala Ile Val Ser Val Arg Asn His Glu Glu Ala His Arg Ala Val
 165 170 175
 Asp Ala Gly Ala Thr Val Val Ala Ile Asp Ile Thr Gly Tyr Thr Gly
 180 185 190
 Ser Leu Thr Leu Pro Glu Ala Phe Ser Gly Ile Thr Gln Phe Met Pro
 195 200 205
 Lys Glu Val Ala Arg Ile Val Leu Gly Gly Cys Ser Ser Pro Lys Glu
 210 215 220
 Leu Met Arg Phe Ala Arg His Ser Ala Asp Ala Ile Phe Val Pro His
 225 230 235 240
 Ala Asp Leu Ala Thr Thr Lys Ser Leu Val Thr Ala Gly Met His Pro
 245 250 255
 Ala Cys Pro Ser Arg
 260

<210> 431

<211> 1545

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1522)

<223> RXA00955

<400> 431

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aagcacgaag agatcgatta ctcagaaaag gagtcttcca atg act agt aat aat 115

634

230	235	240	245	
acc agc cag gaa aac gtc gat ctg gca gcc cgc gaa tta gtc tac ggc				883
Thr Ser Gln Glu Asn Val Asp Leu Ala Ala Arg Glu Leu Val Tyr Gly	250	255	260	
ccc aac aaa gtc tgc gga ctc acc tca cca agt gca gca caa acc gct				931
Pro Asn Lys Val Cys Gly Leu Thr Ser Pro Ser Ala Ala Gln Thr Ala	265	270	275	
cgc gca gcg ggt gcg gtc tac ggc ggg ctc atc ttc gaa gag gca tcg				979
Arg Ala Ala Gly Ala Val Tyr Gly Gly Leu Ile Phe Glu Glu Ala Ser	280	285	290	
cca cgc aat gtt tca cgt gaa aca ttg caa aaa atc atc gcc gca gag				
1027				
Pro Arg Asn Val Ser Arg Glu Thr Leu Gln Lys Ile Ile Ala Ala Glu	295	300	305	
ccc aac ctg cgc tac gtc gcg gtc agc cgt cgc acc tcc ggg tac aag				
1075				
Pro Asn Leu Arg Tyr Val Ala Val Ser Arg Arg Thr Ser Gly Tyr Lys	310	315	320	325
gat ttg ctt gtc gac ggc atc ttc gcc gta caa atc cac gcc cca ctg				
1123				
Asp Leu Leu Val Asp Gly Ile Phe Ala Val Gln Ile His Ala Pro Leu	330	335	340	
cag gac agc gtc gaa gca gaa aag gca ttg atc gcc gcc gtt cgt gaa				
1171				
Gln Asp Ser Val Glu Ala Glu Lys Ala Leu Ile Ala Ala Val Arg Glu	345	350	355	
gag gtt gga ccg cag gtc cag gtc tgg cgc gcg atc tcg atg tcc agc				
1219				
Glu Val Gly Pro Gln Val Gln Val Trp Arg Ala Ile Ser Met Ser Ser	360	365	370	
ccc ttg ggg gct gaa gtg gca gct gcg gtg gag ggt gac gtc gat aag				
1267				
Pro Leu Gly Ala Glu Val Ala Ala Ala Val Glu Gly Asp Val Asp Lys	375	380	385	
cta att ctt gat gcc cat gaa ggt ggc agc ggg gaa gta ttc gac tgg				
1315				
Leu Ile Leu Asp Ala His Glu Gly Gly Ser Gly Glu Val Phe Asp Trp	390	395	400	405
gct acg gtg ccg gcc gct gtg aag gca aag tct ttg ctc gcg gga ggc				
1363				
Ala Thr Val Pro Ala Ala Val Lys Ala Lys Ser Leu Leu Ala Gly Gly	410	415	420	
atc tct ccg gac aac gct gcg cag gca ctc gct gtg ggc tgc gca ggt				
1411				
Ile Ser Pro Asp Asn Ala Ala Gln Ala Leu Ala Val Gly Cys Ala Gly	425	430	435	
ttg gac atc aac tct ggc gtg gaa tac ccc gcc ggt gca ggc acg tgg				
1459				

Leu Asp Ile Asn Ser Gly Val Glu Tyr Pro Ala Gly Ala Gly Thr Trp
 440 445 450

gct ggg gcg aaa gac gcc ggc gcg ctg ctg aaa att tta gcg acc atc
 1507

Ala Gly Ala Lys Asp Ala Gly Ala Leu Leu Lys Ile Leu Ala Thr Ile
 455 460 465

tcc aca ttc cat tac taaaggttta aataggatca tga

1545

Ser Thr Phe His Tyr

470

<210> 432

<211> 474

<212> PRT

<213> Corynebacterium glutamicum

<400> 432

Met Thr Ser Asn Asn Leu Pro Thr Val Leu Glu Ser Ile Val Glu Gly
 1 5 10 15

Arg Arg Gly His Leu Glu Glu Ile Arg Ala Arg Ile Ala His Val Asp
 20 25 30

Val Asp Ala Leu Pro Lys Ser Thr Arg Ser Leu Phe Asp Ser Leu Asn
 35 40 45

Gln Gly Arg Gly Gly Ala Arg Phe Ile Met Glu Cys Lys Ser Ala Ser
 50 55 60

Pro Ser Leu Gly Met Ile Arg Glu His Tyr Gln Pro Gly Glu Ile Ala
 65 70 75 80

Arg Val Tyr Ser Arg Tyr Ala Ser Gly Ile Ser Val Leu Cys Glu Pro
 85 90 95

Asp Arg Phe Gly Gly Asp Tyr Asp His Leu Ala Thr Val Ala Ala Thr
 100 105 110

Ser His Leu Pro Val Leu Cys Lys Asp Phe Ile Ile Asp Pro Val Gln
 115 120 125

Val His Ala Ala Arg Tyr Phe Gly Ala Asp Ala Ile Leu Leu Met Leu
 130 135 140

Ser Val Leu Asp Asp Glu Glu Tyr Ala Ala Leu Ala Ala Glu Ala Ala
 145 150 155 160

Arg Phe Asp Leu Asp Ile Leu Thr Glu Val Ile Asp Glu Glu Glu Val
 165 170 175

Ala Arg Ala Ile Lys Leu Gly Ala Lys Ile Phe Gly Val Asn His Arg
 180 185 190

Asn Leu His Asp Leu Ser Ile Asp Leu Asp Arg Ser Arg Arg Leu Ser
 195 200 205

Lys Leu Ile Pro Ala Asp Ala Val Leu Val Ser Glu Ser Gly Val Arg
 210 215 220

Asp Thr Glu Thr Val Arg Gln Leu Gly Gly His Ser Asn Ala Phe Leu
 225 230 235 240
 Val Gly Ser Gln Leu Thr Ser Gln Glu Asn Val Asp Leu Ala Ala Arg
 245 250 255
 Glu Leu Val Tyr Gly Pro Asn Lys Val Cys Gly Leu Thr Ser Pro Ser
 260 265 270
 Ala Ala Gln Thr Ala Arg Ala Ala Gly Ala Val Tyr Gly Gly Leu Ile
 275 280 285
 Phe Glu Glu Ala Ser Pro Arg Asn Val Ser Arg Glu Thr Leu Gln Lys
 290 295 300
 Ile Ile Ala Ala Glu Pro Asn Leu Arg Tyr Val Ala Val Ser Arg Arg
 305 310 315 320
 Thr Ser Gly Tyr Lys Asp Leu Leu Val Asp Gly Ile Phe Ala Val Gln
 325 330 335
 Ile His Ala Pro Leu Gln Asp Ser Val Glu Ala Glu Lys Ala Leu Ile
 340 345 350
 Ala Ala Val Arg Glu Glu Val Gly Pro Gln Val Gln Val Trp Arg Ala
 355 360 365
 Ile Ser Met Ser Ser Pro Leu Gly Ala Glu Val Ala Ala Ala Val Glu
 370 375 380
 Gly Asp Val Asp Lys Leu Ile Leu Asp Ala His Glu Gly Gly Ser Gly
 385 390 395 400
 Glu Val Phe Asp Trp Ala Thr Val Pro Ala Ala Val Lys Ala Lys Ser
 405 410 415
 Leu Leu Ala Gly Gly Ile Ser Pro Asp Asn Ala Ala Gln Ala Leu Ala
 420 425 430
 Val Gly Cys Ala Gly Leu Asp Ile Asn Ser Gly Val Glu Tyr Pro Ala
 435 440 445
 Gly Ala Gly Thr Trp Ala Gly Ala Lys Asp Ala Gly Ala Leu Leu Lys
 450 455 460
 Ile Leu Ala Thr Ile Ser Thr Phe His Tyr
 465 470

<210> 433

<211> 494

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(471)

<223> RXA02814

<400> 433

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atc ctg gaa cca ctg tgc tca caa ttc gac gcc cca aca gtt cct gaa 96
Ile Leu Glu Pro Leu Cys Ser Gln Phe Asp Ala Pro Thr Val Pro Glu
          20          25          30

ctg acc aaa acc aac gaa atg tgg cac ctc gca aca ccc atc gtt ggc 144
Leu Thr Lys Thr Asn Glu Met Trp His Leu Ala Thr Pro Ile Val Gly
          35          40          45

acc ctc aag tac cca cac atc acc gca cta gaa cta gcc ata cga aca 192
Thr Leu Lys Tyr Pro His Ile Thr Ala Leu Glu Leu Ala Ile Arg Thr
          50          55          60

cac ccc acc ccc gcg atc tgt ggc acc ccc acc gac gcc gcc gaa gcc 240
His Pro Thr Pro Ala Ile Cys Gly Thr Pro Thr Asp Ala Ala Glu Ala
  65          70          75          80

ctc atc atc gaa gcg gaa tcc ccc cga aac ttc tac gcc gga gca gcc 288
Leu Ile Ile Glu Ala Glu Ser Pro Arg Asn Phe Tyr Ala Gly Ala Ala
          85          90          95

ggc tgg tgt gac tcc acc gga gac ggc gaa tac atg gta gcc atc cgc 336
Gly Trp Cys Asp Ser Thr Gly Asp Gly Glu Tyr Met Val Ala Ile Arg
          100          105          110

tgc gcc gaa gta tcc gaa gac gga acc tgg gcc aga gca tgg gca ggc 384
Cys Ala Glu Val Ser Glu Asp Gly Thr Trp Ala Arg Ala Trp Ala Gly
          115          120          125

gga ggc atc gtc gcc gaa tca gac gcc caa gaa gag ttt gat gaa acc 432
Gly Gly Ile Val Ala Glu Ser Asp Ala Gln Glu Glu Phe Asp Glu Thr
          130          135          140

acc gcg aag ctc caa acc atc atg cgc tcg ctt ggt ttg tgagatgtgg 481
Thr Ala Lys Leu Gln Thr Ile Met Arg Ser Leu Gly Leu
          145          150          155

tcttaaaaca ccg 494

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<210> 434

<211> 157

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 434

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Ala Lys Asn Leu Glu Glu His Ser Tyr Val Val Asn His Leu Arg Thr
  1          5          10          15

Ile Leu Glu Pro Leu Cys Ser Gln Phe Asp Ala Pro Thr Val Pro Glu
          20          25          30

Leu Thr Lys Thr Asn Glu Met Trp His Leu Ala Thr Pro Ile Val Gly
          35          40          45

Thr Leu Lys Tyr Pro His Ile Thr Ala Leu Glu Leu Ala Ile Arg Thr
          50          55          60

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His Pro Thr Pro Ala Ile Cys Gly Thr Pro Thr Asp Ala Ala Glu Ala
 65 70 75 80
 Leu Ile Ile Glu Ala Glu Ser Pro Arg Asn Phe Tyr Ala Gly Ala Ala
 85 90 95
 Gly Trp Cys Asp Ser Thr Gly Asp Gly Glu Tyr Met Val Ala Ile Arg
 100 105 110
 Cys Ala Glu Val Ser Glu Asp Gly Thr Trp Ala Arg Ala Trp Ala Gly
 115 120 125
 Gly Gly Ile Val Ala Glu Ser Asp Ala Gln Glu Glu Phe Asp Glu Thr
 130 135 140
 Thr Ala Lys Leu Gln Thr Ile Met Arg Ser Leu Gly Leu
 145 150 155

<210> 435
 <211> 803
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1)..(780)
 <223> RXA00229

<400> 435
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 1 5 10 15
 gac acg ctt ggg tcg cgt gct tcc ggg caa gat tta aat acg ctt ctc 96
 Asp Thr Leu Gly Ser Arg Ala Ser Gly Gln Asp Leu Asn Thr Leu Leu
 20 25 30
 gac gcc gcc ctc tac ctt ggc ttc agc ggc ctg aac atc act cac ccg 144
 Asp Ala Ala Leu Tyr Leu Gly Phe Ser Gly Leu Asn Ile Thr His Pro
 35 40 45
 tac aag caa gca gta tta ccc ctg ctt ggc gaa gtc tcc gaa caa gcc 192
 Tyr Lys Gln Ala Val Leu Pro Leu Leu Gly Glu Val Ser Glu Gln Ala
 50 55 60
 acc caa ctc ggc gca gtg aat act gtc gtt atg gac gcc acc ggc cac 240
 Thr Gln Leu Gly Ala Val Asn Thr Val Val Met Asp Ala Thr Gly His
 65 70 75 80
 acc acc ggc cac aac acc gac gtc tcc gga ttt ggc cgc gga atg gaa 288
 Thr Thr Gly His Asn Thr Asp Val Ser Gly Phe Gly Arg Gly Met Glu
 85 90 95
 gaa ggc ctc ccc aac gcc aag ctc gat tcc gtc gtg cag gtc ggc gcc 336
 Glu Gly Leu Pro Asn Ala Lys Leu Asp Ser Val Val Gln Val Gly Ala
 100 105 110
 ggc ggc gta gaa aac gca gtg gca tac gcc ctg gtc acc cac ggt gtg 384
 Gly Gly Val Glu Asn Ala Val Ala Tyr Ala Leu Val Thr His Gly Val
 115 120 125

cag aaa ctt cag gtc gct gac ctc gac act tcc cgc gcg cag gca ctg 432
 Gln Lys Leu Gln Val Ala Asp Leu Asp Thr Ser Arg Ala Gln Ala Leu
 130 135 140

gca gat gtc atc aac aac gca gtc ggc cgt gaa gcc gtc gtg gga gta 480
 Ala Asp Val Ile Asn Asn Ala Val Gly Arg Glu Ala Val Val Gly Val
 145 150 155 160

gac gcc cgc ggc atc gaa gac gtc atc gcc gcc gcc gac gga gta gtc 528
 Asp Ala Arg Gly Ile Glu Asp Val Ile Ala Ala Ala Asp Gly Val Val
 165 170 175

aac gca acc ccc atg gga atg cca gca cac ccc ggc acc gcc ttt gat 576
 Asn Ala Thr Pro Met Gly Met Pro Ala His Pro Gly Thr Ala Phe Asp
 180 185 190

gtc agc tgc ctc acc aag gat cac tgg gtt ggc gac gtc gtg tac atg 624
 Val Ser Cys Leu Thr Lys Asp His Trp Val Gly Asp Val Val Tyr Met
 195 200 205

ccc atc gaa act gaa ctt ctc aaa gcc gcc cgt gcc ctc ggc tgc gaa 672
 Pro Ile Glu Thr Glu Leu Leu Lys Ala Ala Arg Ala Leu Gly Cys Glu
 210 215 220

acc ctc gac gga acc cgc atg gca atc cac caa gcc gtc gat gcc ttc 720
 Thr Leu Asp Gly Thr Arg Met Ala Ile His Gln Ala Val Asp Ala Phe
 225 230 235 240

cga ctg ttc acc ggc ctc gaa ccc gac gtc tcc cgc atg cgg gaa act 768
 Arg Leu Phe Thr Gly Leu Glu Pro Asp Val Ser Arg Met Arg Glu Thr
 245 250 255

ttc ctg tcc ctc taaaagagtc agtaaacct cga 803
 Phe Leu Ser Leu
 260

<210> 436

<211> 260

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 436

Glu Ala Lys Gly Leu Ala Gln Gly Arg Ala Thr Val Tyr Arg Arg Ile
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Asp Thr Leu Gly Ser Arg Ala Ser Gly Gln Asp Leu Asn Thr Leu Leu
 20 25 30

Asp Ala Ala Leu Tyr Leu Gly Phe Ser Gly Leu Asn Ile Thr His Pro
 35 40 45

Tyr Lys Gln Ala Val Leu Pro Leu Leu Gly Glu Val Ser Glu Gln Ala
 50 55 60

Thr Gln Leu Gly Ala Val Asn Thr Val Val Met Asp Ala Thr Gly His
 65 70 75 80

Thr Thr Gly His Asn Thr Asp Val Ser Gly Phe Gly Arg Gly Met Glu
 85 90 95

Glu Gly Leu Pro Asn Ala Lys Leu Asp Ser Val Val Gln Val Gly Ala
 100 105 110
 Gly Gly Val Glu Asn Ala Val Ala Tyr Ala Leu Val Thr His Gly Val
 115 120 125
 Gln Lys Leu Gln Val Ala Asp Leu Asp Thr Ser Arg Ala Gln Ala Leu
 130 135 140
 Ala Asp Val Ile Asn Asn Ala Val Gly Arg Glu Ala Val Val Gly Val
 145 150 155 160
 Asp Ala Arg Gly Ile Glu Asp Val Ile Ala Ala Ala Asp Gly Val Val
 165 170 175
 Asn Ala Thr Pro Met Gly Met Pro Ala His Pro Gly Thr Ala Phe Asp
 180 185 190
 Val Ser Cys Leu Thr Lys Asp His Trp Val Gly Asp Val Val Tyr Met
 195 200 205
 Pro Ile Glu Thr Glu Leu Leu Lys Ala Ala Arg Ala Leu Gly Cys Glu
 210 215 220
 Thr Leu Asp Gly Thr Arg Met Ala Ile His Gln Ala Val Asp Ala Phe
 225 230 235 240
 Arg Leu Phe Thr Gly Leu Glu Pro Asp Val Ser Arg Met Arg Glu Thr
 245 250 255
 Phe Leu Ser Leu
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 <213> *Corynebacterium glutamicum*

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 <222> (101)..(904)
 <223> RXA02093

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 Met Val Asn Tyr Val 5
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 gac agg gaa aca acc ctg tgc atc tct ctc gct gct cgt cca tcc aac 163
 Asp Arg Glu Thr Thr Leu Cys Ile Ser Leu Ala Ala Arg Pro Ser Asn
 10 15 20
 cat ggt gtt cgt ttc cac aac tgg ctt tac gct gaa ctt gga ttg aac 211
 His Gly Val Arg Phe His Asn Trp Leu Tyr Ala Glu Leu Gly Leu Asn
 25 30 35
 tac ctg tac aag gct gtt gcc cca gca gat atc acc gct gca gtc gca 259

Tyr	Leu	Tyr	Lys	Ala	Val	Ala	Pro	Ala	Asp	Ile	Thr	Ala	Ala	Val	Ala		
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ggt	atc	cgt	ggt	ctg	aac	att	cgc	ggc	gca	ggt	gtc	tcc	atg	cca	tac	307	
Gly	Ile	Arg	Gly	Leu	Asn	Ile	Arg	Gly	Ala	Gly	Val	Ser	Met	Pro	Tyr		
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aag	agc	gat	gtc	atc	cca	ctc	atc	gat	gag	ttg	cat	cct	tcc	gca	gag	355	
Lys	Ser	Asp	Val	Ile	Pro	Leu	Ile	Asp	Glu	Leu	His	Pro	Ser	Ala	Glu		
		70			75				80						85		
cgc	ata	cgt	tct	gtt	aac	acc	atc	gtc	aac	aat	gac	gga	cac	ctt	gtc	403	
Arg	Ile	Arg	Ser	Val	Asn	Thr	Ile	Val	Asn	Asn	Asp	Gly	His	Leu	Val		
				90					95					100			
gga	tac	aac	acc	gac	tac	act	gcg	gtg	tac	cac	ctc	ctt	gaa	gaa	cac	451	
Gly	Tyr	Asn	Thr	Asp	Tyr	Thr	Ala	Val	Tyr	His	Leu	Leu	Glu	Glu	His		
			105					110					115				
cgc	gtg	aac	ccc	aat	gca	cga	gta	gct	atc	aag	gga	tcc	ggc	ggc	atg	499	
Arg	Val	Asn	Pro	Asn	Ala	Arg	Val	Ala	Ile	Lys	Gly	Ser	Gly	Gly	Met		
		120					125					130					
gcc	aat	gct	gtt	gtt	gca	gct	ctt	gct	gag	tat	ggg	ctg	agt	ggc	acc	547	
Ala	Asn	Ala	Val	Val	Ala	Ala	Leu	Ala	Glu	Tyr	Gly	Leu	Ser	Gly	Thr		
		135				140					145						
gtc	gtt	gcc	cgc	aac	cac	acc	acc	ggt	tct	gcg	cta	gct	tcc	cgt	tac	595	
Val	Val	Ala	Arg	Asn	His	Thr	Thr	Gly	Ser	Ala	Leu	Ala	Ser	Arg	Tyr		
		150			155					160					165		
ggt	tgg	gaa	tac	tcc	gca	act	gtt	ccg	gaa	gac	gca	aaa	att	ttg	gtt	643	
Gly	Trp	Glu	Tyr	Ser	Ala	Thr	Val	Pro	Glu	Asp	Ala	Lys	Ile	Leu	Val		
				170				175						180			
aat	gta	acc	cca	atg	gga	atg	aat	gga	cct	gac	caa	gac	gtt	gta	tct	691	
Asn	Val	Thr	Pro	Met	Gly	Met	Asn	Gly	Pro	Asp	Gln	Asp	Val	Val	Ser		
			185					190					195				
ttt	ggt	gag	gat	gaa	gta	gac	cga	gcc	gac	gta	atc	ttt	gac	tgc	gta	739	
Phe	Gly	Glu	Asp	Glu	Val	Asp	Arg	Ala	Asp	Val	Ile	Phe	Asp	Cys	Val		
		200					205					210					
gca	ttc	ccc	gtc	gag	acc	cca	ctg	att	aag	ttg	gcc	aag	gaa	aag	ggt	787	
Ala	Phe	Pro	Val	Glu	Thr	Pro	Leu	Ile	Lys	Leu	Ala	Lys	Glu	Lys	Gly		
		215				220					225						
aag	caa	acc	atc	gac	ggc	gga	gaa	gtt	gcc	gct	ctt	cag	gca	gca	gag	835	
Lys	Gln	Thr	Ile	Asp	Gly	Gly	Glu	Val	Ala	Ala	Leu	Gln	Ala	Ala	Glu		
		230			235				240						245		
cag	ttc	cac	ctc	tac	acc	gga	gtt	ctt	cca	acc	aac	gac	cag	atc	att	883	
Gln	Phe	His	Leu	Tyr	Thr	Gly	Val	Leu	Pro	Thr	Asn	Asp	Gln	Ile	Ile		
			250						255					260			
gct	gcg	gag	gag	ttc	tcc	aag	taaatttctc	tcccctattt	tta							927	
Ala	Ala	Glu	Glu	Phe	Ser	Lys											
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<221> CDS

<222> (101) .. (928)

<223> RXA02791

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                                   Leu Gly Ser His Ile
                                   1 5

act cac cgg gcg gcc gta ctc ggc tca ccc atc gag cat tcc aaa tcc 163
Thr His Arg Ala Ala Val Leu Gly Ser Pro Ile Glu His Ser Lys Ser
                                   10 15 20

cca gtc ctc cac aac acc ggc tat aaa gcc ctc gga ctg gac caa tgg 211
Pro Val Leu His Asn Thr Gly Tyr Lys Ala Leu Gly Leu Asp Gln Trp
                                   25 30 35

gaa tac gac cgc ttt gag tgc acc ggc gac atg ctc ccc ggc atc gtc 259
Glu Tyr Asp Arg Phe Glu Cys Thr Gly Asp Met Leu Pro Gly Ile Val
                                   40 45 50

tcc ggc gct gat gaa acc tac tgc gga ttc tcc gtc acc atg ccg tct 307
Ser Gly Ala Asp Glu Thr Tyr Cys Gly Phe Ser Val Thr Met Pro Ser
                                   55 60 65

aaa ttc gca gct ctt gaa ttc gcc gac gaa gta acc gaa cgc gcc tgc 355
Lys Phe Ala Ala Leu Glu Phe Ala Asp Glu Val Thr Glu Arg Ala Cys
                                   70 75 80 85

gcc atc ggc tcc gca aac acc ttg ctg cgc acg gcc acc gga tgg cgc 403
Ala Ile Gly Ser Ala Asn Thr Leu Leu Arg Thr Ala Thr Gly Trp Arg
                                   90 95 100

gcc gac aac acc gac gtc gac ggc atc agg gga gct ctc ggt gaa ctc 451
Ala Asp Asn Thr Asp Val Asp Gly Ile Arg Gly Ala Leu Gly Glu Leu
                                   105 110 115

ctc ggc ggc gca tca ctg gcc ggc aaa cac gcc atc gtc atc ggc tcc 499
Leu Gly Gly Ala Ser Leu Ala Gly Lys His Ala Ile Val Ile Gly Ser
                                   120 125 130

ggc ggc acc gca cgc ccc gcc atc tgg gca ctc atc gaa gcc ggg gtc 547
Gly Gly Thr Ala Arg Pro Ala Ile Trp Ala Leu Ile Glu Ala Gly Val
                                   135 140 145

gcc cgg atc acg gtg ctc aac cgc tcc gat cgc acc gcc gaa ctg caa 595
Ala Arg Ile Thr Val Leu Asn Arg Ser Asp Arg Thr Ala Glu Leu Gln
                                   150 155 160 165

acg ctt ttc gac gaa acc ccc acc acc ttg gcc tac gcc ccg ctc gag 643
Thr Leu Phe Asp Glu Thr Pro Thr Thr Leu Ala Tyr Ala Pro Leu Glu
                                   170 175 180

cat ctc cac atc gaa gcc gac gtc gta gtc tct aca gtg ccc tcc gca 691
His Leu His Ile Glu Ala Asp Val Val Val Ser Thr Val Pro Ser Ala
                                   185 190 195

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gca atc gca ggc ctc gaa gac acc ctt gcg atc gcc cca gtc ctc gac 739
 Ala Ile Ala Gly Leu Glu Asp Thr Leu Ala Ile Ala Pro Val Leu Asp
 200 205 210

gtc atc tac gac ccc tgg cca aca cca ctc gta gaa gtc aca cga gcc 787
 Val Ile Tyr Asp Pro Trp Pro Thr Pro Leu Val Glu Val Thr Arg Ala
 215 220 225

aaa ggc ctc aaa gct gtc gga ggc cac gtc atg ctg gca cac cag tcc 835
 Lys Gly Leu Lys Ala Val Gly Gly His Val Met Leu Ala His Gln Ser
 230 235 240 245

tac gga cag ttt gaa caa ttc acc gga atg gat gca ccc cgc gat gcc 883
 Tyr Gly Gln Phe Glu Gln Phe Thr Gly Met Asp Ala Pro Arg Asp Ala
 250 255 260

atg cgt gag gct ttg gaa gag tct tta ggc atc tca gaa gaa cac 928
 Met Arg Glu Ala Leu Glu Glu Ser Leu Gly Ile Ser Glu Glu His
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taagtccccg ccacctcctc aac 951

<210> 440

<211> 276

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 440

Leu Gly Ser His Ile Thr His Arg Ala Ala Val Leu Gly Ser Pro Ile
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Glu His Ser Lys Ser Pro Val Leu His Asn Thr Gly Tyr Lys Ala Leu
 20 25 30

Gly Leu Asp Gln Trp Glu Tyr Asp Arg Phe Glu Cys Thr Gly Asp Met
 35 40 45

Leu Pro Gly Ile Val Ser Gly Ala Asp Glu Thr Tyr Cys Gly Phe Ser
 50 55 60

Val Thr Met Pro Ser Lys Phe Ala Ala Leu Glu Phe Ala Asp Glu Val
 65 70 75 80

Thr Glu Arg Ala Cys Ala Ile Gly Ser Ala Asn Thr Leu Leu Arg Thr
 85 90 95

Ala Thr Gly Trp Arg Ala Asp Asn Thr Asp Val Asp Gly Ile Arg Gly
 100 105 110

Ala Leu Gly Glu Leu Leu Gly Gly Ala Ser Leu Ala Gly Lys His Ala
 115 120 125

Ile Val Ile Gly Ser Gly Gly Thr Ala Arg Pro Ala Ile Trp Ala Leu
 130 135 140

Ile Glu Ala Gly Val Ala Arg Ile Thr Val Leu Asn Arg Ser Asp Arg
 145 150 155 160

Thr Ala Glu Leu Gln Thr Leu Phe Asp Glu Thr Pro Thr Thr Leu Ala
 165 170 175

Tyr Ala Pro Leu Glu His Leu His Ile Glu Ala Asp Val Val Val Ser
 180 185 190
 Thr Val Pro Ser Ala Ala Ile Ala Gly Leu Glu Asp Thr Leu Ala Ile
 195 200 205
 Ala Pro Val Leu Asp Val Ile Tyr Asp Pro Trp Pro Thr Pro Leu Val
 210 215 220
 Glu Val Thr Arg Ala Lys Gly Leu Lys Ala Val Gly Gly His Val Met
 225 230 235 240
 Leu Ala His Gln Ser Tyr Gly Gln Phe Glu Gln Phe Thr Gly Met Asp
 245 250 255
 Ala Pro Arg Asp Ala Met Arg Glu Ala Leu Glu Glu Ser Leu Gly Ile
 260 265 270
 Ser Glu Glu His
 275

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 <211> 693
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(670)
 <223> RXA01699

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 aaaaacattg aggaacgaat gaaattcgaa gggttagagg atg gag cgt aat gaa 115
 Met Glu Arg Asn Glu
 1 5
 gtg aat gat caa att cac tta gat cat caa tca gat gac acc tct gaa 163
 Val Asn Asp Gln Ile His Leu Asp His Gln Ser Asp Asp Thr Ser Glu
 10 15 20
 tgc tcc tgc ccg atc gtg gtt ctt gtg ggt ttg cca gga gct gga aaa 211
 Cys Ser Cys Pro Ile Val Val Leu Val Gly Leu Pro Gly Ala Gly Lys
 25 30 35
 tcc acc att gga cgt cga tta gcg cgc gcc tta aac act gaa ctc gtc 259
 Ser Thr Ile Gly Arg Arg Leu Ala Arg Ala Leu Asn Thr Glu Leu Val
 40 45 50
 gac tcc gac gaa ctg att gag cgc gcc acc gga aaa gcc tgt ggc gcc 307
 Asp Ser Asp Glu Leu Ile Glu Arg Ala Thr Gly Lys Ala Cys Gly Ala
 55 60 65
 gtg ttc agc gag ctc ggc gag cca gcc ttc cgc gag ctc gag gcc atc 355
 Val Phe Ser Glu Leu Gly Glu Pro Ala Phe Arg Glu Leu Glu Ala Ile
 70 75 80 85
 cac gtg gcc gaa gca ctg aaa tcc tcc gga gtg gtg agc ttg gga ggc 403

His Val Ala Glu Ala Leu Lys Ser Ser Gly Val Val Ser Leu Gly Gly
 90 95 100
 gga tct gtg ctg aca gaa tcc acc cgt gaa ctg ctc aaa ggc cag gac 451
 Gly Ser Val Leu Thr Glu Ser Thr Arg Glu Leu Leu Lys Gly Gln Asp
 105 110 115
 gtg gtc tgg atc gac gtg cca gta gaa gaa ggc atc agg cgc acc gca 499
 Val Val Trp Ile Asp Val Pro Val Glu Glu Gly Ile Arg Arg Thr Ala
 120 125 130
 aac gag cgt tcc cgc ccc gtg ctg caa gcc gcc gac ccc gcc gag cac 547
 Asn Glu Arg Ser Arg Pro Val Leu Gln Ala Ala Asp Pro Ala Glu His
 135 140 145
 tac cgc aac ctg gtg aaa gtg cgc acc ccg ttg tac gaa gag gtg gca 595
 Tyr Arg Asn Leu Val Lys Val Arg Thr Pro Leu Tyr Glu Glu Val Ala
 150 155 160 165
 acc tac cga ctt cgc acc aac aac cgc agc ccc cag caa gtg gtg gca 643
 Thr Tyr Arg Leu Arg Thr Asn Asn Arg Ser Pro Gln Gln Val Val Ala
 170 175 180
 gca gtg ttg cat cat cta gaa atc gat taattaaacc gggcacctga 690
 Ala Val Leu His His Leu Glu Ile Asp
 185 190
 tta 693

<210> 442

<211> 190

<212> PRT

<213> Corynebacterium glutamicum

<400> 442

Met Glu Arg Asn Glu Val Asn Asp Gln Ile His Leu Asp His Gln Ser
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 Asp Asp Thr Ser Glu Cys Ser Cys Pro Ile Val Val Leu Val Gly Leu
 20 25 30
 Pro Gly Ala Gly Lys Ser Thr Ile Gly Arg Arg Leu Ala Arg Ala Leu
 35 40 45
 Asn Thr Glu Leu Val Asp Ser Asp Glu Leu Ile Glu Arg Ala Thr Gly
 50 55 60
 Lys Ala Cys Gly Ala Val Phe Ser Glu Leu Gly Glu Pro Ala Phe Arg
 65 70 75 80
 Glu Leu Glu Ala Ile His Val Ala Glu Ala Leu Lys Ser Ser Gly Val
 85 90 95
 Val Ser Leu Gly Gly Gly Ser Val Leu Thr Glu Ser Thr Arg Glu Leu
 100 105 110
 Leu Lys Gly Gln Asp Val Val Trp Ile Asp Val Pro Val Glu Glu Gly
 115 120 125
 Ile Arg Arg Thr Ala Asn Glu Arg Ser Arg Pro Val Leu Gln Ala Ala

648

gaa ggc gca ccg ttt tct gca gca gct gca gca gcc gga att gat ccc 546
 Glu Gly Ala Pro Phe Ser Ala Ala Ala Ala Ala Ala Gly Ile Asp Pro
 135 140 145 150
 att tac atc gct ccg gcc aac gcc agc gag aaa acc ctc gag ggt gtc 594
 Ile Tyr Ile Ala Pro Ala Asn Ala Ser Glu Lys Thr Leu Glu Gly Val
 155 160 165
 tcc gcc gca tca aag ggc tac atc tac gcc atc tcc cgc gac ggc gtc 642
 Ser Ala Ala Ser Lys Gly Tyr Ile Tyr Ala Ile Ser Arg Asp Gly Val
 170 175 180
 acc ggc acc gaa cgt gaa tca tcc acc gac ggc ctg tcc gca gtg gtg 690
 Thr Gly Thr Glu Arg Glu Ser Ser Thr Asp Gly Leu Ser Ala Val Val
 185 190 195
 gac aac atc aag aaa ttt gat ggc gca ccc atc ctc ttg ggc ttc ggc 738
 Asp Asn Ile Lys Lys Phe Asp Gly Ala Pro Ile Leu Leu Gly Phe Gly
 200 205 210
 atc tca tcc cct cag cac gtg gca gac gcg att gca gcg ggt gct tcc 786
 Ile Ser Ser Pro Gln His Val Ala Asp Ala Ile Ala Ala Gly Ala Ser
 215 220 225 230
 ggt gcg atc acg ggt tcc gcg atc acc aag atc att gct tcc cac tgc 834
 Gly Ala Ile Thr Gly Ser Ala Ile Thr Lys Ile Ile Ala Ser His Cys
 235 240 245
 gaa ggt gag cac ccg aac ccg tcc acc att cga gat atg gac ggt ttg 882
 Glu Gly Glu His Pro Asn Pro Ser Thr Ile Arg Asp Met Asp Gly Leu
 250 255 260
 aag aag gat ctc act gag ttc atc tct gcg atg aag gca gcg acc aag 930
 Lys Lys Asp Leu Thr Glu Phe Ile Ser Ala Met Lys Ala Ala Thr Lys
 265 270 275
 aag gtt taggccttta aatgtggcaa tgt 959
 Lys Val
 280

<210> 444

<211> 280

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 444

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 Gly Ala Phe Val Pro Phe Ile Met Leu Ser Asp Pro Ser Pro Glu Glu
 20 25 30
 Ala Phe Gln Ile Ile Ser Thr Ala Ile Glu Ala Gly Ala Asp Ala Leu
 35 40 45
 Glu Leu Gly Val Pro Phe Ser Asp Pro Val Ala Asp Gly Pro Thr Val
 50 55 60
 Ala Glu Ser His Leu Arg Ala Leu Asp Gly Gly Ala Thr Val Asp Ser
 65 70 75 80

650

ggc cag ttc gtc gcg gaa tcc ctc ctg cct gct ctc gac cag ctg gag	211
Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala Leu Asp Gln Leu Glu	
25 30 35	
aag gcc ttc gtt gac gcg acc aac agc cca gag ttc cgc gaa gaa ctc	259
Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu Phe Arg Glu Glu Leu	
40 45 50	
ggc ggc tac ctc cgc gat tac ctc ggc cgc cca acc ccg ctg acc gaa	307
Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro Thr Pro Leu Thr Glu	
55 60 65	
tgc tcc aac ctg cca ctc gca ggc gaa ggc aaa ggc ttt gcg cgg atc	355
Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys Gly Phe Ala Arg Ile	
70 75 80 85	
ttc ctc aag cgc gaa gac ctc gtc cac ggc ggt gca cac aaa act aac	403
Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly Ala His Lys Thr Asn	
90 95 100	
cag gtg atc ggc cag gtg ctg ctt gcc aag cgc atg ggc aaa acc cgc	451
Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg Met Gly Lys Thr Arg	
105 110 115	
atc atc gca gag acc ggc gca ggc cag cac ggc acc gcc acc gct ctc	499
Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly Thr Ala Thr Ala Leu	
120 125 130	
gca tgt gcg ctc atg ggc ctc gag tgc gtt gtc tac atg ggc gcc aag	547
Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val Tyr Met Gly Ala Lys	
135 140 145	
gac gtt gcc cgc cag cag ccc aac gtc tac cgc atg cag ctg cac ggc	595
Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg Met Gln Leu His Gly	
150 155 160 165	
gcg aag gtc atc ccc gtg gaa tct ggt tcc ggc acc ctg aag gac gcc	643
Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly Thr Leu Lys Asp Ala	
170 175 180	
gtg aat gaa gcg ctg cgc gat tgg acc gca acc ttc cac gag tcc cac	691
Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr Phe His Glu Ser His	
185 190 195	
tac ctt ctc ggc acc ccc gcc ggc ccg cac cca ttc cca acc atc gtg	739
Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro Phe Pro Thr Ile Val	
200 205 210	
cgt gaa ttc cac aag gtg atc tct gag gaa gcc aag gca cag atg cta	787
Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala Lys Ala Gln Met Leu	
215 220 225	
gag cgc acc ggc aag ctt ccc gac gtt gtg gtc gcc tgt gtc ggt ggt	835
Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val Ala Cys Val Gly Gly	
230 235 240 245	
ggc tcc aac gcc atc ggc atg ttc gca gac ttc att gac gat gaa ggt	883
Gly Ser Asn Ala Ile Gly Met Phe Ala Asp Phe Ile Asp Asp Glu Gly	
250 255 260	

gta gag ctc gtc ggc gct gag cca gcc ggt gaa ggc ctc gac tcc ggc 931
 Val Glu Leu Val Gly Ala Glu Pro Ala Gly Glu Gly Leu Asp Ser Gly
 265 270 275

aag cac ggc gca acc atc acc aac ggt cag atc ggc atc ctg cac ggc 979
 Lys His Gly Ala Thr Ile Thr Asn Gly Gln Ile Gly Ile Leu His Gly
 280 285 290

acc cgt tcc tac ctg atg cgc aac tcc gac ggc caa gtg gaa gag tcc
 1027
 Thr Arg Ser Tyr Leu Met Arg Asn Ser Asp Gly Gln Val Glu Glu Ser
 295 300 305

tac tcc atc tcc gcc gga ctt gat tac cca ggc gtc ggc cca cag cac
 1075
 Tyr Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly Val Gly Pro Gln His
 310 315 320 325

gca cac ctg cac gcc acc ggc cgc gcc acc tac gtt ggt atc acc gac
 1123
 Ala His Leu His Ala Thr Gly Arg Ala Thr Tyr Val Gly Ile Thr Asp
 330 335 340

gcc gaa gcc ctc caa gca ttc cag tac ctc gcc cgc tac gaa ggc atc
 1171
 Ala Glu Ala Leu Gln Ala Phe Gln Tyr Leu Ala Arg Tyr Glu Gly Ile
 345 350 355

atc ccc gca ctg gaa tcc tca cac gcg ttc gcc tac gca ctc aag cgc
 1219
 Ile Pro Ala Leu Glu Ser Ser His Ala Phe Ala Tyr Ala Leu Lys Arg
 360 365 370

gcc aag acc gcc gaa gta
 1237
 Ala Lys Thr Ala Glu Val
 375

<210> 446

<211> 379

<212> PRT

<213> Corynebacterium glutamicum

<400> 446

Met Thr Glu Lys Glu Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr
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Phe Gly Glu Phe Gly Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala
 20 25 30

Leu Asp Gln Leu Glu Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu
 35 40 45

Phe Arg Glu Glu Leu Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro
 50 55 60

Thr Pro Leu Thr Glu Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys
 65 70 75 80

Gly Phe Ala Arg Ile Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly

85										90					95				
Ala	His	Lys	Thr	Asn	Gln	Val	Ile	Gly	Gln	Val	Leu	Leu	Ala	Lys	Arg				
			100					105					110						
Met	Gly	Lys	Thr	Arg	Ile	Ile	Ala	Glu	Thr	Gly	Ala	Gly	Gln	His	Gly				
		115					120					125							
Thr	Ala	Thr	Ala	Leu	Ala	Cys	Ala	Leu	Met	Gly	Leu	Glu	Cys	Val	Val				
	130					135					140								
Tyr	Met	Gly	Ala	Lys	Asp	Val	Ala	Arg	Gln	Gln	Pro	Asn	Val	Tyr	Arg				
145					150					155					160				
Met	Gln	Leu	His	Gly	Ala	Lys	Val	Ile	Pro	Val	Glu	Ser	Gly	Ser	Gly				
				165					170					175					
Thr	Leu	Lys	Asp	Ala	Val	Asn	Glu	Ala	Leu	Arg	Asp	Trp	Thr	Ala	Thr				
			180					185					190						
Phe	His	Glu	Ser	His	Tyr	Leu	Leu	Gly	Thr	Pro	Ala	Gly	Pro	His	Pro				
		195					200					205							
Phe	Pro	Thr	Ile	Val	Arg	Glu	Phe	His	Lys	Val	Ile	Ser	Glu	Glu	Ala				
	210					215					220								
Lys	Ala	Gln	Met	Leu	Glu	Arg	Thr	Gly	Lys	Leu	Pro	Asp	Val	Val	Val				
225					230					235					240				
Ala	Cys	Val	Gly	Gly	Gly	Ser	Asn	Ala	Ile	Gly	Met	Phe	Ala	Asp	Phe				
				245					250					255					
Ile	Asp	Asp	Glu	Gly	Val	Glu	Leu	Val	Gly	Ala	Glu	Pro	Ala	Gly	Glu				
			260					265						270					
Gly	Leu	Asp	Ser	Gly	Lys	His	Gly	Ala	Thr	Ile	Thr	Asn	Gly	Gln	Ile				
		275					280						285						
Gly	Ile	Leu	His	Gly	Thr	Arg	Ser	Tyr	Leu	Met	Arg	Asn	Ser	Asp	Gly				
	290					295					300								
Gln	Val	Glu	Glu	Ser	Tyr	Ser	Ile	Ser	Ala	Gly	Leu	Asp	Tyr	Pro	Gly				
305					310					315					320				
Val	Gly	Pro	Gln	His	Ala	His	Leu	His	Ala	Thr	Gly	Arg	Ala	Thr	Tyr				
				325					330					335					
Val	Gly	Ile	Thr	Asp	Ala	Glu	Ala	Leu	Gln	Ala	Phe	Gln	Tyr	Leu	Ala				
			340					345					350						
Arg	Tyr	Glu	Gly	Ile	Ile	Pro	Ala	Leu	Glu	Ser	Ser	His	Ala	Phe	Ala				
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Tyr	Ala	Leu	Lys	Arg	Ala	Lys	Thr	Ala	Glu	Val									
		370				375													

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<211> 1231

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1231)

<223> FRXA00956

<400> 447

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                                         Met Thr Glu Lys Glu
                                         1                               5

aac ttg ggc ggc tcc acg ctg ctg cct gca tac ttc ggt gaa ttc ggc 163
Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr Phe Gly Glu Phe Gly
                        10                        15                        20

ggc cag ttc gtc gcg gaa tcc ctc ctg cct gct ctc gac cag ctg gag 211
Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala Leu Asp Gln Leu Glu
                        25                        30                        35

aag gcc ttc gtt gac gcg acc aac agc cca gag ttc cgc gaa gaa ctc 259
Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu Phe Arg Glu Glu Leu
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ggc ggc tac ctc cgc gat tac ctc ggc cgc cca acc ccg ctg acc gaa 307
Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro Thr Pro Leu Thr Glu
                        55                        60                        65

tgc tcc aac ctg cca ctc gca ggc gaa ggc aaa ggc ttt gcg cgg atc 355
Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys Gly Phe Ala Arg Ile
                        70                        75                        80                        85

ttc ctc aag cgc gaa gac ctc gtc cac ggc ggt gca cac aaa act aac 403
Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly Ala His Lys Thr Asn
                        90                        95                        100

cag gtg atc ggc cag gtg ctg ctt gcc aag cgc atg ggc aaa acc cgc 451
Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg Met Gly Lys Thr Arg
                        105                        110                        115

atc atc gca gag acc ggc gca ggc cag cac ggc acc gcc acc gct ctc 499
Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly Thr Ala Thr Ala Leu
                        120                        125                        130

gca tgt gcg ctc atg ggc ctc gag tgc gtt gtc tac atg ggc gcc aag 547
Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val Tyr Met Gly Ala Lys
                        135                        140                        145

gac gtt gcc cgc cag cag ccc aac gtc tac cgc atg cag ctg cac ggc 595
Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg Met Gln Leu His Gly
                        150                        155                        160                        165

gcg aag gtc atc ccc gtg gaa tct ggt tcc ggc acc ctg aag gac gcc 643
Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly Thr Leu Lys Asp Ala
                        170                        175                        180

gtg aat gaa gcg ctg cgc gat tgg acc gca acc ttc cac gag tcc cac 691
Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr Phe His Glu Ser His
                        185                        190                        195

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tac ctt ctc ggc acc ccc gcc ggc ccg cac cca ttc cca acc atc gtg	739
Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro Phe Pro Thr Ile Val	
200 205 210	
cggt gaa ttc cac aag gtg atc tct gag gaa gcc aag gca cag atg cta	787
Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala Lys Ala Gln Met Leu	
215 220 225	
gag cgc acc ggc aag ctt ccc gac gtt gtg gtc gcc tgt gtc ggt ggt	835
Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val Ala Cys Val Gly Gly	
230 235 240 245	
ggc tcc aac gcc atc ggc atg ttc gca gac ttc att gac gat gaa ggt	883
Gly Ser Asn Ala Ile Gly Met Phe Ala Asp Phe Ile Asp Asp Glu Gly	
250 255 260	
gta gag ctc gtc ggc gct gag cca gcc ggt gaa ggc ctc gac tcc ggc	931
Val Glu Leu Val Gly Ala Glu Pro Ala Gly Glu Gly Leu Asp Ser Gly	
265 270 275	
aag cac ggc gca acc atc acc aac ggt cag atc ggc atc ctg cac ggc	979
Lys His Gly Ala Thr Ile Thr Asn Gly Gln Ile Gly Ile Leu His Gly	
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acc cgt tcc tac ctg atg cgc aac tcc gac ggc caa gtg gaa gag tcc	
1027	
Thr Arg Ser Tyr Leu Met Arg Asn Ser Asp Gly Gln Val Glu Glu Ser	
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tac tcc atc tcc gcc gga ctt gat tac cca ggc gtc ggc cca cag cac	
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Tyr Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly Val Gly Pro Gln His	
310 315 320 325	
gca cac ctg cac gcc acc ggc cgc gcc acc tac gtt ggt atc acc gac	
1123	
Ala His Leu His Ala Thr Gly Arg Ala Thr Tyr Val Gly Ile Thr Asp	
330 335 340	
gcc gaa gcc ctc caa gca ttc cag tac ctc gcc cgc tac gaa ggc atc	
1171	
Ala Glu Ala Leu Gln Ala Phe Gln Tyr Leu Ala Arg Tyr Glu Gly Ile	
345 350 355	
atc ccc gca ctg gaa tcc tca cac gcg ttc gcc tac gca ctc aag cgc	
1219	
Ile Pro Ala Leu Glu Ser Ser His Ala Phe Ala Tyr Ala Leu Lys Arg	
360 365 370	
gcc aag acc gcc	
1231	
Ala Lys Thr Ala	
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<210> 448

<211> 377

<212> PRT

<213> Corynebacterium glutamicum

<400> 448

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 35 40 45
 Phe Arg Glu Glu Leu Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro
 50 55 60
 Thr Pro Leu Thr Glu Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys
 65 70 75 80
 Gly Phe Ala Arg Ile Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly
 85 90 95
 Ala His Lys Thr Asn Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg
 100 105 110
 Met Gly Lys Thr Arg Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly
 115 120 125
 Thr Ala Thr Ala Leu Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val
 130 135 140
 Tyr Met Gly Ala Lys Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg
 145 150 155 160
 Met Gln Leu His Gly Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly
 165 170 175
 Thr Leu Lys Asp Ala Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr
 180 185 190
 Phe His Glu Ser His Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro
 195 200 205
 Phe Pro Thr Ile Val Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala
 210 215 220
 Lys Ala Gln Met Leu Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val
 225 230 235 240
 Ala Cys Val Gly Gly Gly Ser Asn Ala Ile Gly Met Phe Ala Asp Phe
 245 250 255
 Ile Asp Asp Glu Gly Val Glu Leu Val Gly Ala Glu Pro Ala Gly Glu
 260 265 270
 Gly Leu Asp Ser Gly Lys His Gly Ala Thr Ile Thr Asn Gly Gln Ile
 275 280 285
 Gly Ile Leu His Gly Thr Arg Ser Tyr Leu Met Arg Asn Ser Asp Gly
 290 295 300
 Gln Val Glu Glu Ser Tyr Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly
 305 310 315 320
 Val Gly Pro Gln His Ala His Leu His Ala Thr Gly Arg Ala Thr Tyr

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ggtcctgtcta	ttttgccacc	acatgcggag	gtacgcagtt	atg	agt	tca	gtt	tcg	115							
				Met	Ser	Ser	Val	Ser	5							
				1												
ctg	cag	gat	ttt	gat	gca	gag	cga	att	ggc	ttg	ttc	cac	gag	gac	att	163
Leu	Gln	Asp	Phe	Asp	Ala	Glu	Arg	Ile	Gly	Leu	Phe	His	Glu	Asp	Ile	
				10					15					20		
aag	cgc	aag	ttt	gat	gag	ctc	aag	tca	aaa	aat	ctg	aag	ctg	gat	ctt	211
Lys	Arg	Lys	Phe	Asp	Glu	Leu	Lys	Ser	Lys	Asn	Leu	Lys	Leu	Asp	Leu	
			25					30					35			
act	cgc	ggc	aag	cct	tcg	tcg	gag	cag	ttg	gat	ttc	gct	gat	gag	ttg	259
Thr	Arg	Gly	Lys	Pro	Ser	Ser	Glu	Gln	Leu	Asp	Phe	Ala	Asp	Glu	Leu	
			40				45					50				
ttg	gcg	ttg	cct	ggc	aag	ggc	gat	ttc	aag	gct	gcg	gat	ggc	act	gat	307
Leu	Ala	Leu	Pro	Gly	Lys	Gly	Asp	Phe	Lys	Ala	Ala	Asp	Gly	Thr	Asp	
	55					60					65					
gtc	cgt	aac	tat	ggc	ggg	ctg	gat	ggc	atc	ggt	gat	att	cgc	cag	att	355
Val	Arg	Asn	Tyr	Gly	Gly	Leu	Asp	Gly	Ile	Val	Asp	Ile	Arg	Gln	Ile	
	70				75				80						85	
tgg	gcg	gat	ttg	ctg	ggc	ggt	cct	gtg	gag	cag	gtc	ttg	gcg	ggg	gat	403
Trp	Ala	Asp	Leu	Leu	Gly	Val	Pro	Val	Glu	Gln	Val	Leu	Ala	Gly	Asp	
				90					95					100		
gct	tcg	agc	ttg	aac	atc	atg	ttt	gat	gtg	atc	agc	tgg	tcg	tac	att	451
Ala	Ser	Ser	Leu	Asn	Ile	Met	Phe	Asp	Val	Ile	Ser	Trp	Ser	Tyr	Ile	
			105					110					115			
ttc	ggc	aac	aat	gat	tcg	gtt	cag	cct	tgg	tcg	aag	gaa	gaa	acc	gtt	499
Phe	Gly	Asn	Asn	Asp	Ser	Val	Gln	Pro	Trp	Ser	Lys	Glu	Glu	Thr	Val	
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aag tgg att tgc cct gtt ccg ggc tat gat cgc cat ttc tcc atc acg	547
Lys Trp Ile Cys Pro Val Pro Gly Tyr Asp Arg His Phe Ser Ile Thr	
135 140 145	
gag cgt ttc ggc ttt gag atg att tct gtg cca atg aat gaa gac ggc	595
Glu Arg Phe Gly Phe Glu Met Ile Ser Val Pro Met Asn Glu Asp Gly	
150 155 160 165	
cct gat atg gat gct gtt gag gaa ttg gtg aag aat ccg cag gtt aag	643
Pro Asp Met Asp Ala Val Glu Glu Leu Val Lys Asn Pro Gln Val Lys	
170 175 180	
ggc atg tgg gtt gtt ccg gtg ttt tct aac ccg act ggt ttc acg gtg	691
Gly Met Trp Val Val Pro Val Phe Ser Asn Pro Thr Gly Phe Thr Val	
185 190 195	
aca gaa gac gtc gca aag cgt cta agc gca atg gaa acc gca gct ccg	739
Thr Glu Asp Val Ala Lys Arg Leu Ser Ala Met Glu Thr Ala Ala Pro	
200 205 210	
gac ttc cgc gtt gtg tgg gat aat gcc tac gcc gtt cat acg ctg acc	787
Asp Phe Arg Val Val Trp Asp Asn Ala Tyr Ala Val His Thr Leu Thr	
215 220 225	
gat gaa ttc cct gag gtt atc gat atc gtc ggg ctt ggt gag gcc gct	835
Asp Glu Phe Pro Glu Val Ile Asp Ile Val Gly Leu Gly Glu Ala Ala	
230 235 240 245	
ggc aac ccg aac cgt ttc tgg gcg ttc act tct act tcg aag atc act	883
Gly Asn Pro Asn Arg Phe Trp Ala Phe Thr Ser Thr Ser Lys Ile Thr	
250 255 260	
ctc gcg ggt gcg ggc gtg tcg ttc ttc ctc acc tct gcg gag aac cgc	931
Leu Ala Gly Ala Gly Val Ser Phe Phe Leu Thr Ser Ala Glu Asn Arg	
265 270 275	
aag tgg tac acc ggc cat gcg ggt atc cgt ggc att ggc cct aac aag	979
Lys Trp Tyr Thr Gly His Ala Gly Ile Arg Gly Ile Gly Pro Asn Lys	
280 285 290	
gtc aat cag ttg gct cat gcg cgt tac ttt ggc gat gct gag gga gtg	
1027	
Val Asn Gln Leu Ala His Ala Arg Tyr Phe Gly Asp Ala Glu Gly Val	
295 300 305	
cgc gcg gtg atg cgt aag cat gct gcg tcg ttg gct ccg aag ttc aac	
1075	
Arg Ala Val Met Arg Lys His Ala Ala Ser Leu Ala Pro Lys Phe Asn	
310 315 320 325	
aag gtt ctg gag att ctg gat tct cgc ctt gct gag tac ggt gtc gcg	
1123	
Lys Val Leu Glu Ile Leu Asp Ser Arg Leu Ala Glu Tyr Gly Val Ala	
330 335 340	
cag tgg act gtc cct gcg ggc ggt tac ttc att tcc ctt gat gtg gtt	
1171	
Gln Trp Thr Val Pro Ala Gly Gly Tyr Phe Ile Ser Leu Asp Val Val	
345 350 355	

cct ggt acg gcg tct cgc gtg gct gag ttg gct aag gaa gcc ggc atc
 1219
 Pro Gly Thr Ala Ser Arg Val Ala Glu Leu Ala Lys Glu Ala Gly Ile
 360 365 370

gcg ttg acg ggt gcg ggt tct tct tac ccg ctg cgt cag gat ccg gag
 1267
 Ala Leu Thr Gly Ala Gly Ser Ser Tyr Pro Leu Arg Gln Asp Pro Glu
 375 380 385

aac aaa aat ctc cgt ttg gca ccg tcg ctg cct cca gtt gag gaa ctt
 1315
 Asn Lys Asn Leu Arg Leu Ala Pro Ser Leu Pro Pro Val Glu Glu Leu
 390 395 400 405

gag gtt gcc atg gat ggc gtg gct acc tgt gtg ctg ttg gca gca gcg
 1363
 Glu Val Ala Met Asp Gly Val Ala Thr Cys Val Leu Leu Ala Ala Ala
 410 415 420

gag cat tac gct aac taaaagtgaac tacagcggag aca
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 Glu His Tyr Ala Asn
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<210> 450

<211> 426

<212> PRT

<213> Corynebacterium glutamicum

<400> 450

Met Ser Ser Val Ser Leu Gln Asp Phe Asp Ala Glu Arg Ile Gly Leu
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Phe His Glu Asp Ile Lys Arg Lys Phe Asp Glu Leu Lys Ser Lys Asn
 20 25 30

Leu Lys Leu Asp Leu Thr Arg Gly Lys Pro Ser Ser Glu Gln Leu Asp
 35 40 45

Phe Ala Asp Glu Leu Leu Ala Leu Pro Gly Lys Gly Asp Phe Lys Ala
 50 55 60

Ala Asp Gly Thr Asp Val Arg Asn Tyr Gly Gly Leu Asp Gly Ile Val
 65 70 75 80

Asp Ile Arg Gln Ile Trp Ala Asp Leu Leu Gly Val Pro Val Glu Gln
 85 90 95

Val Leu Ala Gly Asp Ala Ser Ser Leu Asn Ile Met Phe Asp Val Ile
 100 105 110

Ser Trp Ser Tyr Ile Phe Gly Asn Asn Asp Ser Val Gln Pro Trp Ser
 115 120 125

Lys Glu Glu Thr Val Lys Trp Ile Cys Pro Val Pro Gly Tyr Asp Arg
 130 135 140

His Phe Ser Ile Thr Glu Arg Phe Gly Phe Glu Met Ile Ser Val Pro
 145 150 155 160

Met Asn Glu Asp Gly Pro Asp Met Asp Ala Val Glu Glu Leu Val Lys
 165 170 175
 Asn Pro Gln Val Lys Gly Met Trp Val Val Pro Val Phe Ser Asn Pro
 180 185 190
 Thr Gly Phe Thr Val Thr Glu Asp Val Ala Lys Arg Leu Ser Ala Met
 195 200 205
 Glu Thr Ala Ala Pro Asp Phe Arg Val Val Trp Asp Asn Ala Tyr Ala
 210 215 220
 Val His Thr Leu Thr Asp Glu Phe Pro Glu Val Ile Asp Ile Val Gly
 225 230 235 240
 Leu Gly Glu Ala Ala Gly Asn Pro Asn Arg Phe Trp Ala Phe Thr Ser
 245 250 255
 Thr Ser Lys Ile Thr Leu Ala Gly Ala Gly Val Ser Phe Phe Leu Thr
 260 265 270
 Ser Ala Glu Asn Arg Lys Trp Tyr Thr Gly His Ala Gly Ile Arg Gly
 275 280 285
 Ile Gly Pro Asn Lys Val Asn Gln Leu Ala His Ala Arg Tyr Phe Gly
 290 295 300
 Asp Ala Glu Gly Val Arg Ala Val Met Arg Lys His Ala Ala Ser Leu
 305 310 315 320
 Ala Pro Lys Phe Asn Lys Val Leu Glu Ile Leu Asp Ser Arg Leu Ala
 325 330 335
 Glu Tyr Gly Val Ala Gln Trp Thr Val Pro Ala Gly Gly Tyr Phe Ile
 340 345 350
 Ser Leu Asp Val Val Pro Gly Thr Ala Ser Arg Val Ala Glu Leu Ala
 355 360 365
 Lys Glu Ala Gly Ile Ala Leu Thr Gly Ala Gly Ser Ser Tyr Pro Leu
 370 375 380
 Arg Gln Asp Pro Glu Asn Lys Asn Leu Arg Leu Ala Pro Ser Leu Pro
 385 390 395 400
 Pro Val Glu Glu Leu Glu Val Ala Met Asp Gly Val Ala Thr Cys Val
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 Leu Leu Ala Ala Ala Glu His Tyr Ala Asn
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<210> 451

<211> 1143

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) .. (1120)

<223> RXN00448

<400> 451

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catagagata accgtagtag gtatgtgcca cacttgtcag gtg act acc aaa gac 115
                               Val Thr Thr Lys Asp
                               1                               5

att tcc cgc cca gta tgc atc ctg ggc ctc ggc ctc atc ggc gga tcc 163
Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly Leu Ile Gly Gly Ser
                10                15                20

ctc ctc cgc gac ctc cat gca gcc aac cac tcc gtc ttc ggc tac aac 211
Leu Leu Arg Asp Leu His Ala Ala Asn His Ser Val Phe Gly Tyr Asn
                25                30                35

cgc tca cgc tcc ggc gct aaa tca gcc gtc gac gaa ggc ttc gac gtt 259
Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp Glu Gly Phe Asp Val
                40                45                50

tcc gcc gat ctt gaa gca acc ctc cag cgt gca gcc gcc gaa gat gcg 307
Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala Ala Glu Asp Ala
                55                60                65

ctc atc gtc ctc gcg gtc ccc atg acc gca atc gat tcg ctt ctc gac 355
Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile Asp Ser Leu Leu Asp
                70                75                80                85

gcc gtc cac acc cac gca cca aac aac ggc ttc acc gac gtc gta tcc 403
Ala Val His Thr His Ala Pro Asn Asn Gly Phe Thr Asp Val Val Ser
                90                95                100

gta aaa acc gcc gtc tac gac gca gta aaa gcc cgc aac atg caa cac 451
Val Lys Thr Ala Val Tyr Asp Ala Val Lys Ala Arg Asn Met Gln His
                105                110                115

cgt tat gtg gga tcc cac ccc atg gca ggc acc gcc aac tcc ggc tgg 499
Arg Tyr Val Gly Ser His Pro Met Ala Gly Thr Ala Asn Ser Gly Trp
                120                125                130

agc gca tcc atg gac gga ctg ttc aaa cga gca gta tgg gtg gtc acc 547
Ser Ala Ser Met Asp Gly Leu Phe Lys Arg Ala Val Trp Val Val Thr
                135                140                145

ttc gac cag ctt ttc gac ggc acc gac atc aac tcc acc tgg atc agc 595
Phe Asp Gln Leu Phe Asp Gly Thr Asp Ile Asn Ser Thr Trp Ile Ser
                150                155                160                165

atc tgg aaa gac gtc gtc caa atg gca ctc gcc gtg ggc gct gaa gtt 643
Ile Trp Lys Asp Val Val Gln Met Ala Leu Ala Val Gly Ala Glu Val
                170                175                180

gtc cca tcc cga gtt ggc cca cac gat gca gca gca gca cga gtg tct 691
Val Pro Ser Arg Val Gly Pro His Asp Ala Ala Ala Ala Arg Val Ser
                185                190                195

cat tta aca cac atc ctg gct gaa acc ctc gcc atc gtc ggt gac aac 739
His Leu Thr His Ile Leu Ala Glu Thr Leu Ala Ile Val Gly Asp Asn
                200                205                210

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ggt ggc gca ctg tct ctc tct tta gcc gct ggc agc tac cgc gac tcc 787
 Gly Gly Ala Leu Ser Leu Ser Leu Ala Ala Gly Ser Tyr Arg Asp Ser
 215 220 225
 acc cgc gtt gca ggc acc gac cca gga ctc gtc cgc gcc atg tgt gaa 835
 Thr Arg Val Ala Gly Thr Asp Pro Gly Leu Val Arg Ala Met Cys Glu
 230 235 240 245
 agc aac gcc ggc cca ctg gtc aaa gcc ctc gac gaa gca ctg gcg atc 883
 Ser Asn Ala Gly Pro Leu Val Lys Ala Leu Asp Glu Ala Leu Ala Ile
 250 255 260
 ctc cac gaa gcc cgc gaa ggc ctc acc gca gaa cag cca aac atc gag 931
 Leu His Glu Ala Arg Glu Gly Leu Thr Ala Glu Gln Pro Asn Ile Glu
 265 270 275
 caa ctt gcc gac aac ggc tac cga tcc cgc atc cgc tac gaa gcc cgc 979
 Gln Leu Ala Asp Asn Gly Tyr Arg Ser Arg Ile Arg Tyr Glu Ala Arg
 280 285 290
 tcc ggc cag cga cgc gcc aaa gaa tcc gtt agc cct acc atc acc tca
 1027
 Ser Gly Gln Arg Arg Ala Lys Glu Ser Val Ser Pro Thr Ile Thr Ser
 295 300 305
 tcc agg cca gtg ctc cgt ctc cac ccg ggc aca cca aac tgg gag aag
 1075
 Ser Arg Pro Val Leu Arg Leu His Pro Gly Thr Pro Asn Trp Glu Lys
 310 315 320 325
 cag ctc atc cac gct gaa acc ctc ggc gca cgg atc gaa gtg ttc
 1120
 Gln Leu Ile His Ala Glu Thr Leu Gly Ala Arg Ile Glu Val Phe
 330 335 340
 tagttttatc ggctgatgat tct
 1143

<210> 452

<211> 340

<212> PRT

<213> Corynebacterium glutamicum

<400> 452

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 20 25 30
 Val Phe Gly Tyr Asn Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp
 35 40 45
 Glu Gly Phe Asp Val Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala
 50 55 60
 Ala Ala Glu Asp Ala Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile
 65 70 75 80
 Asp Ser Leu Leu Asp Ala Val His Thr His Ala Pro Asn Asn Gly Phe

[illegible]

<400> 453

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1				5					10					15		

gca	tcc	atg	gac	gga	ctg	ttc	aaa	cga	gca	gta	tgg	gtg	gtc	acc	ttc	96
Ala	Ser	Met	Asp	Gly	Leu	Phe	Lys	Arg	Ala	Val	Trp	Val	Val	Thr	Phe	
			20					25					30			

gac	cag	ctt	ttc	gac	ggc	acc	gac	atc	aac	tcc	acc	tgg	atc	agc	atc	144
Asp	Gln	Leu	Phe	Asp	Gly	Thr	Asp	Ile	Asn	Ser	Thr	Trp	Ile	Ser	Ile	
		35					40					45				

tgg	aaa	gac	gtc	gtc	caa	atg	gca	ctc	gcc	gtg	ggc	gct	gaa	gtt	gtc	192
Trp	Lys	Asp	Val	Val	Gln	Met	Ala	Leu	Ala	Val	Gly	Ala	Glu	Val	Val	
	50					55					60					

cca	tcc	cga	gtt	ggc	cca	cac	gat	gca	gca	gca	gca	cga	gtg	tct	cat	240
Pro	Ser	Arg	Val	Gly	Pro	His	Asp	Ala	Ala	Ala	Ala	Arg	Val	Ser	His	
65				70						75					80	

tta	aca	cac	atc	ctg	gct	gaa	acc	ctc	gcc	atc	gtc	ggt	gac	aac	ggt	288
Leu	Thr	His	Ile	Leu	Ala	Glu	Thr	Leu	Ala	Ile	Val	Gly	Asp	Asn	Gly	
				85					90					95		

ggc	gca	ctg	tct	ctc	tct	tta	gcc	gct	ggc	agc	tac	cgc	gac	tcc	acc	336
Gly	Ala	Leu	Ser	Leu	Ser	Leu	Ala	Ala	Gly	Ser	Tyr	Arg	Asp	Ser	Thr	
			100					105					110			

cgc	gtt	gca	ggc	acc	gac	cca	gga	ctc	gtc	cgc	gcc	atg	tgt	gaa	agc	384
Arg	Val	Ala	Gly	Thr	Asp	Pro	Gly	Leu	Val	Arg	Ala	Met	Cys	Glu	Ser	
		115					120					125				

aac	gcc	ggc	cca	ctg	gtc	aaa	gcc	ctc	gac	gaa	gca	ctg	gcg	atc	ctc	432
Asn	Ala	Gly	Pro	Leu	Val	Lys	Ala	Leu	Asp	Glu	Ala	Leu	Ala	Ile	Leu	
	130					135					140					

cac	gaa	gcc	cgc	gaa	ggc	ctc	acc	gca	gaa	cag	cca	aac	atc	gag	caa	480
His	Glu	Ala	Arg	Glu	Gly	Leu	Thr	Ala	Glu	Gln	Pro	Asn	Ile	Glu	Gln	
145					150					155					160	

ctt	gcc	gac	aac	ggc	tac	cga	tcc	cgc	atc	cgc	tac	gaa	gcc	cgc	tcc	528
Leu	Ala	Asp	Asn	Gly	Tyr	Arg	Ser	Arg	Ile	Arg	Tyr	Glu	Ala	Arg	Ser	
				165					170					175		

ggc	cag	cga	cgc	gcc	aaa	gaa	tcc	gtt	agc	cct	acc	atc	acc	tca	tcc	576
Gly	Gln	Arg	Arg	Ala	Lys	Glu	Ser	Val	Ser	Pro	Thr	Ile	Thr	Ser	Ser	
			180					185					190			

agg	cca	gtg	ctc	cgt	ctc	cac	ccg	ggc	aca	cca	aac	tgg	gag	aag	cag	624
Arg	Pro	Val	Leu	Arg	Leu	His	Pro	Gly	Thr	Pro	Asn	Trp	Glu	Lys	Gln	
		195					200					205				

ctc	atc	cac	gct	gaa	acc	ctc	ggc	gca	cgg	atc	gaa	gtg	ttc			666
Leu	Ile	His	Ala	Glu	Thr	Leu	Gly	Ala	Arg	Ile	Glu	Val	Phe			
	210					215					220					

tagttttatc	ggctgatgat	tct														689
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<210> 454

<211> 222

<212> PRT

<213> Corynebacterium glutamicum

<400> 454

Tyr Val Gly Ser His Pro Met Ala Gly Thr Ala Asn Ser Gly Trp Ser
 1 5 10 15

Ala Ser Met Asp Gly Leu Phe Lys Arg Ala Val Trp Val Val Thr Phe
 20 25 30

Asp Gln Leu Phe Asp Gly Thr Asp Ile Asn Ser Thr Trp Ile Ser Ile
 35 40 45

Trp Lys Asp Val Val Gln Met Ala Leu Ala Val Gly Ala Glu Val Val
 50 55 60

Pro Ser Arg Val Gly Pro His Asp Ala Ala Ala Arg Val Ser His
 65 70 75 80

Leu Thr His Ile Leu Ala Glu Thr Leu Ala Ile Val Gly Asp Asn Gly
 85 90 95

Gly Ala Leu Ser Leu Ser Leu Ala Ala Gly Ser Tyr Arg Asp Ser Thr
 100 105 110

Arg Val Ala Gly Thr Asp Pro Gly Leu Val Arg Ala Met Cys Glu Ser
 115 120 125

Asn Ala Gly Pro Leu Val Lys Ala Leu Asp Glu Ala Leu Ala Ile Leu
 130 135 140

His Glu Ala Arg Glu Gly Leu Thr Ala Glu Gln Pro Asn Ile Glu Gln
 145 150 155 160

Leu Ala Asp Asn Gly Tyr Arg Ser Arg Ile Arg Tyr Glu Ala Arg Ser
 165 170 175

Gly Gln Arg Arg Ala Lys Glu Ser Val Ser Pro Thr Ile Thr Ser Ser
 180 185 190

Arg Pro Val Leu Arg Leu His Pro Gly Thr Pro Asn Trp Glu Lys Gln
 195 200 205

Leu Ile His Ala Glu Thr Leu Gly Ala Arg Ile Glu Val Phe
 210 215 220

<210> 455

<211> 346

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(346)

<223> FRXA00452

<400> 455

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                               Val Thr Thr Lys Asp
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att tcc cgc cca gta tgc atc ctg ggc ctc ggc ctc atc ggc gga tcc 163
Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly Leu Ile Gly Gly Ser
                10                15                20

ctc ctc cgc gac ctc cat gca gcc aac cac tcc gtc ttc ggc tac aac 211
Leu Leu Arg Asp Leu His Ala Ala Asn His Ser Val Phe Gly Tyr Asn
                25                30                35

cgc tca cgc tcc ggc gct aaa tca gcc gtc gac gaa ggc ttc gac gtt 259
Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp Glu Gly Phe Asp Val
                40                45                50

tcc gcc gat ctt gaa gca acc ctc cag cgt gca gcc gcc gaa gat gcg 307
Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala Ala Ala Glu Asp Ala
                55                60                65

ctc atc gtc ctc gcg gtc ccc atg acc gca atc gat tcg 346
Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile Asp Ser
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<210> 456

<211> 82

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 456

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Val Thr Thr Lys Asp Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly
 1                5                10                15

Leu Ile Gly Gly Ser Leu Leu Arg Asp Leu His Ala Ala Asn His Ser
                20                25                30

Val Phe Gly Tyr Asn Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp
                35                40                45

Glu Gly Phe Asp Val Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala
 50                55                60

Ala Ala Glu Asp Ala Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile
 65                70                75                80

Asp Ser

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<210> 457

<211> 1248

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1225)

<223> RXA00584

<400> 457

667

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 Ser Asp Asp Gly Ala Leu Ser Val Val Glu Thr Ala Gly Asn Ser Asn
 230 235 240 245
 tcc cac atc att ttg cgc ggc ggt acc tcc ggc ccg aat cat gat gca 883
 Ser His Ile Ile Leu Arg Gly Gly Thr Ser Gly Pro Asn His Asp Ala
 250 255 260
 gct tcg gtg gag gcc gtc gtc gag aag ctt ggt gaa aac gct cgt ctc 931
 Ala Ser Val Glu Ala Val Val Glu Lys Leu Gly Glu Asn Ala Arg Leu
 265 270 275
 atg atc gat gct tcc cat gct aac tcc ggc aag gat cat atc cga cag 979
 Met Ile Asp Ala Ser His Ala Asn Ser Gly Lys Asp His Ile Arg Gln
 280 285 290
 gtt gag gtt gtt cgt gaa atc gca gag cag att tct ggc ggt tct gaa
 1027
 Val Glu Val Val Arg Glu Ile Ala Glu Gln Ile Ser Gly Gly Ser Glu
 295 300 305
 gct gtg gct gga atc atg att gag tcc ttc ctc gtt ggt ggc gca cag
 1075
 Ala Val Ala Gly Ile Met Ile Glu Ser Phe Leu Val Gly Gly Ala Gln
 310 315 320 325
 aac ctt gat cct gcg aaa ttg cgc atc aat ggc ggt gaa ggc ctg gtg
 1123
 Asn Leu Asp Pro Ala Lys Leu Arg Ile Asn Gly Gly Glu Gly Leu Val
 330 335 340
 tac gga cag tct gtg acc gat aag tgc atc gat att gac acc acc atc
 1171
 Tyr Gly Gln Ser Val Thr Asp Lys Cys Ile Asp Ile Asp Thr Thr Ile
 345 350 355
 gat ttg ctc gct gag ctg gcc gca gca gta agg gaa cgc cga gca gca
 1219
 Asp Leu Leu Ala Glu Leu Ala Ala Ala Val Arg Glu Arg Arg Ala Ala
 360 365 370
 gcc aag taattaaggg cgctagactg tta
 1248
 Ala Lys
 375

<210> 458

<211> 375

<212> PRT

<213> Corynebacterium glutamicum

<400> 458

Met His Ser Pro Glu Arg Gln Glu Lys Met Ser Ser Pro Val Ser Leu
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Glu Asn Ala Ala Ser Thr Ser Asn Lys Arg Val Val Ala Phe His Glu
 20 25 30

Leu Pro Ser Pro Thr Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys

35					40					45						
Gln	Ala	Ser	Lys	Val	Glu	Gln	Asp	Arg	Gln	Asp	Ile	Ala	Asp	Ile	Phe	
50					55					60						
Ala	Gly	Asp	Asp	Asp	Arg	Leu	Val	Val	Val	Val	Gly	Pro	Cys	Ser	Val	
65					70					75					80	
His	Asp	Pro	Glu	Ala	Ala	Ile	Asp	Tyr	Ala	Asn	Arg	Leu	Ala	Pro	Leu	
85					90					95						
Ala	Lys	Arg	Leu	Asp	Gln	Asp	Leu	Lys	Ile	Val	Met	Arg	Val	Tyr	Phe	
100					105					110						
Glu	Lys	Pro	Arg	Thr	Ile	Val	Gly	Trp	Lys	Gly	Leu	Ile	Asn	Asp	Pro	
115					120					125						
His	Leu	Asn	Glu	Thr	Tyr	Asp	Ile	Pro	Glu	Gly	Leu	Arg	Ile	Ala	Arg	
130					135					140						
Lys	Val	Leu	Ile	Asp	Val	Val	Asn	Leu	Asp	Leu	Pro	Val	Gly	Cys	Glu	
145					150					155					160	
Phe	Leu	Glu	Pro	Asn	Ser	Pro	Gln	Tyr	Tyr	Ala	Asp	Thr	Val	Ala	Trp	
165					170					175						
Gly	Ala	Ile	Gly	Ala	Arg	Thr	Thr	Glu	Ser	Gln	Val	His	Arg	Gln	Leu	
180					185					190						
Ala	Ser	Gly	Met	Ser	Met	Pro	Ile	Gly	Phe	Lys	Asn	Gly	Thr	Asp	Gly	
195					200					205						
Asn	Ile	Gln	Val	Ala	Val	Asp	Ala	Val	Gln	Ala	Ala	Gln	Asn	Pro	His	
210					215					220						
Phe	Phe	Phe	Gly	Thr	Ser	Asp	Asp	Gly	Ala	Leu	Ser	Val	Val	Glu	Thr	
225					230					235					240	
Ala	Gly	Asn	Ser	Asn	Ser	His	Ile	Ile	Leu	Arg	Gly	Gly	Thr	Ser	Gly	
245					250					255						
Pro	Asn	His	Asp	Ala	Ala	Ser	Val	Glu	Ala	Val	Val	Glu	Lys	Leu	Gly	
260					265					270						
Glu	Asn	Ala	Arg	Leu	Met	Ile	Asp	Ala	Ser	His	Ala	Asn	Ser	Gly	Lys	
275					280					285						
Asp	His	Ile	Arg	Gln	Val	Glu	Val	Val	Arg	Glu	Ile	Ala	Glu	Gln	Ile	
290					295					300						
Ser	Gly	Gly	Ser	Glu	Ala	Val	Ala	Gly	Ile	Met	Ile	Glu	Ser	Phe	Leu	
305					310					315					320	
Val	Gly	Gly	Ala	Gln	Asn	Leu	Asp	Pro	Ala	Lys	Leu	Arg	Ile	Asn	Gly	
325					330					335						
Gly	Glu	Gly	Leu	Val	Tyr	Gly	Gln	Ser	Val	Thr	Asp	Lys	Cys	Ile	Asp	
340					345					350						
Ile	Asp	Thr	Thr	Ile	Asp	Leu	Leu	Ala	Glu	Leu	Ala	Ala	Ala	Val	Arg	
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Glu Arg Arg Ala Ala Ala Lys
370 375

<210> 459

<211> 1983

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1960)

<223> RXA00579

<400> 459

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gtgctttttct cggtgttttg tggttttgtc agaggatgtc atg cgc gtt tta att 115
               Met Arg Val Leu Ile
               1 5

att gat aat tat gat tct ttc acg ttt aat ctc gcc acc tat gtg gaa 163
Ile Asp Asn Tyr Asp Ser Phe Thr Phe Asn Leu Ala Thr Tyr Val Glu
               10 15 20

gag gtt acg ggt cag gca cct gtg gtg gtg cct aat gat caa gaa ata 211
Glu Val Thr Gly Gln Ala Pro Val Val Val Pro Asn Asp Gln Glu Ile
               25 30 35

gat gag atg ctt ttc gac gcc gtc atc ctc tca cct ggc ccg ggc cac 259
Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser Pro Gly Pro Gly His
               40 45 50

gcc ggc gtt gcg gct gat ttt ggt atc tgt gca ggc gtc att gag cgt 307
Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala Gly Val Ile Glu Arg
               55 60 65

gca cgc gtt ccg att ttg ggt gtg tgt tta ggc cac cag ggc att gcg 355
Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly His Gln Gly Ile Ala
               70 75 80 85

ttg gcc tat ggc ggt gat gtt gat ttg gcg ccc agg ccg gtc cac ggt 403
Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro Arg Pro Val His Gly
               90 95 100

gag gtt tcg cag atc acc cat gat ggt tca ggt tta ttt gca ggc atc 451
Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly Leu Phe Ala Gly Ile
               105 110 115

cct gaa acg ttt gag gcg gtg cgt tat cac tcg atg gtg gca acc cgc 499
Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser Met Val Ala Thr Arg
               120 125 130

ttg ccg gag tca ttg aaa gct aca gct acc agc gat gat ggt ttg atc 547
Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser Asp Asp Gly Leu Ile
               135 140 145

atg gca ttg gca cat gaa gtg ctt ccg cag tgg ggt gtg caa ttt cat 595
Met Ala Leu Ala His Glu Val Leu Pro Gln Trp Gly Val Gln Phe His
               150 155 160 165

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ccg gaa tct att ggt gga caa ttc ggc cat cag atc att aag aac ttc	643
Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln Ile Ile Lys Asn Phe	
170 175 180	
ctt aat tta gcg cgc aca tat cgc tgg caa ctc acg gag aaa act att	691
Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu Thr Glu Lys Thr Ile	
185 190 195	
ccg ctc agc gtt gat tca gca gcg gtt ttt gaa aca ttc ttt gcc cat	739
Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu Thr Phe Phe Ala His	
200 205 210	
tcc tcc cat gct ttt tgg ctc gat gat gcc caa gga acc agc tat ctt	787
Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln Gly Thr Ser Tyr Leu	
215 220 225	
ggg gat gcc agc ggt cct ctc gca cgc aca aaa acc cat aat gtc ggc	835
Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys Thr His Asn Val Gly	
230 235 240 245	
gag ggg gat ttc ttc acc tgg cta aag gag gat ctc gcc gcc aac tca	883
Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp Leu Ala Ala Asn Ser	
250 255 260	
gtt gcg ccc ggt caa ggt ttt cgt ctt ggc tgg gtt ggt tac gtt ggt	931
Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp Val Gly Tyr Val Gly	
265 270 275	
tat gag ctt aaa gcg gaa gct ggc gca cgg gct gcg cac act tcg agt	979
Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala Ala His Thr Ser Ser	
280 285 290	
ctt ccg gat gcg cac ctc att ttt gcc gat cgc gcc atc gca gtg gaa	
1027	
Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg Ala Ile Ala Val Glu	
295 300 305	
tcg gat cag gtt cgg ttg ctg gcg ttg ggg gag cag gac gag tgg ttt	
1075	
Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu Gln Asp Glu Trp Phe	
310 315 320 325	
gaa gaa acc atc aag aag ctg cat aat ctt gtc gcc ccg cgg ata cct	
1123	
Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val Ala Pro Arg Ile Pro	
330 335 340	
gcg tcc gga cac ctc gct ttg cag gtt cga gat tcc aaa gat gag tat	
1171	
Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp Ser Lys Asp Glu Tyr	
345 350 355	
ctc gac aaa att cgc aga gcc cag gag ctg att act cgc gcc gaa tcg	
1219	
Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile Thr Arg Gly Glu Ser	
360 365 370	
tat gaa atc tgc ctg acc aca aaa ctt cag ggc acc act gat gtg gcc	
1267	
Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly Thr Thr Asp Val Ala	

375	380	385
cct ctg gct gcc tat cta gca ctg cgt ggg gcc aat ccc acc gca tat 1315		
Pro Leu Ala Ala Tyr	Leu Ala Leu Arg Gly Ala Asn Pro Thr Ala Tyr 395	400 405
ggt gcg tat ctt cag ctg ggg gat acc tct att ttg agt tcc tcg ccg 1363		
Gly Ala Tyr Leu	Gln Leu Gly Asp Thr Ser Ile Leu Ser Ser Ser Pro 410 415 420	
gag cgg ttc atc acc att gat tcg gca ggg tat gtg gaa tca aag ccc 1411		
Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr Val Glu Ser Lys Pro 425 430 435		
att aaa ggc acc agg ccg cgt ggg cga aca gcg caa gaa gac caa gaa 1459		
Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala Gln Glu Asp Gln Glu 440 445 450		
atc att gct gag ctg cgc agt aat cct aaa gat cgt gca gaa aac ttg 1507		
Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp Arg Ala Glu Asn Leu 455 460 465		
atg atc gtg gat ttg gtc cgc aac gac tta gcc cgc ggc gct ttg ccc 1555		
Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala Arg Gly Ala Leu Pro 470 475 480 485		
acc aca gtt aaa aca tcc aag ctt ttc gac gtc gaa acc tac gcc aca 1603		
Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val Glu Thr Tyr Ala Thr 490 495 500		
gtc cac caa ctt gtc agc acc gtc tct gca gag ttg ggg cca cgc agt 1651		
Val His Gln Leu Val Ser Thr Val Ser Ala Glu Leu Gly Pro Arg Ser 505 510 515		
ccg att gag tgc gtg cgc gca gca ttc ccc ggt ggt tcg atg act ggt 1699		
Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly Gly Ser Met Thr Gly 520 525 530		
gcc cca aag ctg cgc acc atg gag atc atc gat gag ctg gag gca gct 1747		
Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp Glu Leu Glu Ala Ala 535 540 545		
cct cgc ggt att tac tca ggt ggc ttg gga tat ttt tcc ctc gac ggc 1795		
Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr Phe Ser Leu Asp Gly 550 555 560 565		
gca gtt gat ctc tcc atg gtg atc aga act ctc gtc atc cag aac aat 1843		
Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu Val Ile Gln Asn Asn 570 575 580		

cac gtg gag tac gga gtg ggc ggt gca ctt ctt gct ctg tct gat ccg
1891

His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu Ala Leu Ser Asp Pro
585 590 595

gag gct gag tgg gag gaa atc cgc gtt aaa tca cgg cct ctg ctg aat
1939

Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser Arg Pro Leu Leu Asn
600 605 610

ttg ttt ggg gtt gaa ttc cca tgacgtacct cgtgtgggac ggt
1983

Leu Phe Gly Val Glu Phe Pro
615 620

<210> 460

<211> 620

<212> PRT

<213> Corynebacterium glutamicum

<400> 460

Met Arg Val Leu Ile Ile Asp Asn Tyr Asp Ser Phe Thr Phe Asn Leu
1 5 10 15

Ala Thr Tyr Val Glu Glu Val Thr Gly Gln Ala Pro Val Val Val Pro
20 25 30

Asn Asp Gln Glu Ile Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser
35 40 45

Pro Gly Pro Gly His Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala
50 55 60

Gly Val Ile Glu Arg Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly
65 70 75 80

His Gln Gly Ile Ala Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro
85 90 95

Arg Pro Val His Gly Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly
100 105 110

Leu Phe Ala Gly Ile Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser
115 120 125

Met Val Ala Thr Arg Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser
130 135 140

Asp Asp Gly Leu Ile Met Ala Leu Ala His Glu Val Leu Pro Gln Trp
145 150 155 160

Gly Val Gln Phe His Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln
165 170 175

Ile Ile Lys Asn Phe Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu
180 185 190

Thr Glu Lys Thr Ile Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu
195 200 205

Thr Phe Phe Ala His Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln
 210 215 220
 Gly Thr Ser Tyr Leu Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys
 225 230 235 240
 Thr His Asn Val Gly Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp
 245 250 255
 Leu Ala Ala Asn Ser Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp
 260 265 270
 Val Gly Tyr Val Gly Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala
 275 280 285
 Ala His Thr Ser Ser Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg
 290 295 300
 Ala Ile Ala Val Glu Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu
 305 310 315 320
 Gln Asp Glu Trp Phe Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val
 325 330 335
 Ala Pro Arg Ile Pro Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp
 340 345 350
 Ser Lys Asp Glu Tyr Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile
 355 360 365
 Thr Arg Gly Glu Ser Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly
 370 375 380
 Thr Thr Asp Val Ala Pro Leu Ala Ala Tyr Leu Ala Leu Arg Gly Ala
 385 390 395 400
 Asn Pro Thr Ala Tyr Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile
 405 410 415
 Leu Ser Ser Ser Pro Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr
 420 425 430
 Val Glu Ser Lys Pro Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala
 435 440 445
 Gln Glu Asp Gln Glu Ile Ile Ala Glu Leu Arg Ser -Asn Pro Lys Asp
 450 455 460
 Arg Ala Glu Asn Leu Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala
 465 470 475 480
 Arg Gly Ala Leu Pro Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val
 485 490 495
 Glu Thr Tyr Ala Thr Val His Gln Leu Val Ser Thr Val Ser Ala Glu
 500 505 510
 Leu Gly Pro Arg Ser Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly
 515 520 525

Gly Ser Met Thr Gly Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp
 530 535 540

Glu Leu Glu Ala Ala Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr
 545 550 555 560

Phe Ser Leu Asp Gly Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu
 565 570 575

Val Ile Gln Asn Asn His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu
 580 585 590

Ala Leu Ser Asp Pro Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser
 595 600 605

Arg Pro Leu Leu Asn Leu Phe Gly Val Glu Phe Pro
 610 615 620

<210> 461
 <211> 747
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(724)
 <223> RXA00958

<400> 461
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ccattgcgct tgctgctggt tccacttttg aggtcatccg atg aca cac gtt gtt 115
 Met Thr His Val Val
 1 5

ctc att gat aat cac gat tct ttt gtc tac aac ctg gtg gat gcg ttc 163
 Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn Leu Val Asp Ala Phe
 10 15 20

gcc gtg gcc ggt tat aag tgc acg gtg ttc cgc aat acg gtg cca gtg 211
 Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg Asn Thr Val Pro Val
 25 30 35

gaa acc att ttg gca gcc aac ccg gac ctg atc tgc ctt tca cct gga 259
 Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile Cys Leu Ser Pro Gly
 40 45 -50

cct ggt tac cct gcc gat gcg ggc aac atg atg gcg ctg atc gag cgc 307
 Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met Ala Leu Ile Glu Arg
 55 60 65

aca ctc ggc cag att cct tta ctg ggt att tgc ctc ggc tac cag gca 355
 Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys Leu Gly Tyr Gln Ala
 70 75 80 85

ctc atc gaa tac cac ggc ggc aag gtt gag cct tgt ggc cct gtg cac 403
 Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro Cys Gly Pro Val His
 90 95 100

ggc acc acc gac aac atg atc ctt act gat gca gg'z gtg cag agc cct 451

Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala Gly Val Gln Ser Pro
 105 110 115
 gtt ttt gca ggt ctt gcc act gat gtt gag cct gat cat cca gaa atc 499
 Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro Asp His Pro Glu Ile
 120 125 130
 cca ggc cgc aag gtt cca att ggc cgt tat cac tca ctg ggc tgc gtg 547
 Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His Ser Leu Gly Cys Val
 135 140 145
 gtt gcc cca gac ggt att gaa tca cta ggt acc tgt tcc tcg gag att 595
 Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr Cys Ser Ser Glu Ile
 150 155 160 165
 ggt gat gtc atc atg gcg gca cgc acc acc gat gga aag gcc att ggc 643
 Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp Gly Lys Ala Ile Gly
 170 175 180
 ctg cag ttt cac cct gag tca gtg cta agc cca acg ggt cct gtc att 691
 Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro Thr Gly Pro Val Ile
 185 190 195
 ttg tcc cgc tgt gtc gaa cag ctt ctc gcg aac taataaaaaa aggatttgat 744
 Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn
 200 205
 tca 747

<210> 462

<211> 208

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 462

Met Thr His Val Val Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn
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 Leu Val Asp Ala Phe Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg
 20 25 30
 Asn Thr Val Pro Val Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile
 35 40 45
 Cys Leu Ser Pro Gly Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met
 50 55 60
 Ala Leu Ile Glu Arg Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys
 65 70 75 80
 Leu Gly Tyr Gln Ala Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro
 85 90 95
 Cys Gly Pro Val His Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala
 100 105 110
 Gly Val Gln Ser Pro Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro
 115 120 125
 Asp His Pro Glu Ile Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His

130	135	140
Ser Leu Gly Cys Val Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr		
145	150	155 160
Cys Ser Ser Glu Ile Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp		
	165	170 175
Gly Lys Ala Ile Gly Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro		
	180	185 190
Thr Gly Pro Val Ile Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn		
	195	200 205

<210> 463
 <211> 469
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(469)
 <223> RXN03007

<400> 463
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gaacagcttc tcgcgaacta ataaaaaaag gatttgattc atg act tct cca gca 115
 Met Thr Ser Pro Ala
 1 5

aca ctg aaa gtt ctc aac gcc tac ttg gat aac ccc act cca acc ctg 163
 Thr Leu Lys Val Leu Asn Ala Tyr Leu Asp Asn Pro Thr Pro Thr Leu
 10 15 20

gag gag gca att gag gtg ttc acc ccg ctg acc gtg ggt gaa tac gat 211
 Glu Glu Ala Ile Glu Val Phe Thr Pro Leu Thr Val Gly Glu Tyr Asp
 25 30 35

gac gtg cac atc gca gcg ctg ctt gcc acc atc cgt act cgc ggt gag 259
 Asp Val His Ile Ala Ala Leu Leu Ala Thr Ile Arg Thr Arg Gly Glu
 40 45 50

cag ttc gct gat att gcc ggc gct gcc aag gcg ttc ctc gcg gcg gct 307
 Gln Phe Ala Asp Ile Ala Gly Ala Ala Lys Ala Phe Leu Ala Ala Ala
 55 60 65

cgt ccg ttc ccg att act ggc gca ggt ttg cta gat tcc gct ggt act 355
 Arg Pro Phe Pro Ile Thr Gly Ala Gly Leu Leu Asp Ser Ala Gly Thr
 70 75 80 85

ggt ggc gac ggt gcc aac acc atc aac atc acc acc ggc gca tcc ctg 403
 Gly Gly Asp Gly Ala Asn Thr Ile Asn Ile Thr Thr Gly Ala Ser Leu
 90 95 100

atc gca gca tcc ggt gga gtg aag ctg gtt aag cac ggc aac cgt tcg 451
 Ile Ala Ala Ser Gly Gly Val Lys Leu Val Lys His Gly Asn Arg Ser

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<210> 464
<211> 123
<212> PRT
<213> Corynebacterium glutamicum
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<210> 465
<211> 564
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(541)  
<223> RXN02918
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678

25	30	35	
acc ctg ttc ggg gat tta ggt tta gac gga ctc tct gga aac tac acc			259
Thr Leu Phe Gly Asp Leu Gly Leu Asp Gly Leu Ser Gly Asn Tyr Thr			
40	45	50	
gac act gag att gac ggc tac ggc gac gca ttc ctg ctg gtt gca gcg			307
Asp Thr Glu Ile Asp Gly Tyr Gly Asp Ala Phe Leu Leu Val Ala Ala			
55	60	65	
cta tcc gtg ttg atg gct gaa aac aaa gca aca ggt ggc gtg aat ctg			355
Leu Ser Val Leu Met Ala Glu Asn Lys Ala Thr Gly Gly Val Asn Leu			
70	75	80	85
ggt gag ctt ggg gga gct gat aaa tcg atc cgg ctg cat gtt gaa tcc			403
Gly Glu Leu Gly Gly Ala Asp Lys Ser Ile Arg Leu His Val Glu Ser			
90	95	100	
aag gag aac acc caa atc aac acc gca ttg aag tat ttt gcg ctc tcc			451
Lys Glu Asn Thr Gln Ile Asn Thr Ala Leu Lys Tyr Phe Ala Leu Ser			
105	110	115	
cca gaa gac cac gca gca gca gat cgc ttc gat gag gat gac ctg tct			499
Pro Glu Asp His Ala Ala Ala Asp Arg Phe Asp Glu Asp Asp Leu Ser			
120	125	130	
gag ctt gcc aac ttg agt gaa gag ctg cgc gga cag ctg gac			541
Glu Leu Ala Asn Leu Ser Glu Glu Leu Arg Gly Gln Leu Asp			
135	140	145	
taattgtctc ccatttaagg agt			564

<210> 466

<211> 147

<212> PRT

<213> Corynebacterium glutamicum

<400> 466

Met Ser Glu Ile Leu Glu Thr Tyr Trp Ala Pro His Phe Gly Lys Thr			
1	5	10	15
Glu Glu Ala Thr Ala Leu Val Ser Tyr Leu Ala Gln Ala Ser Gly Asp			
20	25	30	
Pro Ile Glu Val His Thr Leu Phe Gly Asp Leu Gly Leu Asp Gly Leu			
35	40	45	
Ser Gly Asn Tyr Thr Asp Thr Glu Ile Asp Gly Tyr Gly Asp Ala Phe			
50	55	60	
Leu Leu Val Ala Ala Leu Ser Val Leu Met Ala Glu Asn Lys Ala Thr			
65	70	75	80
Gly Gly Val Asn Leu Gly Glu Leu Gly Gly Ala Asp Lys Ser Ile Arg			
85	90	95	
Leu His Val Glu Ser Lys Glu Asn Thr Gln Ile Asn Thr Ala Leu Lys			
100	105	110	
Tyr Phe Ala Leu Ser Pro Glu Asp His Ala Ala Ala Asp Arg Phe Asp			

680

gag tgt cgc ctc cca ctg act ggc gcg aag tgc gtg gac atg att gtc 595
 Glu Cys Arg Leu Pro Leu Thr Gly Ala Lys Cys Val Asp Met Ile Val
 150 155 160 165

acc acc cac gct gtg ttc tct gtg gac cct gaa gaa ggc ctc acg ctc 643
 Thr Thr His Ala Val Phe Ser Val Asp Pro Glu Glu Gly Leu Thr Leu
 170 175 180

atc gag tgc gcc gac ggt gtc acc gtt gag gaa ctc cgc gaa atc acc 691
 Ile Glu Cys Ala Asp Gly Val Thr Val Glu Glu Leu Arg Glu Ile Thr
 185 190 195

gaa gcc gat ttc aaa gtt gct taagcaaacg ctgcgcaatt aag 735
 Glu Ala Asp Phe Lys Val Ala
 200

<210> 468

<211> 204

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 468

Met Ala Ala Arg Val Ala Gln Glu Leu Glu Asp Gly Gln Tyr Val Asn
 1 5 10 15

Leu Gly Ile Gly Met Pro Thr Leu Ile Pro Gly Tyr Leu Pro Glu Gly
 20 25 30

Leu Glu Val Ile Leu His Ser Glu Asn Gly Val Leu Gly Val Gly Pro
 35 40 45

Tyr Pro Thr Glu Glu Glu Leu Asp Pro Glu Leu Ile Asn Ala Gly Lys
 50 55 60

Glu Thr Ile Thr Val Ala Pro Gly Ala Ser Tyr Phe Ser Ser Ser Asp
 65 70 75 80

Ser Phe Ala Met Ile Arg Ser Lys Ser Val Asp Val Ala Val Leu Gly
 85 90 95

Val Met Glu Val Ser Gln Tyr Gly Asp Leu Ala Asn Trp Met Ile Pro
 100 105 110

Gly Lys Leu Val Lys Gly Met Gly Gly Ala Met Asp Leu Val His Gly
 115 120 125

Ala Ser Lys Ile Ile Ala Met Thr Asp His Ile Thr Lys Lys Gly Ala
 130 135 140

Pro Lys Ile Leu Lys Glu Cys Arg Leu Pro Leu Thr Gly Ala Lys Cys
 145 150 155 160

Val Asp Met Ile Val Thr Thr His Ala Val Phe Ser Val Asp Pro Glu
 165 170 175

Glu Gly Leu Thr Leu Ile Glu Cys Ala Asp Gly Val Thr Val Glu Glu
 180 185 190

Leu Arg Glu Ile Thr Glu Ala Asp Phe Lys Val Ala

195

200

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<210> 469
<211> 876
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(853)  
<223> RXN01115
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<400> 469															
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gccagggtct tgcagctgtc tttgaaaagg agaactaaaa atg gct att ttg cac 115															
Met Ala Ile Leu His 5															
agc gtt tcc tac gga act tcc gac aac acc ttg gtg ttc att ggc tcg 163															
Ser Val Ser Tyr Gly Thr Ser Asp Asn Thr Leu Val Phe Ile Gly Ser 20															
ttg ggt tcc acc acc gac atg tgg ctg cca cag ctg gat gcc ttg cat 211															
Leu Gly Ser Thr Thr Asp Met Trp Leu Pro Gln Leu Asp Ala Leu His 35															
aag gat ttc cgc gtc atc gct gtt gat cac cgc gga cat ggt ctg tct 259															
Lys Asp Phe Arg Val Ile Ala Val Asp His Arg Gly His Gly Leu Ser 50															
gaa ctc atc gaa ggc acc ccc act gtg gcg gat ctg gcg cag gat gtg 307															
Glu Leu Ile Glu Gly Thr Pro Thr Val Ala Asp Leu Ala Gln Asp Val 65															
ctg gat acc ctc gat gac ctg ggt gtc gga aac ttc ggc gtc atc gga 355															
Leu Asp Thr Leu Asp Asp Leu Gly Val Gly Asn Phe Gly Val Ile Gly 85															
cta tct ctc ggc gga gcg gtt gca caa tac ttg gcg gcc acc tct gat 403															
Leu Ser Leu Gly Gly Ala Val Ala Gln Tyr Leu Ala Ala Thr Ser Asp 100															
cgt gtc acc aag gca gca ttc atg tgt acc gct gca aaa ttc ggc gag 451															
Arg Val Thr Lys Ala Ala Phe Met Cys Thr Ala Ala Lys Phe Gly Glu 115															
ccc cag ggc tgg cta gat cgc gcc gca gcg tgc cgc gaa aac ggc act 499															
Pro Gln Gly Trp Leu Asp Arg Ala Ala Ala Cys Arg Glu Asn Gly Thr 130															
ggg tct ctg tcc gaa gct gtg atc cag cgc tgg ttc tcc ccc act tgg 547															
Gly Ser Leu Ser Glu Ala Val Ile Gln Arg Trp Phe Ser Pro Thr Trp 145															
ttg gag aac aac cca gcg tcc cgc gag cac ttc gaa gcc atg gtt gcc 595															
Leu Glu Asn Asn Pro Ala Ser Arg Glu His Phe Glu Ala Met Val Ala 165															
ggc acc cca tct gag ggt tac gcg ctg tgc tgc gag gcg ttg gca acc 643															

Gly Thr Pro Ser Glu Gly Tyr Ala Leu Cys Cys Glu Ala Leu Ala Thr
 170 175 180

tgg gat ttc acc gat cgc ctg gga gaa atc acc gtg cca gtg ctc acc 691
 Trp Asp Phe Thr Asp Arg Leu Gly Glu Ile Thr Val Pro Val Leu Thr
 185 190 195

atc gca ggt gcc gat gac ccc tcc act cct cca gca acc gtg cag atc 739
 Ile Ala Gly Ala Asp Asp Pro Ser Thr Pro Pro Ala Thr Val Gln Ile
 200 205 210

att gcc gat ggc gtt ggc ggc gag tcc cgc gca gag gtc cta agc cca 787
 Ile Ala Asp Gly Val Gly Gly Glu Ser Arg Ala Glu Val Leu Ser Pro
 215 220 225

gcc gcg cac gta cca acc gtg gaa cgt cca aac gag gta aat gaa ctg 835
 Ala Ala His Val Pro Thr Val Glu Arg Pro Asn Glu Val Asn Glu Leu
 230 235 240 245

cta gca cag cat ttc gct taatgttgta ggcattgttca caa 876
 Leu Ala Gln His Phe Ala
 250

<210> 470

<211> 251

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 470

Met Ala Ile Leu His Ser Val Ser Tyr Gly Thr Ser Asp Asn Thr Leu
 1 5 10 15

Val Phe Ile Gly Ser Leu Gly Ser Thr Thr Asp Met Trp Leu Pro Gln
 20 25 30

Leu Asp Ala Leu His Lys Asp Phe Arg Val Ile Ala Val Asp His Arg
 35 40 45

Gly His Gly Leu Ser Glu Leu Ile Glu Gly Thr Pro Thr Val Ala Asp
 50 55 60

Leu Ala Gln Asp Val Leu Asp Thr Leu Asp Asp Leu Gly Val Gly Asn
 65 70 75 80

Phe Gly Val Ile Gly Leu Ser Leu Gly Gly Ala Val Ala Gln Tyr Leu
 85 90 95

Ala Ala Thr Ser Asp Arg Val Thr Lys Ala Ala Phe Met Cys Thr Ala
 100 105 110

Ala Lys Phe Gly Glu Pro Gln Gly Trp Leu Asp Arg Ala Ala Ala Cys
 115 120 125

Arg Glu Asn Gly Thr Gly Ser Leu Ser Glu Ala Val Ile Gln Arg Trp
 130 135 140

Phe Ser Pro Thr Trp Leu Glu Asn Asn Pro Ala Ser Arg Glu His Phe
 145 150 155 160

Glu Ala Met Val Ala Gly Thr Pro Ser Glu Gly Tyr Ala Leu Cys Cys

684

105	110	115	
gtt ttg gaa ccg tat tac gat gcg tat gcg gcg gct att gcg ttg gcg Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu Ala 120 125 130			499
ggg gcg acg cgg gtg gcg gtt cct ttg cag gag gtg gag aac tcg tgg Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser Trp 135 140 145			547
gat gtg gat gtc gat aag ttg cat gcg gcg gtg act aag aag acg cgg Asp Val Asp Val Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr Arg 150 155 160 165			595
atg att atc gtt aat tcg ccg cat aat ccg acg ggt tcg gtg ttt tct Met Ile Ile Val Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe Ser 170 175 180			643
aag aag gcg ttg aag cag ttg gcg ggt gtt gct cgt gcg tat gac ttg Lys Lys Ala Leu Lys Gln Leu Ala Gly Val Ala Arg Ala Tyr Asp Leu 185 190 195			691
ttg gtg ttg tca gat gag gtg tat gag cat ctt gtt ttt gat gat cag Leu Val Leu Ser Asp Glu Val Tyr Glu His Leu Val Phe Asp Asp Gln 200 205 210			739
aag cat gtg agt gtc gcg aag ctg ccc ggt atg tgg gat cgc acg gtg Lys His Val Ser Val Ala Lys Leu Pro Gly Met Trp Asp Arg Thr Val 215 220 225			787
acg gtg tcg tcg gcg gcg aaa acg ttc aat gtg act ggt tgg aag acg Thr Val Ser Ser Ala Ala Lys Thr Phe Asn Val Thr Gly Trp Lys Thr 230 235 240 245			835
ggg tgg gcg ttg gca ccg gag ccg ttg ttg gag gcg gtg ttg aag gcg Gly Trp Ala Leu Ala Pro Glu Pro Leu Leu Glu Ala Val Leu Lys Ala 250 255 260			883
aag cag ttt atg tct tat gtg ggg gct aca cct ttt cag ccg gct gtg Lys Gln Phe Met Ser Tyr Val Gly Ala Thr Pro Phe Gln Pro Ala Val 265 270 275			931
gcg cat gcg att gaa cat gag cag aag tgg gtg tca aag atg tct aag Ala His Ala Ile Glu His Glu Gln Lys Trp Val Ser Lys Met Ser Lys 280 285 290			979
ggg ctt gag ctc aag cgg gat att ttg cgt act gcg tta gat aag gcg 1027 Gly Leu Glu Leu Lys Arg Asp Ile Leu Arg Thr Ala Leu Asp Lys Ala 295 300 305			
ggg ctg aag act cat gac agt atg ggc acg tat ttc atc gtt gcg gat 1075 Gly Leu Lys Thr His Asp Ser Met Gly Thr Tyr Phe Ile Val Ala Asp 310 315 320 325			
att ggg gat cgt gat ggt gcg gag ttc tgt ttt gag ttg att gag aag 1123 Ile Gly Asp Arg Asp Gly Ala Glu Phe Cys Phe Glu Leu Ile Glu Lys 330 335 340			

gtt ggg gtg gcg gcg att ccg gtg cag gcg ttt gtg gat cat ccg aag
 1171
 Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe Val Asp His Pro Lys
 345 350 355

aag tgg tcg tcg aag gtt cgt ttt gcg ttt tgc aaa aaa gaa gag acg
 1219
 Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys Lys Lys Glu Glu Thr
 360 365 370

ctc cgc gaa gct gcg gag cgt ctc aag ggg att aag aaa cta
 1261
 Leu Arg Glu Ala Ala Glu Arg Leu Lys Gly Ile Lys Lys Leu
 375 380 385

tagtttgaac aggttggttg ggg
 1284

<210> 472

<211> 387

<212> PRT

<213> Corynebacterium glutamicum

<400> 472

Met Ser Asn Asp Phe Val Val Ser Arg Leu Arg Pro Phe Gly Glu Thr
 1 5 10 15

Ile Phe Ala Thr Met Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn
 20 25 30

Leu Gly Gln Gly Phe Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu
 35 40 45

Ile Ala Ser Glu Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly
 50 55 60

Arg Gly Asp Ala Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu
 65 70 75 80

Arg Phe Asp Leu Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val
 85 90 95

Gly Ala Thr Glu Ala Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro
 100 105 110

Gly Asp Glu Val Ile Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala
 115 120 125

Ala Ile Ala Leu Ala Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu
 130 135 140

Val Glu Asn Ser Trp Asp Val Asp Val Asp Lys Leu His Ala Ala Val
 145 150 155 160

Thr Lys Lys Thr Arg Met Ile Ile Val Asn Ser Pro His Asn Pro Thr
 165 170 175

Gly Ser Val Phe Ser Lys Lys Ala Leu Lys Gln Leu Ala Gly Val Ala
 180 185 190

Arg Ala Tyr Asp Leu Leu Val Leu Ser Asp Glu Val Tyr Glu His Leu
195 200 205

Val Phe Asp Asp Gln Lys His Val Ser Val Ala Lys Leu Pro Gly Met
210 215 220

Trp Asp Arg Thr Val Thr Val Ser Ser Ala Ala Lys Thr Phe Asn Val
225 230 235 240

Thr Gly Trp Lys Thr Gly Trp Ala Leu Ala Pro Glu Pro Leu Leu Glu
245 250 255

Ala Val Leu Lys Ala Lys Gln Phe Met Ser Tyr Val Gly Ala Thr Pro
260 265 270

Phe Gln Pro Ala Val Ala His Ala Ile Glu His Glu Gln Lys Trp Val
275 280 285

Ser Lys Met Ser Lys Gly Leu Glu Leu Lys Arg Asp Ile Leu Arg Thr
290 295 300

Ala Leu Asp Lys Ala Gly Leu Lys Thr His Asp Ser Met Gly Thr Tyr
305 310 315 320

Phe Ile Val Ala Asp Ile Gly Asp Arg Asp Gly Ala Glu Phe Cys Phe
325 330 335

Glu Leu Ile Glu Lys Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe
340 345 350

Val Asp His Pro Lys Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys
355 360 365

Lys Lys Glu Glu Thr Leu Arg Glu Ala Ala Glu Arg Leu Lys Gly Ile
370 375 380

Lys Lys Leu
385

<210> 473

<211> 607

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(607)

<223> FRXA00116

<400> 473

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ttctaggctt agaccctttg gtgaaacgat ttttgcaacc atg acc cag cga gct 115
Met Thr Gln Arg Ala
1 5

gtt gag gcg ggt gca atc aat ctt ggt cag ggc ttt cct gat gag gat 163
Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly Phe Pro Asp Glu Asp
10 15 20

ggt cct cgt cgg atg tta gag atc gcg tcg gag cag att ctc ggg gga 211
 Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu Gln Ile Leu Gly Gly
 25 30 35

aat aat cag tat tcg gcg ggg cgt ggg gat gct tcg ttg agg gca gct 259
 Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala Ser Leu Arg Ala Ala
 40 45 50

gtg gct cgt gat cat ttg gag agg ttt gat ctg gag tac aac cct gat 307
 Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu Glu Tyr Asn Pro Asp
 55 60 65

tcg gag gtg ttg atc acg gtg ggg gcc act gag gcg att acg gcg act 355
 Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu Ala Ile Thr Ala Thr
 70 75 80 85

gtg ttg ggt ttg gtg gag cct ggg gat gaa gtg atc gtt ttg gaa ccg 403
 Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val Ile Val Leu Glu Pro
 90 95 100

tat tac gat gcg tat gcg gcg gct att gcg ttg gcg ggg gcg acg cgg 451
 Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu Ala Gly Ala Thr Arg
 105 110 115

gtg gcg gtt cct ttg cag gag gtg gag aac tcg tgg gat gtg gat gtc 499
 Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser Trp Asp Val Asp Val
 120 125 130

gat aag ttg cat gcg gcg gtg act aag aag acg cgg atg att atc gtt 547
 Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr Arg Met Ile Ile Val
 135 140 145

aat tcg ccg cat aat ccg acg ggt tcg gtg ttt tct aag aag gcg ttg 595
 Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe Ser Lys Lys Ala Leu
 150 155 160 165

aag cag ttg gcg 607
 Lys Gln Leu Ala

<210> 474

<211> 169

<212> PRT

<213> Corynebacterium glutamicum

<400> 474

Met Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly
 1 5 10 15

Phe Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu
 20 25 30

Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala
 35 40 45

Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu
 50 55 60

Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu
 65 70 75 80

ctg aaa aat acc ggc gac cgc gtc tat aca tcc ttg act cca atg cag 451
 Leu Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser Leu Thr Pro Met Gln
 105 110 115

 tta ctt aaa gca atg gac tcc ttg caa ggc att gaa gcc ctg aaa ctt 499
 Leu Leu Lys Ala Met Asp Ser Leu Gln Gly Ile Glu Ala Leu Lys Leu
 120 125 130

 ttt gat gtc att ctt gtt ggc ggt gct gca ttg tct aag cag gcc cga 547
 Phe Asp Val Ile Leu Val Gly Gly Ala Ala Leu Ser Lys Gln Ala Arg
 135 140 145

 att tct gcg gag cag cta gac atc aac att gtc acc acc tac ggc tcc 595
 Ile Ser Ala Glu Gln Leu Asp Ile Asn Ile Val Thr Thr Tyr Gly Ser
 150 155 160 165

 tca gag act tca ggt ggc tgc gtt tat gat ggc aag ccc att ccc ggc 643
 Ser Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly Lys Pro Ile Pro Gly
 170 175 180

 gcg aaa gtc cgt att tcg gat gag cgc att gag ttg ggt ggc ccg atg 691
 Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu Leu Gly Gly Pro Met
 185 190 195

 att gcg cag ggc tac aga aat gca cct gaa cat ccg gat ttc gcc aac 739
 Ile Ala Gln Gly Tyr Arg Asn Ala Pro Glu His Pro Asp Phe Ala Asn
 200 205 210

 gag ggt tgg ttt acc acc tct gat tca ggt gaa ctc cac gac ggg att 787
 Glu Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu Leu His Asp Gly Ile
 215 220 225

 ctc acc gtg act ggt cgc gtg gat acc cgt cat tgattccggt ggattgaagt 840
 Leu Thr Val Thr Gly Arg Val Asp Thr Arg His
 230 235 240

 tgc 843

<210> 476

<211> 240

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 476

Leu Leu Arg Asp Ser Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile
 1 5 10 15

 Ala Leu Val Met Ala Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala
 20 25 30

 Gln Leu Thr Pro Leu Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln
 35 40 45

 Phe Leu Gly Gly Glu Gly Gln Trp Leu Leu Ala Met Pro Ala His His
 50 55 60

 Ile Ala Gly Met Gln Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu
 65 70 75 80

 Pro Leu Ala Ile Asp Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala

85										90					95				
Gly	Ala	Ala	Ala	Glu	Leu	Lys	Asn	Thr	Gly	Asp	Arg	Val	Tyr	Thr	Ser				
			100						105					110					
Leu	Thr	Pro	Met	Gln	Leu	Leu	Lys	Ala	Met	Asp	Ser	Leu	Gln	Gly	Ile				
		115					120					125							
Glu	Ala	Leu	Lys	Leu	Phe	Asp	Val	Ile	Leu	Val	Gly	Gly	Ala	Ala	Leu				
	130					135					140								
Ser	Lys	Gln	Ala	Arg	Ile	Ser	Ala	Glu	Gln	Leu	Asp	Ile	Asn	Ile	Val				
145					150					155					160				
Thr	Thr	Tyr	Gly	Ser	Ser	Glu	Thr	Ser	Gly	Gly	Cys	Val	Tyr	Asp	Gly				
				165					170					175					
Lys	Pro	Ile	Pro	Gly	Ala	Lys	Val	Arg	Ile	Ser	Asp	Glu	Arg	Ile	Glu				
			180					185					190						
Leu	Gly	Gly	Pro	Met	Ile	Ala	Gln	Gly	Tyr	Arg	Asn	Ala	Pro	Glu	His				
	195						200					205							
Pro	Asp	Phe	Ala	Asn	Glu	Gly	Trp	Phe	Thr	Thr	Ser	Asp	Ser	Gly	Glu				
	210					215					220								
Leu	His	Asp	Gly	Ile	Leu	Thr	Val	Thr	Gly	Arg	Val	Asp	Thr	Arg	His				
225					230					235					240				

<210> 477

<211> 1017

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(994)

<223> RXS00393

<400> 477

tctattcatt tcacaatagc gtttcacact ccccatagc ctgccgaacg tatttcaagc 60

aattgcgcga	tcgagtatgt	gatggggaaa	gatagagggt	atg	tct	cac	acg	gaa	115
				Met	Ser	His	Thr	Glu	
				1				5	

ccc	cag	ccg	aat	tct	gta	act	ttg	tcc	gat	tgg	att	caa	ggc	gca	cgc	163
Pro	Gln	Pro	Asn	Ser	Val	Thr	Leu	Ser	Asp	Trp	Ile	Gln	Gly	Ala	Arg	
				10					15					20		

ccg	cgt	acc	tgg	gca	aat	gcg	ttc	gcg	cct	gtc	att	gcc	ggc	tca	ggc	211
Pro	Arg	Thr	Trp	Ala	Asn	Ala	Phe	Ala	Pro	Val	Ile	Ala	Gly	Ser	Gly	
			25				30						35			

gtc	gcc	gct	ttt	cat	gat	ggc	ttt	gtg	tgg	tgg	aag	gcc	ttg	ctg	gcg	259
Val	Ala	Ala	Phe	His	Asp	Gly	Phe	Val	Trp	Trp	Lys	Ala	Leu	Leu	Ala	
		40					45					50				

ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp 55 60 65	307
tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu 70 75 80 85	355
cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala 90 95 100	403
gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser 105 110 115	451
ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu 120 125 130	499
ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggg Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly 135 140 145	547
ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met 150 155 160 165	595
gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala 170 175 180	643
gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn 185 190 195	691
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att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp 230 235 240 245	835
cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala 250 255 260	883
ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccc gtc atc Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Val Ile 265 270 275	931
ggc tca aca ggg cgc gcc atg gcg ttg tgg gcc gtg ctc acg ggc ctg Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala Val Leu Thr Gly Leu 280 285 290	979

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 Ala Leu Ala Phe Ser
 295

<210> 478
 <211> 298
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 478
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 35 40 45
 Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val
 50 55 60
 Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp
 65 70 75 80
 Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys
 85 90 95
 Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala
 100 105 110
 Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly
 115 120 125
 Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro
 130 135 140
 Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly
 145 150 155 160
 Leu Val Ala Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser
 165 170 175
 Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly
 180 185 190
 Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr
 195 200 205
 Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys
 210 215 220
 Leu Phe Leu Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu
 225 230 235 240
 Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu
 245 250 255
 Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp

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	Met Ser His Thr Glu	5
	1	
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Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg		
	10 15 20	
ccg cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt 211		
Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly		
	25 30 35	
gtc gcc gct ttt cat gat ggt ttt gtg tgg tgg aag gcc ttg ctg gcg 259		
Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala		
	40 45 50	
ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat 307		
Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp		
	55 60 65	
tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg 355		
Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu		
	70 75 80 85	
cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg 403		
Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala		
	90 95 100	
gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc 451		
Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser		
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ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg 499		
Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu		
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Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly		
	135 140 145	

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 Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met
 150 155 160 165

 gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc 643
 Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala
 170 175 180

 gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac 691
 Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn
 185 190 195

 aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc 739
 Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu
 200 205 210

 gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg 787
 Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu
 215 220 225

 att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg 835
 Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp
 230 235 240 245

 cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca 883
 Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala
 250 255 260

 ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccg tca tcg 931
 Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Ser Ser
 265 270 275

 gct caa cag ggc gcg cca tgg cgt tgt ggg ccg tgc tca cgg gcc tgg 979
 Ala Gln Gln Gly Ala Pro Trp Arg Cys Gly Pro Cys Ser Arg Ala Trp
 280 285 290

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 1005
 His

<210> 480
 <211> 294
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 480
 Met Ser His Thr Glu Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp
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 Ile Gln Gly Ala Arg Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val
 20 25 30

 Ile Ala Gly Ser Gly Val Ala Ala Phe His Asp Gly Phe Val Trp Trp
 35 40 45

 Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val
 50 55 60

Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp
 65 70 75 80
 Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys
 85 90 95
 Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala
 100 105 110
 Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly
 115 120 125
 Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro
 130 135 140
 Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly
 145 150 155 160
 Leu Val Ala Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser
 165 170 175
 Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly
 180 185 190
 Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr
 195 200 205
 Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys
 210 215 220
 Leu Phe Leu Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu
 225 230 235 240
 Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu
 245 250 255
 Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp
 260 265 270
 Leu Ile Pro Ser Ser Ala Gln Gln Gly Ala Pro Trp Arg Cys Gly Pro
 275 280 285
 Cys Ser Arg Ala Trp His
 290

<210> 481

<211> 987

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(964)

<223> RXS00446

<400> 481

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 Met Gly Ala Val Glu

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ctc	cgt	gag	gct	ctt	gca	gag	cat	tta	gag	gtt	gag	ttt	gac	cag	gtc				163
Leu	Arg	Glu	Ala	Leu	Ala	Glu	His	Leu	Glu	Val	Glu	Phe	Asp	Gln	Val				
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acg	gta	ggt	tgc	ggc	tgc	tct	gcg	ctg	tgt	caa	cag	ctg	gtt	cag	gca				211
Thr	Val	Gly	Cys	Gly	Ser	Ser	Ala	Leu	Cys	Gln	Gln	Leu	Val	Gln	Ala				
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acg	tgc	gct	cag	ggc	gat	gag	gtc	att	ttt	cca	tgg	cgc	agc	ttt	gag				259
Thr	Cys	Ala	Gln	Gly	Asp	Glu	Val	Ile	Phe	Pro	Trp	Arg	Ser	Phe	Glu				
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Pro	Leu	Thr	Ala	Asp	Gln	Asn	His	Asp	Leu	Asp	Ala	Met	Ala	Ala	Ala				
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atc	act	gat	aag	acc	cgc	ctc	att	ttc	atc	tgc	aac	ccc	aac	aat	cct				403
Ile	Thr	Asp	Lys	Thr	Arg	Leu	Ile	Phe	Ile	Cys	Asn	Pro	Asn	Asn	Pro				
				90					95					100					
tgc	ggc	acc	acc	atc	acc	cag	gcg	cag	ttt	gat	aat	ttc	atg	gaa	aag				451
Ser	Gly	Thr	Thr	Ile	Thr	Gln	Ala	Gln	Phe	Asp	Asn	Phe	Met	Glu	Lys				
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Val	Pro	Asn	Asp	Val	Val	Val	Gly	Leu	Asp	Glu	Ala	Tyr	Phe	Glu	Phe				
		120					125					130							
aac	cgc	gcg	gac	gac	acc	cca	gtt	gcc	act	gag	gaa	atc	cac	cgc	cac				547
Asn	Arg	Ala	Asp	Asp	Thr	Pro	Val	Ala	Thr	Glu	Glu	Ile	His	Arg	His				
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gac	aac	gtg	att	ggt	ttg	cgc	acg	ttc	tcc	aag	gcg	tat	ggc	ctg	gcg				595
Asp	Asn	Val	Ile	Gly	Leu	Arg	Thr	Phe	Ser	Lys	Ala	Tyr	Gly	Leu	Ala				
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Gly	Leu	Arg	Val	Gly	Tyr	Ala	Phe	Gly	Asn	Ala	Glu	Ile	Ile	Ala	Ala				
			170					175						180					
atg	aat	aag	gtg	gct	att	cct	ttc	gcg	gtg	aat	tca	gca	gct	cag	gcg				691
Met	Asn	Lys	Val	Ala	Ile	Pro	Phe	Ala	Val	Asn	Ser	Ala	Ala	Gln	Ala				
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		200					205					210							
gag	gaa	acc	gtc	gaa	aag	cgt	gat	gct	gtg	gtg	tca	gcg	ctt	ggt	gct				787
Glu	Glu	Thr	Val	Glu	Lys	Arg	Asp	Ala	Val	Val	Ser	Ala	Leu	Gly	Ala				
	215					220					225								
gcg	ccg	acg	cag	gcc	aat	ttc	gtc	tgg	ctg	ccg	ggc	gag	ggc	gcc	gct				835
Ala	Pro	Thr	Gln	Ala	Asn	Phe	Val	Trp	Leu	Pro	Gly	Glu	Gly	Ala	Ala				
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 Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile Arg Ala Phe
 250 255 260

ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa act gac aag 931
 Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu Thr Asp Lys
 265 270 275

ctg ctg cgc gcg tgg gag gcc atc aat gct ggg tagtctttgg cgttttgcgg 984
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 280 285

tgc 987

<210> 482

<211> 288

<212> PRT

<213> Corynebacterium glutamicum

<400> 482

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 20 25 30

Gln Leu Val Gln Ala Thr Cys Ala Gln Gly Asp Glu Val Ile Phe Pro
 35 40 45

Trp Arg Ser Phe Glu Ala Tyr Pro Ile Phe Ala Gln Val Ala Gly Ala
 50 55 60

Thr Pro Val Ala Ile Pro Leu Thr Ala Asp Gln Asn His Asp Leu Asp
 65 70 75 80

Ala Met Ala Ala Ala Ile Thr Asp Lys Thr Arg Leu Ile Phe Ile Cys
 85 90 95

Asn Pro Asn Asn Pro Ser Gly Thr Thr Ile Thr Gln Ala Gln Phe Asp
 100 105 110

Asn Phe Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu
 115 120 125

Ala Tyr Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu
 130 135 140

Glu Ile His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys
 145 150 155 160

Ala Tyr Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala
 165 170 175

Glu Ile Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn
 180 185 190

Ser Ala Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu
 195 200 205

Leu Met Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val
 210 215 220
 Ser Ala Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro
 225 230 235 240
 Gly Glu Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile
 245 250 255
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 260 265 270
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 275 280 285

<210> 483
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 <212> DNA
 <213> *Corynebacterium glutamicum*

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 <222> (1)..(522)
 <223> FRXA00446

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 Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile
 20 25 30
 cac cgc cac gac aac gtg att ggt ttg cgc acg ttc tcc aag gcg tat 144
 His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr
 35 40 45
 ggc ctg gcg ggc ttg cgt gtt ggt tac gcc ttc gga aac gca gag atc 192
 Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile
 50 55 60
 atc gca gcg atg aat aag gtg gct att cct ttc gcg gtg aat tca gca 240
 Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala
 65 70 75 80
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 Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met
 85 90 95
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 Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala
 100 105 110
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 Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu
 115 120 125

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 Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile
 130 135 140
 cgc gcg ttc ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa 480
 Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu
 145 150 155 160
 act gac aag ctg ctg cgc gcg tgg gag gcc atc aat gct ggg 522
 Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
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 tagtcctttgg cggttttgagg tgc 545

<210> 484
 <211> 174
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 484
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 Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile
 20 25 30
 His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr
 35 40 45
 Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile
 50 55 60
 Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala
 65 70 75 80
 Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met
 85 90 95
 Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala
 100 105 110
 Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu
 115 120 125
 Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile
 130 135 140
 Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu
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 Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
 165 170

<210> 485
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1207)

<223> RXS00618

<400> 485

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cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc 163
Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys
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Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala
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Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly
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Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr
                        55 60 65

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Val Ala Met Pro Thr Pro Gly Tyr Pro Ala Tyr Arg Asn Ile Leu Glu
                        105 110 115

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Ser Leu Gly Ala Lys Val Leu Asn Leu Arg Cys Thr Ala Glu Thr Arg
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ttc cag cca acc gct caa atg ttg gag gaa ctg cca cac aag ccg aag 547
Phe Gln Pro Thr Ala Gln Met Leu Glu Glu Leu Pro His Lys Pro Lys
                        135 140 145

gct gtt att gtc acc agc cca gga aac cca acg ggc acc atc att gat 595
Ala Val Ile Val Thr Ser Pro Gly Asn Pro Thr Gly Thr Ile Ile Asp
                        150 155 160 165

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Pro Glu Glu Leu Glu Arg Ile Ala Lys Trp Cys Asp Asp Asn Asp Ala
                        170 175 180

gtt ctt atc tct gat gag gac tac cac ggc atg agc ttt ggt cgt ccg 691
Val Leu Ile Ser Asp Glu Asp Tyr His Gly Met Ser Phe Gly Arg Pro
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ctg gca act gcg cat cag ttt tcc aag aac gcc atc gtg gtg ggt acc 739

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 Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg Val Gly Trp Ile Ile
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 gtt cca gat gag ctg gtc aca ccg att gaa aac ctg cag gct tct ctt 835
 Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn Leu Gln Ala Ser Leu
 230 235 240 245
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 Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala Gly Arg Ala Ala Phe
 250 255 260
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 Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His Val Glu Ala Tyr Arg
 265 270 275
 gag gcc cgg gag gtg ttc gtc gat aag ctc cct gaa atc ggg ctt ggc 979
 Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro Glu Ile Gly Leu Gly
 280 285 290
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 Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu Trp Val Asp Val Ser
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 Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu Arg Leu Leu Asp Glu
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 330 335 340
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 His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr Ile
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<210> 486

<211> 369

<212> PRT

<213> Corynebacterium glutamicum

<400> 486

Met Gln Met Leu Asp Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp
 1 5 10 15

Thr Leu Met Phe Cys Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala
 20 25 30
 Val Ile Glu Glu Ala Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr
 35 40 45
 Thr Glu Val Ile Gly Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp
 50 55 60
 His Ser Ala Thr Tyr Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val
 65 70 75 80
 Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr Leu
 85 90 95
 Asp His Gly Asp Tyr Val Ala Met Pro Thr Pro Gly Tyr Pro Ala Tyr
 100 105 110
 Arg Asn Ile Leu Glu Ser Leu Gly Ala Lys Val Leu Asn Leu Arg Cys
 115 120 125
 Thr Ala Glu Thr Arg Phe Gln Pro Thr Ala Gln Met Leu Glu Glu Leu
 130 135 140
 Pro His Lys Pro Lys Ala Val Ile Val Thr Ser Pro Gly Asn Pro Thr
 145 150 155 160
 Gly Thr Ile Ile Asp Pro Glu Glu Leu Glu Arg Ile Ala Lys Trp Cys
 165 170 175
 Asp Asp Asn Asp Ala Val Leu Ile Ser Asp Glu Asp Tyr His Gly Met
 180 185 190
 Ser Phe Gly Arg Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala
 195 200 205
 Ile Val Val Gly Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg
 210 215 220
 Val Gly Trp Ile Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn
 225 230 235 240
 Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala
 245 250 255
 Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His
 260 265 270
 Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro
 275 280 285
 Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu
 290 295 300
 Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu
 305 310 315 320
 Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe
 325 330 335
 Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser

340

345

350

Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys
355 360 365

Lys

<210> 487

<211> 657

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) .. (634)

<223> FRXA00618

<400> 487

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				Met	Ser	Phe	Gly	Arg	5							
				1												
ccg	ctg	gca	act	gcg	cat	cag	ttt	tcc	aag	aac	gcc	atc	gtg	gtg	ggt	163
Pro	Leu	Ala	Thr	Ala	His	Gln	Phe	Ser	Lys	Asn	Ala	Ile	Val	Val	Gly	20
				10					15							
acc	ttg	tcc	aag	tac	ttc	tcc	atg	acg	ggt	tgg	cgc	gtg	ggt	tgg	atc	211
Thr	Leu	Ser	Lys	Tyr	Phe	Ser	Met	Thr	Gly	Trp	Arg	Val	Gly	Trp	Ile	35
			25					30								
atc	gtt	cca	gat	gag	ctg	gtc	aca	ccg	att	gaa	aac	ctg	cag	gct	tct	259
Ile	Val	Pro	Asp	Glu	Leu	Val	Thr	Pro	Ile	Glu	Asn	Leu	Gln	Ala	Ser	50
		40					45									
ctt	tcc	ttg	tgt	gct	cct	gcc	atc	ggg	cag	gct	gcg	gga	cgc	gca	gcc	307
Leu	Ser	Leu	Cys	Ala	Pro	Ala	Ile	Gly	Gln	Ala	Ala	Gly	Arg	Ala	Ala	65
	55					60										
ttc	act	ttg	gag	gct	ggg	gcc	gaa	ctt	gat	gcc	cac	gtt	gaa	gcg	tat	355
Phe	Thr	Leu	Glu	Ala	Gly	Ala	Glu	Leu	Asp	Ala	His	Val	Glu	Ala	Tyr	85
70					75				80							
cgc	gag	gcc	cgg	gag	gtg	ttc	gtc	gat	aag	ctc	cct	gaa	atc	ggg	ctt	403
Arg	Glu	Ala	Arg	Glu	Val	Phe	Val	Asp	Lys	Leu	Pro	Glu	Ile	Gly	Leu	95
				90					95					100		
ggc	act	ttc	gcc	gac	ccg	gat	ggc	ggc	ctg	tat	ttg	tgg	gtc	gat	gtt	451
Gly	Thr	Phe	Ala	Asp	Pro	Asp	Gly	Gly	Leu	Tyr	Leu	Trp	Val	Asp	Val	110
			105										115			
tct	gca	tac	acc	gat	gat	tca	gag	gaa	tgg	gca	ttg	cgt	ttg	ctc	gat	499
Ser	Ala	Tyr	Thr	Asp	Asp	Ser	Glu	Glu	Trp	Ala	Leu	Arg	Leu	Leu	Asp	120
			120				125					130				
gaa	gcg	ggc	gtg	gcc	gtc	gcg	ccg	ggt	gtt	gat	ttt	gat	cct	gag	gaa	547
Glu	Ala	Gly	Val	Ala	Val	Ala	Pro	Gly	Val	Asp	Phe	Asp	Pro	Glu	Glu	135
	135					140					145					

ggc cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc 595
 Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr
 150 155 160 165

att gaa ggt gtg cgc aaa atc gga gaa ttc atc aaa aaa tagcagcgac 644
 Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys Lys
 170 175

taggttagtt tcg 657

<210> 488

<211> 178

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 488

Met Ser Phe Gly Arg Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn
 1 5 10 15

Ala Ile Val Val Gly Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp
 20 25 30

Arg Val Gly Trp Ile Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu
 35 40 45

Asn Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala
 50 55 60

Ala Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala
 65 70 75 80

His Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu
 85 90 95

Pro Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr
 100 105 110

Leu Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala
 115 120 125

Leu Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp
 130 135 140

Phe Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala
 145 150 155 160

Ser Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile
 165 170 175

Lys Lys

<210> 489

<211> 385

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS
 <222> (101)..(385)
 <223> FRXA00627

<400> 489

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gaagccaagc actagaagca atgttcagcc gtttcgcgtc atg cag atg ttg gac 115
                                         Met Gln Met Leu Asp
                                         1 5
cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc 163
Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys
                        10 15 20
gct ggc cag ccg tca act ggt gcg cca gaa gca gtc atc gaa gaa gca 211
Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala
                        25 30 35
gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt 259
Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly
                        40 45 50
gat cgt gag ttc cgt gaa cgc atc gcc gat tgg cac tct gct act tat 307
Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr
                        55 60 65
gac gta gac acc aac cct gac aat gtt att gtc acc acc ggt tct tca 355
Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val Thr Thr Gly Ser Ser
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ggt gga ttc gtg gca tcg ttt atc gcc acc 385
Gly Gly Phe Val Ala Ser Phe Ile Ala Thr
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<210> 490
 <211> 95
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 490

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Met Gln Met Leu Asp Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp
  1 5 10 15
Thr Leu Met Phe Cys Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala
      20 25 30
Val Ile Glu Glu Ala Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr
      35 40 45
Thr Glu Val Ile Gly Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp
      50 55 60
His Ser Ala Thr Tyr Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val
      65 70 75 80
Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr
      85 90 95

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```

gat gtt gag cgc atc atc aac gtt gcc cca ggc atc gtg atc gtg gat 691
Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly Ile Val Ile Val Asp
185 190 195

gaa gct tat gcg gaa ttc tcc cca tca cct tca gca acc act ctt ctg 739
Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser Ala Thr Thr Leu Leu
200 205 210

gag aag tac cca acc aag ctg gtg gtg tcc cgc acc atg agt aag gct 787
Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg Thr Met Ser Lys Ala
215 220 225

ttt gat ttc gca ggt gga cgc ctc ggc tac ttc gtg gcc aac cca gcg 835
Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe Val Ala Asn Pro Ala
230 235 240 245

ttt atc gac gcc gtg atg cta gtc cgc ctt ccg tat cat ctt tca gcg 883
Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro Tyr His Leu Ser Ala
250 255 260

ctg agc caa gca gcc gca atc gta gcg ctg cgt cac tcc gct gac acg 931
Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg His Ser Ala Asp Thr
265 270 275

ctg gga acc gtc gaa aag ctc tct gta gag cgt gtt cgc gtg gca gca 979
Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg Val Arg Val Ala Ala
280 285 290

cgc ttg gag gaa ctg ggc tac gct gtg gtt cca agt gag tcc aac ttt
1027
Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro Ser Glu Ser Asn Phe
295 300 305

gtg ttc ttt gga gat ttc tcc gat cag cac gcg gca tgg cag gca ttt
1075
Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala Ala Trp Gln Ala Phe
310 315 320 325

ttg gat agg gga gtg ctc atc cgc gat gtg gga atc gct ggg cac ttg
1123
Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly Ile Ala Gly His Leu
330 335 340

cgc act acc att ggt gtg cct gag gaa aat gat gcg ttt ttg gac gca
1171
Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp Ala Phe Leu Asp Ala
345 350 355

gct gca gag atc atc aag ctg aac ctg taagagagaa gaatttttca
1218
Ala Ala Glu Ile Ile Lys Leu Asn Leu
360 365

tga
1221

<210> 492
<211> 366
<212> PRT
<213> Corynebacterium glutamicum

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<400> 492

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Met Thr Lys Ile Thr Leu Ser Asp Leu Pro Leu Arg Glu Glu Leu Arg
 1           5           10           15

Gly Glu His Ala Tyr Gly Ala Pro Gln Leu Asn Val Asp Ile Arg Leu
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Asn Thr Asn Glu Asn Pro Tyr Pro Pro Ser Glu Ala Leu Val Ala Asp
          35           40           45

Leu Val Ala Thr Val Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro
 50           55           60

Glu Arg Asp Ala Val Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr
 65           70           75           80

Lys Gln Thr Gly Val Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn
          85           90           95

Gly Ser Asn Glu Ile Leu Gln Gln Leu Leu Gln Ala Phe Gly Gly Pro
          100          105          110

Gly Arg Thr Ala Leu Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile
          115          120          125

Leu Ala Lys Gly Thr His Thr Glu Phe Ile Ala Val Ser Arg Gly Ala
          130          135          140

Asp Phe Arg Ile Asp Met Asp Val Ala Leu Glu Glu Ile Arg Ala Lys
          145          150          155          160

Gln Pro Asp Ile Val Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp
          165          170          175

Val Thr Ser Leu Asp Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly
          180          185          190

Ile Val Ile Val Asp Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser
          195          200          205

Ala Thr Thr Leu Leu Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg
          210          215          220

Thr Met Ser Lys Ala Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe
          225          230          235          240

Val Ala Asn Pro Ala Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro
          245          250          255

Tyr His Leu Ser Ala Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg
          260          265          270

His Ser Ala Asp Thr Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg
          275          280          285

Val Arg Val Ala Ala Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro
          290          295          300

Ser Glu Ser Asn Phe Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala
          305          310          315          320

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Ala Trp Gln Ala Phe Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly
 325 330 335

Ile Ala Gly His Leu Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp
 340 345 350

Ala Phe Leu Asp Ala Ala Ala Glu Ile Ile Lys Leu Asn Leu
 355 360 365

<210> 493

<211> 1752

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1729)

<223> RXS02315

<400> 493

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gaatcgtatc cgtacctgga gacgatctag actgttgctgc atg tcc agc acg cca 115
 Met Ser Ser Thr Pro
 1 5

gct caa gat ctt gcc cgc gcc gtt att gat tcc ctc gca cca cac gtc 163
 Ala Gln Asp Leu Ala Arg Ala Val Ile Asp Ser Leu Ala Pro His Val
 10 15 20

act gac gtg gtg tta tgc cca gga tcc agg aac tca ccg ttg tgc ctt 211
 Thr Asp Val Val Leu Cys Pro Gly Ser Arg Asn Ser Pro Leu Ser Leu
 25 30 35

gag ttg ctg gcg cgg cag gat ctg cgt gtc cat gtg cgt atc gac gag 259
 Glu Leu Leu Ala Arg Gln Asp Leu Arg Val His Val Arg Ile Asp Glu
 40 45 50

cgc agc gcc tca ttt ttg gcg ctg tcc cta gcg cgt acc cag gcc cgg 307
 Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala Arg Thr Gln Ala Arg
 55 60 65

ccg gtg gct gtg gtg atg acc tcc ggc acg gct gta gct aac tgc ctg 355
 Pro Val Ala Val Val Met Thr Ser Gly Thr Ala Val Ala Asn Cys Leu
 70 75 80 85

cct gct gtt gct gaa gct gcg cat gcc cat atc ccg ttg att gtg ctc 403
 Pro Ala Val Ala Glu Ala Ala His Ala His Ile Pro Leu Ile Val Leu
 90 95 100

tct gct gac cgt cct gca cat ttg gtg gga acg ggg gcg agc caa acg 451
 Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr Gly Ala Ser Gln Thr
 105 110 115

att aac cag acc ggt att ttt ggt gat ctt gca ccg acg gtc ggt atc 499
 Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala Pro Thr Val Gly Ile
 120 125 130

act gag ctg gat cag gta gcg cag att gct gaa agc ctt gct cag ggg 547

Thr	Glu	Leu	Asp	Gln	Val	Ala	Gln	Ile	Ala	Glu	Ser	Leu	Ala	Gln	Gly		
135						140					145						
gct	tcc	cag	att	ccg	cgt	cat	ttc	aat	ctt	gca	ctt	gat	gtt	cct	ttg	595	
Ala	Ser	Gln	Ile	Pro	Arg	His	Phe	Asn	Leu	Ala	Leu	Asp	Val	Pro	Leu		
150					155					160					165		
ggt	gct	cct	gaa	ctg	cca	gag	ctt	cat	ggg	gag	gca	gtt	gga	gca	tca	643	
Val	Ala	Pro	Glu	Leu	Pro	Glu	Leu	His	Gly	Glu	Ala	Val	Gly	Ala	Ser		
				170					175					180			
tgg	acg	cat	cgc	tgg	atc	aac	cac	ggg	gag	gtg	acc	gtg	gac	ctg	ggg	691	
Trp	Thr	His	Arg	Trp	Ile	Asn	His	Gly	Glu	Val	Thr	Val	Asp	Leu	Gly		
			185					190					195				
gag	cac	acc	ctc	gtg	att	gcc	ggg	gat	gaa	gca	tgg	gaa	gtg	gaa	ggg	739	
Glu	His	Thr	Leu	Val	Ile	Ala	Gly	Asp	Glu	Ala	Trp	Glu	Val	Glu	Gly		
		200					205					210					
ctg	gaa	gat	gtg	ccc	acc	atc	gct	gaa	cct	act	gca	cca	aag	cct	tat	787	
Leu	Glu	Asp	Val	Pro	Thr	Ile	Ala	Glu	Pro	Thr	Ala	Pro	Lys	Pro	Tyr		
	215					220					225						
aat	ccg	gtg	cac	cca	ctg	gct	gct	gaa	atc	ttg	ctg	aag	gag	cag	gtc	835	
Asn	Pro	Val	His	Pro	Leu	Ala	Ala	Glu	Ile	Leu	Leu	Lys	Glu	Gln	Val		
230					235					240					245		
tcc	gcg	gaa	ggc	tat	gtg	gta	aac	acc	agg	cct	gat	cat	gtg	atc	gtg	883	
Ser	Ala	Glu	Gly	Tyr	Val	Val	Asn	Thr	Arg	Pro	Asp	His	Val	Ile	Val		
				250					255					260			
gtg	gga	cac	ccc	acg	ctg	cac	cgc	gga	gtg	ttg	aag	ttg	atg	tca	gat	931	
Val	Gly	His	Pro	Thr	Leu	His	Arg	Gly	Val	Leu	Lys	Leu	Met	Ser	Asp		
			265					270					275				
cct	ggc	att	aaa	tta	act	gtg	ctt	tca	cgc	acc	gat	atc	atc	act	gat	979	
Pro	Gly	Ile	Lys	Leu	Thr	Val	Leu	Ser	Arg	Thr	Asp	Ile	Ile	Thr	Asp		
		280					285					290					
ccc	ggc	cgc	cat	gcc	gat	cag	gtg	ggc	agc	aca	gtg	aaa	gtc	acc	ggc		
1027																	
Pro	Gly	Arg	His	Ala	Asp	Gln	Val	Gly	Ser	Thr	Val	Lys	Val	Thr	Gly		
	295					300					305						
acc	cag	gaa	aag	cag	tgg	cta	aag	atc	tgt	tgc	gca	gca	tca	gaa	ctt		
1075																	
Thr	Gln	Glu	Lys	Gln	Trp	Leu	Lys	Ile	Cys	Ser	Ala	Ala	Ser	Glu	Leu		
310					315					320					325		
gcg	gcc	gat	ggg	gtg	cgt	gac	gtc	ctg	gac	aac	caa	gaa	ttc	ggg	ttc		
1123																	
Ala	Ala	Asp	Gly	Val	Arg	Asp	Val	Leu	Asp	Asn	Gln	Glu	Phe	Gly	Phe		
				330					335					340			
acc	ggc	ctc	cat	gtt	gcc	gca	gcc	gtg	gcg	gat	acc	tta	ggc	acc	ggc		
1171																	
Thr	Gly	Leu	His	Val	Ala	Ala	Ala	Val	Ala	Asp	Thr	Leu	Gly	Thr	Gly		
			345					350					355				
gat	act	ctc	ttt	gct	gca	gca	tcc	aac	tca	atc	cgt	gac	ctc	tcc	ctg		
1219																	

Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile Arg Asp Leu Ser Leu
 360 365 370
 gtg ggt atg cct ttt gat ggc gtg gat acc ttc tcc cca cga ggt gtc
 1267
 Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe Ser Pro Arg Gly Val
 375 380 385
 gca ggc att gat ggt tct gtt gct caa gca atc ggc act tca ctt gct
 1315
 Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile Gly Thr Ser Leu Ala
 390 395 400 405
 gtg cag tcc cgc cac ccc gat gaa atc cgc gcg cca cgc act gtg gcc
 1363
 Val Gln Ser Arg His Pro Asp Glu Ile Arg Ala Pro Arg Thr Val Ala
 410 415 420
 ctt ctg ggc gat ctg tcg ttc ctt cac gat att ggc gga ctg ctc atc
 1411
 Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile Gly Gly Leu Leu Ile
 425 430 435
 ggc cct gat gaa cca cgc cca gaa aac ctc acc atc gtg gtc tcc aac
 1459
 Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr Ile Val Val Ser Asn
 440 445 450
 gac aac ggt ggc gga atc ttc gaa ctc cta gaa acc ggc gca gat ggt
 1507
 Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu Thr Gly Ala Asp Gly
 455 460 465
 ctc cgc ccc aac ttc gag cgt gct ttc ggt acc cca cac gac gcg tcc
 1555
 Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr Pro His Asp Ala Ser
 470 475 480 485
 atc gcg gat ctc tgc gca ggc tac ggc att gaa cac caa gtg gta gac
 1603
 Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu His Gln Val Val Asp
 490 495 500
 aac ctc caa gac ctc atc atc gcg cta gtt gat acc acc gaa gta tcc
 1651
 Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp Thr Thr Glu Val Ser
 505 510 515
 gga ttc acc att att gaa gct tcg acc gtc cga gat acc cgc cgt gca
 1699
 Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg Asp Thr Arg Arg Ala
 520 525 530
 caa cag caa gct ctc atg gac acg gtg cac taaatggagt ggtaccaagt
 1749
 Gln Gln Gln Ala Leu Met Asp Thr Val His
 535 540
 gcg
 1752

<210> 494
 <211> 543
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 494

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Met Ser Ser Thr Pro Ala Gln Asp Leu Ala Arg Ala Val Ile Asp Ser
 1           5           10           15

Leu Ala Pro His Val Thr Asp Val Val Leu Cys Pro Gly Ser Arg Asn
           20           25           30

Ser Pro Leu Ser Leu Glu Leu Leu Ala Arg Gln Asp Leu Arg Val His
           35           40           45

Val Arg Ile Asp Glu Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala
           50           55           60

Arg Thr Gln Ala Arg Pro Val Ala Val Val Met Thr Ser Gly Thr Ala
           65           70           75           80

Val Ala Asn Cys Leu Pro Ala Val Ala Glu Ala Ala His Ala His Ile
           85           90           95

Pro Leu Ile Val Leu Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr
           100          105          110

Gly Ala Ser Gln Thr Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala
           115          120          125

Pro Thr Val Gly Ile Thr Glu Leu Asp Gln Val Ala Gln Ile Ala Glu
           130          135          140

Ser Leu Ala Gln Gly Ala Ser Gln Ile Pro Arg His Phe Asn Leu Ala
           145          150          155          160

Leu Asp Val Pro Leu Val Ala Pro Glu Leu Pro Glu Leu His Gly Glu
           165          170          175

Ala Val Gly Ala Ser Trp Thr His Arg Trp Ile Asn His Gly Glu Val
           180          185          190

Thr Val Asp Leu Gly Glu His Thr Leu Val Ile Ala Gly Asp Glu Ala
           195          200          205

Trp Glu Val Glu Gly Leu Glu Asp Val Pro Thr Ile Ala Glu Pro Thr
           210          215          220

Ala Pro Lys Pro Tyr Asn Pro Val His Pro Leu Ala Ala Glu Ile Leu
           225          230          235          240

Leu Lys Glu Gln Val Ser Ala Glu Gly Tyr Val Val Asn Thr Arg Pro
           245          250          255

Asp His Val Ile Val Val Gly His Pro Thr Leu His Arg Gly Val Leu
           260          265          270

Lys Leu Met Ser Asp Pro Gly Ile Lys Leu Thr Val Leu Ser Arg Thr
           275          280          285

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Asp Ile Ile Thr Asp Pro Gly Arg His Ala Asp Gln Val Gly Ser Thr
 290 295 300
 Val Lys Val Thr Gly Thr Gln Glu Lys Gln Trp Leu Lys Ile Cys Ser
 305 310 315 320
 Ala Ala Ser Glu Leu Ala Ala Asp Gly Val Arg Asp Val Leu Asp Asn
 325 330 335
 Gln Glu Phe Gly Phe Thr Gly Leu His Val Ala Ala Ala Val Ala Asp
 340 345 350
 Thr Leu Gly Thr Gly Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile
 355 360 365
 Arg Asp Leu Ser Leu Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe
 370 375 380
 Ser Pro Arg Gly Val Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile
 385 390 395 400
 Gly Thr Ser Leu Ala Val Gln Ser Arg His Pro Asp Glu Ile Arg Ala
 405 410 415
 Pro Arg Thr Val Ala Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile
 420 425 430
 Gly Gly Leu Leu Ile Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr
 435 440 445
 Ile Val Val Ser Asn Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu
 450 455 460
 Thr Gly Ala Asp Gly Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr
 465 470 475 480
 Pro His Asp Ala Ser Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu
 485 490 495
 His Gln Val Val Asp Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp
 500 505 510
 Thr Thr Glu Val Ser Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg
 515 520 525
 Asp Thr Arg Arg Ala Gln Gln Gln Ala Leu Met Asp Thr Val His
 530 535 540

<210> 495

<211> 1434

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1411)

<223> RXS02550

<400> 495

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				Val	Thr	Thr	Asp	Lys		
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cgc	aaa	acc	tct	aag	acc	acc	gac	acc	gcc	
Arg	Lys	Thr	Ser	Lys	Thr	Thr	Asp	Thr	Ala	
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									Ala	
									Val	
									Gly	
									Ala	
									20	
163										
gat	cag	gca	gcg	cgt	ccc	act	cgg	cga	aca	
Asp	Gln	Ala	Ala	Arg	Pro	Thr	Arg	Arg	Thr	
				25				30	Thr	
									Thr	
									Arg	
									Arg	
									Ile	
									Phe	
									Asp	
									35	
211										
cag	tcg	gag	aag	atg	aag	gac	gtg	ctg	tac	
Gln	Ser	Glu	Lys	Met	Lys	Asp	Val	Leu	Tyr	
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									Ile	
									Arg	
									Gly	
									Pro	
									Val	
									50	
259										
gcc	gcg	gag	gcg	gaa	cgc	atg	gag	ctt	gat	
Ala	Ala	Glu	Ala	Glu	Arg	Met	Glu	Leu	Asp	
				55				60	Gly	
									His	
									Asn	
									Ile	
									Leu	
									Lys	
									65	
307										
ctc	aac	acg	gga	aat	cca	gcc	gtg	ttc	gga	
Leu	Asn	Thr	Gly	Asn	Pro	Ala	Val	Phe	Gly	
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									Asp	
									Ala	
									Pro	
									Asp	
									Val	
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355										
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Ile	Met	Arg	Asp	Met	Ile	Ala	Asn	Leu	Pro	
				90				95	Thr	
									Ser	
									Gln	
									Gly	
									Tyr	
									Ser	
									100	
403										
acc	tcc	aaa	ggc	att	att	ccg	gcc	cgg	cga	
Thr	Ser	Lys	Gly	Ile	Ile	Pro	Ala	Arg	Ala	
				105				110	Val	
									Val	
									Val	
									Thr	
									Arg	
									Tyr	
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gaa	gtt	gtg	ccc	gga	ttc	ccc	cac	ttc	gat	
Glu	Val	Val	Pro	Gly	Phe	Pro	His	Phe	Asp	
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									Val	
									Asp	
									Val	
									Phe	
									Leu	
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ggc	aac	ggt	gtc	tca	gaa	cta	atc	acc	atg	
Gly	Asn	Gly	Val	Ser	Glu	Leu	Ile	Thr	Met	
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									Thr	
									Gln	
									Ala	
									Leu	
									Leu	
									145	
547										
aac	gac	ggc	gat	gaa	gtt	ctt	atc	ccc	gca	
Asn	Asp	Gly	Asp	Glu	Val	Leu	Ile	Pro	Ala	
				150				155	Pro	
									Pro	
									Asp	
									Tyr	
									Pro	
									Leu	
									Trp	
									165	
595										
act	gcc	gca	acc	tcc	ctg	gct	ggt	ggt	aag	
Thr	Ala	Ala	Thr	Ser	Leu	Ala	Gly	Gly	Lys	
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									Pro	
									Val	
									His	
									Tyr	
									Leu	
									Cys	
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643										
gat	gag	gaa	gat	gac	tgg	aac	cca	tcc	atc	
Asp	Glu	Glu	Asp	Asp	Trp	Asn	Pro	Ser	Ile	
				185				190	Glu	
									Asp	
									Ile	
									Lys	
									Ser	
									Lys	
									195	
691										
atc	tca	gag	aaa	acc	aaa	gct	att	gtg	gtg	
Ile	Ser	Glu	Lys	Thr	Lys	Ala	Ile	Val	Val	
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									Asn	
									Pro	
									Asn	
									Asn	
									Pro	
									210	
739										
acg	gga	gct	gtc	tac	ccg	cgc	cgg	gtg	ttg	
Thr	Gly	Ala	Val	Tyr	Pro	Arg	Val	Leu	Glu	
				215				220	Gln	
									Ile	
									Val	
									Glu	
									Ile	
									225	
787										

gca cgc gag cat gac ctg ctg att ttg gcc gat gaa atc tac gac cgc 835
 Ala Arg Glu His Asp Leu Leu Ile Leu Ala Asp Glu Ile Tyr Asp Arg
 230 235 240 245

att ctc tac gat gat gcc gag cac atc agc ctg gca acc ctt gca cca 883
 Ile Leu Tyr Asp Asp Ala Glu His Ile Ser Leu Ala Thr Leu Ala Pro
 250 255 260

gat ctc ctt tgc atc aca tac aac ggt cta tcc aag gca tac cgc gtc 931
 Asp Leu Leu Cys Ile Thr Tyr Asn Gly Leu Ser Lys Ala Tyr Arg Val
 265 270 275

gca gga tac cga gct ggc tgg atg gta ttg act gga cca aag caa tac 979
 Ala Gly Tyr Arg Ala Gly Trp Met Val Leu Thr Gly Pro Lys Gln Tyr
 280 285 290

gca cgt gga ttt att gag ggc ctc gaa ctc ctc gca ggc act cga ctc
 1027
 Ala Arg Gly Phe Ile Glu Gly Leu Glu Leu Leu Ala Gly Thr Arg Leu
 295 300 305

tgc cca aat gtc cca gct cag cac gct att cag gta gct ctg ggt gga
 1075
 Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln Val Ala Leu Gly Gly
 310 315 320 325

cgc cag tcc atc tac gac ctc act ggc gaa cac ggc cga ctc ctg gaa
 1123
 Arg Gln Ser Ile Tyr Asp Leu Thr Gly Glu His Gly Arg Leu Leu Glu
 330 335 340

cag cgc aac atg gca tgg acg aaa ctc aac gaa atc cca ggt gtc agc
 1171
 Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu Ile Pro Gly Val Ser
 345 350 355

tgt gtg aaa cca atg gga gct cta tac gcg ttc ccc aag ctc gac ccc
 1219
 Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe Pro Lys Leu Asp Pro
 360 365 370

aac gtg tac gaa atc cac gac gac acc caa ctc atg ctg gat ctt ctc
 1267
 Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu Met Leu Asp Leu Leu
 375 380 385

cgt gcc gag aaa atc ctc atg gtt cag ggc act ggc ttc aac tgg cca
 1315
 Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr Gly Phe Asn Trp Pro
 390 395 400 405

cat cac gat cac ttc cga gtg gtc acc ctg cca tgg gca tcc cag ttg
 1363
 His His Asp His Phe Arg Val Val Thr Leu Pro Trp Ala Ser Gln Leu
 410 415 420

gaa aac gca att gag cgc ctg ggt aac ttc ctg tcc act tac aag cag
 1411
 Glu Asn Ala Ile Glu Arg Leu Gly Asn Phe Leu Ser Thr Tyr Lys Gln
 425 430 435

tagtagttgt taggattcac cac
1434

<210> 496

<211> 437

<212> PRT

<213> Corynebacterium glutamicum

<400> 496

Val Thr Thr Asp Lys Arg Lys Thr Ser Lys Thr Thr Asp Thr Ala Asn
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Lys Ala Val Gly Ala Asp Gln Ala Ala Arg Pro Thr Arg Arg Thr Thr
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Arg Arg Ile Phe Asp Gln Ser Glu Lys Met Lys Asp Val Leu Tyr Glu
35 40 45

Ile Arg Gly Pro Val Ala Ala Glu Ala Glu Arg Met Glu Leu Asp Gly
50 55 60

His Asn Ile Leu Lys Leu Asn Thr Gly Asn Pro Ala Val Phe Gly Phe
65 70 75 80

Asp Ala Pro Asp Val Ile Met Arg Asp Met Ile Ala Asn Leu Pro Thr
85 90 95

Ser Gln Gly Tyr Ser Thr Ser Lys Gly Ile Ile Pro Ala Arg Arg Ala
100 105 110

Val Val Thr Arg Tyr Glu Val Val Pro Gly Phe Pro His Phe Asp Val
115 120 125

Asp Asp Val Phe Leu Gly Asn Gly Val Ser Glu Leu Ile Thr Met Thr
130 135 140

Thr Gln Ala Leu Leu Asn Asp Gly Asp Glu Val Leu Ile Pro Ala Pro
145 150 155 160

Asp Tyr Pro Leu Trp Thr Ala Ala Thr Ser Leu Ala Gly Gly Lys Pro
165 170 175

Val His Tyr Leu Cys Asp Glu Glu Asp Asp Trp Asn Pro Ser Ile Glu
180 185 190

Asp Ile Lys Ser Lys Ile Ser Glu Lys Thr Lys Ala Ile Val Val Ile
195 200 205

Asn Pro Asn Asn Pro Thr Gly Ala Val Tyr Pro Arg Arg Val Leu Glu
210 215 220

Gln Ile Val Glu Ile Ala Arg Glu His Asp Leu Leu Ile Leu Ala Asp
225 230 235 240

Glu Ile Tyr Asp Arg Ile Leu Tyr Asp Asp Ala Glu His Ile Ser Leu
245 250 255

Ala Thr Leu Ala Pro Asp Leu Leu Cys Ile Thr Tyr Asn Gly Leu Ser
260 265 270

Lys Ala Tyr Arg Val Ala Gly Tyr Arg Ala Gly Trp Met Val Leu Thr
 275 280 285
 Gly Pro Lys Gln Tyr Ala Arg Gly Phe Ile Glu Gly Leu Glu Leu Leu
 290 295 300
 Ala Gly Thr Arg Leu Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln
 305 310 315 320
 Val Ala Leu Gly Gly Arg Gln Ser Ile Tyr Asp Leu Thr Gly Glu His
 325 330 335
 Gly Arg Leu Leu Glu Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu
 340 345 350
 Ile Pro Gly Val Ser Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe
 355 360 365
 Pro Lys Leu Asp Pro Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu
 370 375 380
 Met Leu Asp Leu Leu Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr
 385 390 395 400
 Gly Phe Asn Trp Pro His His Asp His Phe Arg Val Val Thr Leu Pro
 405 410 415
 Trp Ala Ser Gln Leu Glu Asn Ala Ile Glu Arg Leu Gly Asn Phe Leu
 420 425 430
 Ser Thr Tyr Lys Gln
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<210> 497

<211> 1080

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1057)

<223> RXS02319

<400> 497

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 agaccttggc catttcggca gaggcttaag gttaaagatt atg agc aac tac agc 115
 Met Ser Asn Tyr Ser
 1 5
 acc gac aac cct ttt gat ccc acc caa tgg gcc acc gtt cca ggt ttt 163
 Thr Asp Asn Pro Phe Asp Pro Thr Gln Trp Ala Thr Val Pro Gly Phe
 10 15 20
 gaa gaa ttc acc gac atc acc tac cac cgc cac gtg ggc acc acc cgc 211
 Glu Glu Phe Thr Asp Ile Thr Tyr His Arg His Val Gly Thr Thr Arg
 25 30 35
 gcc gat ggc atc gtg cgc atc gcc ttc gac cgc ccc gaa gtt cgc aat 259
 Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg Pro Glu Val Arg Asn

40	45	50	
gct ttc cgc ccc cac acc gtc gac gag ctt tac caa gcc ctc gac cac Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr Gln Ala Leu Asp His 55 60 65			307
gcg cgc cgg acc cca gat gtt gga acc atc ctg ctc acc ggc aac ggc Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu Leu Thr Gly Asn Gly 70 75 80 85			355
ccc agc gaa aaa gac ggt ggc tgg gcg ttc tgc tcc ggc ggc gac caa Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys Ser Gly Gly Asp Gln 90 95 100			403
cgc atc cgc ggg cgc tcc ggc tac caa tac gcc acc gaa cac gcg cgc Arg Ile Arg 105 Arg Ser Gly Tyr Gln Tyr Ala Thr Glu His Ala Arg 110 115			451
gac gat gcc acc gct gat gtc ttc acg gta gat att gcc cgc acc aaa Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp Ile Ala Arg Thr Lys 120 125 130			499
gtt gaa ggc gga cgc ctc cac att ttg gaa gtc caa cgc ctc atc cgc Val Glu Gly Gly Arg Leu His Ile Leu Glu Val Gln Arg Leu Ile Arg 135 140 145			547
acc atg cct aaa gtt gtc atc gca gta gtc aac ggc tgg gca gcc ggc Thr Met Pro Lys Val Val Ile Ala Val Val Asn Gly Trp Ala Ala Gly 150 155 160 165			595
ggt ggg cac tcc ctc cat gtc gtt tgc gac ctc acc atc gct tcc cgc Gly Gly His Ser 170 Leu His Val Val Cys Asp Leu Thr Ile Ala Ser Arg 175 180			643
caa gaa gca cgc ttc aag caa acc gac gct gac gtg gga tcc ttc gac Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp Val Gly Ser Phe Asp 185 190 195			691
gct ggc tac ggc tcc gcc tac cta gcg aaa atg gtc gga cag aaa aac Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met Val Gly Gln Lys Asn 200 205 210			739
gcc cgc gaa atc ttc ttc ctc gga cgc acc tac gac gcc gaa cgc atg Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr Asp Ala Glu Arg Met 215 220 225			787
caa caa atg ggc gca gtc aac atc gtg gcc gac cac ggc gac cta gaa Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp His Gly Asp Leu Glu 230 235 240 245			835
aaa gaa gcc atc caa gca gcc cgc gaa atc aac acc aaa tcc ccc acc Lys Glu Ala Ile 250 Gln Ala Ala Arg Glu Ile Asn Thr Lys Ser Pro Thr 255 260			883
ggg caa cgc atg ctg aaa ttc gcc ttc aat ctc acc gac gat ggc ctc Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu Thr Asp Asp Gly Leu 265 270 275			931
atg gga caa caa gtc ttc gcc ggc gaa gcc acc cgc ctg gcc tac atg Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr Arg Leu Ala Tyr Met 280 285 290			979

acg gat gaa gcc gta gag ggt aag gaa gca ttc cta gaa aag cgc gaa
1027

Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe Leu Glu Lys Arg Glu
295 300 305

ccc aac tgg aat gaa ttc cct tac tac tac tagtgagttc atgggggtcct
1077

Pro Asn Trp Asn Glu Phe Pro Tyr Tyr Tyr
310 315

aaa
1080

<210> 498

<211> 319

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 498

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20 25 30

Val Gly Thr Thr Arg Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg
35 40 45

Pro Glu Val Arg Asn Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr
50 55 60

Gln Ala Leu Asp His Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu
65 70 75 80

Leu Thr Gly Asn Gly Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys
85 90 95

Ser Gly Gly Asp Gln Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala
100 105 110

Thr Glu His Ala Arg Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp
115 120 125

Ile Ala Arg Thr Lys Val Glu Gly Gly Arg Leu His Ile Leu Glu Val
130 135 140

Gln Arg Leu Ile Arg Thr Met Pro Lys Val Val Ile Ala Val Val Asn
145 150 155 160

Gly Trp Ala Ala Gly Gly Gly His Ser Leu His Val Val Cys Asp Leu
165 170 175

Thr Ile Ala Ser Arg Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp
180 185 190

Val Gly Ser Phe Asp Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met
195 200 205

Val Gly Gln Lys Asn Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr

210	215	220
Asp Ala Glu Arg Met Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp		
225	230	235 240
His Gly Asp Leu Glu Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn		
	245	250 255
Thr Lys Ser Pro Thr Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu		
	260	265 270
Thr Asp Asp Gly Leu Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr		
	275	280 285
Arg Leu Ala Tyr Met Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe		
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Leu Glu Lys Arg Glu Pro Asn Trp Asn Glu Phe Pro Tyr Tyr Tyr		
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<211> 384

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(361)

<223> RXS02908

<400> 499

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                                   Leu Lys Leu His Pro
                                   1 5
gag gta ctg gaa cgt gcc atc gca gat att aaa ggt gtc acc gcg gcg 163
Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys Gly Val Thr Ala Ala
                                   10 15 20
tgt gtt gtg ggt att ccc gat ccc cga tta ggc caa gca att gtg gcc 211
Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly Gln Ala Ile Val Ala
                                   25 30 35
gcg tac tcc gga tcg atc agt ccg tct gaa gtt att gaa ggc ctc gac 259
Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val Ile Glu Gly Leu Asp
                                   40 45 50
gat cta cct cgt tgg cag ctt ccc aaa cgg ctg aag cat ctg gaa tct 307
Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu Lys His Leu Glu Ser
                                   55 60 65
ttg ccc agc att ggt cct gga aaa gct gat cga cgt gct atc gcg aag 355
Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg Arg Ala Ile Ala Lys
                                   70 75 80 85
ctg ttt tagtcttcat tcttgctggc tgc 384
Leu Phe

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						Met Thr Ser Arg Thr										
						1 5										
ccg ctt gtt tct gtt ctt cct gat ttt ccg tgg gat tcg ctc gct tcc	163															
Pro Leu Val Ser Val Leu Pro Asp Phe Pro Trp Asp Ser Leu Ala Ser																
10 15 20																
gca aaa gcc aaa gct gcg tct cac ccg gat ggg atc gtg aat ctt tct																211
Ala Lys Ala Lys Ala Ala Ser His Pro Asp Gly Ile Val Asn Leu Ser																
25 30 35																
gtt ggc act ccg gtt gat ccg gtc gcg ccc agc att cag atc gcg ttg																259
Val Gly Thr Pro Val Asp Pro Val Ala Pro Ser Ile Gln Ile Ala Leu																
40 45 50																
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Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln Thr Ile Gly Thr Pro																
55 60 65																
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Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu Arg Arg Tyr Asn Met
 70 75 80 85
 aca aag ctt gtc gac gcc tcc ctc ctc ccc gtc gtg ggt acc aag gag 403
 Thr Lys Leu Val Asp Ala Ser Leu Leu Pro Val Val Gly Thr Lys Glu
 90 95 100
 gca att gcc ctt ctt cca ttc gcg ttg ggt att tcc ggc acc gtt gtc 451
 Ala Ile Ala Leu Leu Pro Phe Ala Leu Gly Ile Ser Gly Thr Val Val
 105 110 115
 atc cca gag att gcg tac cca acc tac gaa gtc gct gtc gtg gcc gca 499
 Ile Pro Glu Ile Ala Tyr Pro Thr Tyr Glu Val Ala Val Val Ala Ala
 120 125 130
 gga tgc acc gtg ttg cgt tct gat tcg ctg ttt aag ctc ggc ccg cag 547
 Gly Cys Thr Val Leu Arg Ser Asp Ser Leu Phe Lys Leu Gly Pro Gln
 135 140 145
 atc ccg tcg atg atg ttt atc aac tca cca tcc aac ccc aca ggc aag 595
 Ile Pro Ser Met Met Phe Ile Asn Ser Pro Ser Asn Pro Thr Gly Lys
 150 155 160 165
 gtt ctg ggc atc cca cac ttg cgc aag gtt gtg aag tgg gcg cag gaa 643
 Val Leu Gly Ile Pro His Leu Arg Lys Val Val Lys Trp Ala Gln Glu
 170 175 180
 aac aac gtg atc ctc gca gct gat gaa tgc tac ttg ggt ctt ggc tgg 691
 Asn Asn Val Ile Leu Ala Ala Asp Glu Cys Tyr Leu Gly Leu Gly Trp
 185 190 195
 gac gat gaa aac cca ccg atc tca att ttg gat cca cgt gtc tgc gat 739
 Asp Asp Glu Asn Pro Pro Ile Ser Ile Leu Asp Pro Arg Val Cys Asp
 200 205 210
 ggc gac cac acc aac ttg atc gcc att cac tcg ctg 775
 Gly Asp His Thr Asn Leu Ile Ala Ile His Ser Leu
 215 220 225
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 <211> 225
 <212> PRT
 <213> *Corynebacterium glutamicum*
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 20 25 30
 Ile Val Asn Leu Ser Val Gly Thr Pro Val Asp Pro Val Ala Pro Ser
 35 40 45
 Ile Gln Ile Ala Leu Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln
 50 55 60
 Thr Ile Gly Thr Pro Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu
 65 70 75 80

Arg Arg Tyr Asn Met Thr Lys Leu Val Asp Ala Ser Leu Leu Pro Val
 85 90 95
 Val Gly Thr Lys Glu Ala Ile Ala Leu Leu Pro Phe Ala Leu Gly Ile
 100 105 110
 Ser Gly Thr Val Val Ile Pro Glu Ile Ala Tyr Pro Thr Tyr Glu Val
 115 120 125
 Ala Val Val Ala Ala Gly Cys Thr Val Leu Arg Ser Asp Ser Leu Phe
 130 135 140
 Lys Leu Gly Pro Gln Ile Pro Ser Met Met Phe Ile Asn Ser Pro Ser
 145 150 155 160
 Asn Pro Thr Gly Lys Val Leu Gly Ile Pro His Leu Arg Lys Val Val
 165 170 175
 Lys Trp Ala Gln Glu Asn Asn Val Ile Leu Ala Ala Asp Glu Cys Tyr
 180 185 190
 Leu Gly Leu Gly Trp Asp Asp Glu Asn Pro Pro Ile Ser Ile Leu Asp
 195 200 205
 Pro Arg Val Cys Asp Gly Asp His Thr Asn Leu Ile Ala Ile His Ser
 210 215 220

Leu
 225

<210> 503
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(367)
 <223> RXS03026

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 Met Pro Gly Lys Ile
 1 5
 ctc ctt ctc aac ggc cca aac ctg aac atg ctg ggc aaa cgc gag cct 163
 Leu Leu Leu Asn Gly Pro Asn Leu Asn Met Leu Gly Lys Arg Glu Pro
 10 15 20
 gac att tac gga cac gac acc ttg gaa gac gtc gtc gcg ctg gca acc 211
 Asp Ile Tyr Gly His Asp Thr Leu Glu Asp Val Val Ala Leu Ala Thr
 25 30 35
 gct gag gct gcg aaa cac ggc ctt gag gtt gag gcg ctg cag agc aat 259
 Ala Glu Ala Ala Lys His Gly Leu Glu Val Glu Ala Leu Gln Ser Asn
 40 45 50
 cac caa ggt gag cta atc gat gcg ctg cac aac gct cgc ggg acc cac 307

His Gln Gly Glu Leu Ile Asp Ala Leu His Asn Ala Arg Gly Thr His
 55 60 65
 atc ggt tgc gtg att aac ccc ggc ggc ctg act aca ctt cgg tgg cgc 355
 Ile Gly Cys Val Ile Asn Pro Gly Gly Leu Thr Thr Leu Arg Trp Arg
 70 75 80 85
 ttt tgg atg ctg tgaaggcgtc tgagcttcct acc 390
 Phe Trp Met Leu

<210> 504
 <211> 89
 <212> PRT
 <213> Corynebacterium glutamicum

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 Val Ala Leu Ala Thr Ala Glu Ala Ala Lys His Gly Leu Glu Val Glu
 35 40 45
 Ala Leu Gln Ser Asn His Gln Gly Glu Leu Ile Asp Ala Leu His Asn
 50 55 60
 Ala Arg Gly Thr His Ile Gly Cys Val Ile Asn Pro Gly Gly Leu Thr
 65 70 75 80
 Thr Leu Arg Trp Arg Phe Trp Met Leu
 85

<210> 505
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(598)
 <223> RXS03074

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 Met Thr Gln Ser Ala
 1 5
 cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163
 Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn
 10 15 20
 gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211
 Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu
 25 30 35

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Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu
      40                      45                      50

ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307
Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile
      55                      60                      65

gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355
Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala
      70                      75                      80                      85

gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403
Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala
      90                      95                      100

att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451
Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala
      105                      110                      115

ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499
Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg
      120                      125                      130

gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547
Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr
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gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595
Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys
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<211> 166

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 506

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      20                      25                      30

Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
      35                      40                      45

Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
      50                      55                      60

Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
      65                      70                      75                      80

Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
      85                      90                      95

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Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr
 100 105 110

Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr
 115 120 125

Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe
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Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr
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Glu Ala Pro Ile Lys Gln
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 <211> 3075
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 <213> Corynebacterium glutamicum

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 <222> (101)..(3052)
 <223> RXC01434

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 Val Leu Gly Ala Val
 1 5

ctg aca tcg ctg gtt att ccg gtc ctt acc cgc gcg gaa aaa gaa gac 163
 Leu Thr Ser Leu Val Ile Pro Val Leu Thr Arg Ala Glu Lys Glu Asp
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gcc gac ggc ggt tcc ggg ttc ttc agg cgg ctg ctc acc ctg tcg gtg 211
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acg ctg ctg ggt ggt gtc acc atc ctg tcg att atc ggc gcg ccg ctg 259
 Thr Leu Leu Gly Gly Val Thr Ile Leu Ser Ile Ile Gly Ala Pro Leu
 40 45 50

ctg aca cgg atg atg ctg tcc tct gag gga caa gtc-aac gtg gtc atg 307
 Leu Thr Arg Met Met Leu Ser Ser Glu Gly Gln Val Asn Val Val Met
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 Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln Ile Phe Phe Tyr Gly
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ctg ttt gcc ctg ttc atg gct gtg ttg aac acc cgt gaa gtg ttc aaa 403
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 90 95 100

ccc ggc gcg tgg gca cct gtt gtc aac aat gtg atc acc ttg acc gtg 451
 Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val Ile Thr Leu Thr Val
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ctg ggc gtg tac atg gtg ctg cct gcg cgt ttg cac ccg cat gag cag	499
Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu His Pro His Glu Gln	
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Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu Gly Val Gly Thr Thr	
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Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile Pro Tyr Leu Arg Arg	
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Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile Asp Ala Arg Leu Lys	
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Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val Tyr Val Ala Ile Ser	
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Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala Ser Ile Ala Asp Asp	
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gct gcg ccg ttt att tat cag cag cac tgg atg ttg ctg caa gtt cct	787
Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met Leu Leu Gln Val Pro	
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Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala Ile Met Pro Arg Leu	
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Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala Val Val Ser Asp Leu	
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Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu Ile Pro Ile Val Val	
265 270 275	
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Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn Gly Leu Phe Ala Tyr	
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Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu Val Leu Leu His Leu	
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1123	
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 1171
 Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser Leu Leu Ala Pro Leu
 345 350 355

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 1219
 Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu Leu Gly Ala Ala Asn
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ggt ttc agt ttc atc acc ggc gcg gtc atc ggc gcg tat ctg ttg cgc
 1267
 Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly Ala Tyr Leu Leu Arg
 375 380 385

aac aaa ctc ggc ctg ttg ggt atg cgc tct ttg gct aaa acc tcc ctg
 1315
 Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu Ala Lys Thr Ser Leu
 390 395 400 405

tgg gcg ttg ggc tct gcg gcg gtt ggt gca gca gca gca tgg gcg ttg
 1363
 Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala Ala Ala Trp Ala Leu
 410 415 420

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 1411
 Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe Leu Leu Gly Thr Leu
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agc tcc gta ggc tac ttg ttg aac ctg gct gtg ttg ggt gtc ttc ttc
 1459
 Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val Leu Gly Val Phe Phe
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atc ttc gtc acc ggc atc gtg ttg tca cgt tct ggt ttg ccg gag gtc
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 Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser Gly Leu Pro Glu Val
 455 460 465

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 Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val Gly Glu Val Ser Glu
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 1651
 Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser Glu Phe Ala Ala Thr
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 Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val Arg Gly Pro Arg Leu
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 Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe Arg Leu Leu Ala Asp
 535 540 545

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 His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln Ala Arg Glu Ile Ala
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 Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp Thr Ser Gly Asn Ala
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cca ttt gcg cca ctg tct tcg gca gcc gca gcg ggc atc gcc tac gag
 1891
 Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Ala Gly Ile Ala Tyr Glu
 585 590 595

gtg cag cgc cgc acc aag aag ctg gcc agc ttg ggc agc ttg gcg gta
 1939
 Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu Gly Ser Leu Ala Val
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gcc ccc aac atc cac tcc gag gcg tac cgc aac ggt tgc ctc att gtg
 1987
 Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn Gly Cys Leu Ile Val
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 2035
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 630 635 640 645

gcc gat ccc cgc gcc gcc gcg ttc gcg ctc gcg gaa cta act gaa acc
 2083
 Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala Glu Leu Thr Glu Thr
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 680 685 690

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2323
Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala Thr Glu Asp Asn Pro
730 735 740

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2371
Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr Cys Gly Leu Phe Thr
745 750 755

gag gaa cca acc cac ctt gtg gtg aag aag gaa aag aca cca aag cct
2419
Glu Glu Pro Thr His Leu Val Val Lys Lys Glu Lys Thr Pro Lys Pro
760 765 770

gcg aca cgt gat ggt ttc ggt gcc tcc gac tac acc gtc aag ggc atg
2467
Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr Thr Val Lys Gly Met
775 780 785

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Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val Ser Leu Val Ala Ala
790 795 800 805

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Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser Ser Thr Asn Glu Gln
810 815 820

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825 830 835

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2659
Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln Ala Arg Thr Trp Asp
840 845 850

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2707
Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr Asp Gly Asn Thr Ser
855 860 865

acc gca tgg acc tcc acc ggc ggc gac ggc ctc cta gtt gac ctg tcc
2755
Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu Leu Val Asp Leu Ser
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2851
Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr Ala Phe Asn Asp Ala
905 910 915

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2899
Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile Gly Thr Val Asp Tyr
920 925 930

tcc ggc cgc agt ctc agc cac agc atc cgc gat tcc tcc aag ctt ccg
2947
Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp Ser Ser Lys Leu Pro
935 940 945

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2995
Gly Gln Val Glu Ser Val Val Ile Leu Val Asp Glu Val Arg Ser Ser
950 955 960 965

caa acc tca gac acc aat cca cag atg cag atc gct gaa gta caa ctt
3043
Gln Thr Ser Asp Thr Asn Pro Gln Met Gln Ile Ala Glu Val Gln Leu
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3075
Val Gly Trp

<210> 508
<211> 984
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 508
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35 40 45
Ile Gly Ala Pro Leu Leu Thr Arg Met Met Leu Ser Ser Glu Gly Gln
50 55 60
Val Asn Val Val Met Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln
65 70 75 80
Ile Phe Phe Tyr Gly Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr
85 90 95
Arg Glu Val Phe Lys Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val
100 105 110
Ile Thr Leu Thr Val Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu
115 120 125
His Pro His Glu Gln Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu
130 135 140
Gly Val Gly Thr Thr Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile
145 150 155 160

Pro Tyr Leu Arg Arg Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile
 165 170 175
 Asp Ala Arg Leu Lys Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val
 180 185 190
 Tyr Val Ala Ile Ser Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala
 195 200 205
 Ser Ile Ala Asp Asp Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met
 210 215 220
 Leu Leu Gln Val Pro Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala
 225 230 235 240
 Ile Met Pro Arg Leu Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala
 245 250 255
 Val Val Ser Asp Leu Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu
 260 265 270
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 275 280 285
 Gly Leu Phe Ala Tyr Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu
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 Gly Trp Thr Leu Ser Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu
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 325 330 335
 Pro Thr Phe Ile Ile Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser
 340 345 350
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 355 360 365
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 370 375 380
 Ala Tyr Leu Leu Arg Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu
 385 390 395 400
 Ala Lys Thr Ser Leu Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala
 405 410 415
 Ala Ala Trp Ala Leu Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe
 420 425 430
 Leu Leu Gly Thr Leu Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val
 435 440 445
 Leu Gly Val Phe Phe Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser
 450 455 460
 Gly Leu Pro Glu Val Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro
 465 470 475 480

Gly Leu Ser Arg Phe Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val
 485 490 495
 Gly Glu Val Ser Glu Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser
 500 505 510
 Glu Phe Ala Ala Thr Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val
 515 520 525
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 530 535 540
 Arg Leu Leu Ala Asp His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln
 545 550 555 560
 Ala Arg Glu Ile Ala Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp
 565 570 575
 Thr Ser Gly Asn Ala Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Ala
 580 585 590
 Gly Ile Ala Tyr Glu Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu
 595 600 605
 Gly Ser Leu Ala Val Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn
 610 615 620
 Gly Cys Leu Ile Val Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala
 625 630 635 640
 Val Ala Glu Ser Gly Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala
 645 650 655
 Glu Leu Thr Glu Thr Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala
 660 665 670
 Gly Leu Asp Asn Lys Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala
 675 680 685
 Val Leu Ala Leu Pro Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp
 690 695 700
 Ala Lys Ser Leu Ala Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu
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 725 730 735
 Thr Glu Asp Asn Pro Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr
 740 745 750
 Cys Gly Leu Phe Thr Glu Glu Pro Thr His Leu Val Val Lys Lys Glu
 755 760 765
 Lys Thr Pro Lys Pro Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr
 770 775 780
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 Ser Leu Val Ala Ala Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser

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Gly	Thr	Val	Asp	Tyr	Ser	Gly	Arg	Ser	Leu	Ser	His	Ser	Ile	Arg	Asp
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Ser	Ser	Lys	Leu	Pro	Gly	Gln	Val	Glu	Ser	Val	Val	Ile	Leu	Val	Asp
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<211> 930

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(907)

<223> RXC02080

<400> 509

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Leu	Gln	Ile	Val	Glu	Leu	Gly	Ala	Ile	Phe	Gly	Ala	Gly	Phe	Leu	Ala	
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Gly	Ser	Ile	Asn	Val	Ile	Val	Gly	Ala	Gly	Thr	Leu	Val	Ser	Phe	Pro	
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acc atc ggc atc gtt cct gga agt att tcg ggt gtg gtt gct tat aga	307
Thr Ile Gly Ile Val Pro Gly Ser Ile Ser Gly Val Val Ala Tyr Arg	
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Arg Glu Leu His Ala His Val Lys Thr Ile Arg Phe Leu Leu Pro Ala	
70 75 80 85	
tca atc ctc gga ggg atc acc ggc gcc tcg ctc ttg ctg cat ttc tcc	403
Ser Ile Leu Gly Gly Ile Thr Gly Ala Ser Leu Leu Leu His Phe Ser	
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Ala Asp Val Phe Thr Ala Val Ile Pro Trp Leu Ile Gly Phe Gly Thr	
105 110 115	
ctg ttg gtt atc gca ggt cca tca att aag aag cat gtt ggc gct cat	499
Leu Leu Val Ile Ala Gly Pro Ser Ile Lys Lys His Val Gly Ala His	
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Thr Ser Gly Gly Ile Ser Ala Gly Phe Arg Gln Leu Pro Phe Pro Ser	
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Arg Thr Thr Phe Ile Val Ser Val Cys Gly Ala Leu Leu Leu Gly Met	
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Tyr Gly Gly Tyr Phe Ser Ala Ala Gln Gly Ile Leu Leu Ile Ala Leu	
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Leu Gly Ile Thr Ser Thr Leu Gln Met Gln Glu Leu Asn Ala Ile Lys	
185 190 195	
aac ctc aca gtg gcg gca gtt aat ctc atc gca gcc agt gtt ttt ata	739
Asn Leu Thr Val Ala Ala Val Asn Leu Ile Ala Ala Ser Val Phe Ile	
200 205 210	
atc atc tcc cct gag ttg atc tcc tgg ccg acc gtt gcc tta atc gcg	787
Ile Ile Ser Pro Glu Leu Ile Ser Trp Pro Thr Val Ala Leu Ile Ala	
215 220 225	
ctt ggc tca gct tta ggt gga tac atc ggc gga cgg tac gcc cgc cga	835
Leu Gly Ser Ala Leu Gly Gly Tyr Ile Gly Gly Arg Tyr Ala Arg Arg	
230 235 240 245	
ctt cgc ccc agt gtt ttt aga gca ttt gtg gtc atc gtc gga atc acc	883
Leu Arg Pro Ser Val Phe Arg Ala Phe Val Val Ile Val Gly Ile Thr	
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Thr Val Ile Val Met Thr Ile Gly	
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 510

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           20           25           30

Leu Val Ser Phe Pro Ile Leu Val Phe Leu Gly Leu Pro Pro Leu Thr
           35           40           45

Ala Thr Ile Ala Asn Thr Ile Gly Ile Val Pro Gly Ser Ile Ser Gly
 50           55           60

Val Val Ala Tyr Arg Arg Glu Leu His Ala His Val Lys Thr Ile Arg
 65           70           75           80

Phe Leu Leu Pro Ala Ser Ile Leu Gly Gly Ile Thr Gly Ala Ser Leu
           85           90           95

Leu Leu His Phe Ser Ala Asp Val Phe Thr Ala Val Ile Pro Trp Leu
           100          105          110

Ile Gly Phe Gly Thr Leu Leu Val Ile Ala Gly Pro Ser Ile Lys Lys
 115           120           125

His Val Gly Ala His Thr Ser Gly Gly Ile Ser Ala Gly Phe Arg Gln
 130           135           140

Leu Pro Phe Pro Ser Arg Thr Thr Phe Ile Val Ser Val Cys Gly Ala
 145           150           155           160

Leu Leu Leu Gly Met Tyr Gly Gly Tyr Phe Ser Ala Ala Gln Gly Ile
           165           170           175

Leu Leu Ile Ala Leu Leu Gly Ile Thr Ser Thr Leu Gln Met Gln Glu
           180           185           190

Leu Asn Ala Ile Lys Asn Leu Thr Val Ala Ala Val Asn Leu Ile Ala
 195           200           205

Ala Ser Val Phe Ile Ile Ile Ser Pro Glu Leu Ile Ser Trp Pro Thr
 210           215           220

Val Ala Leu Ile Ala Leu Gly Ser Ala Leu Gly Gly Tyr Ile Gly Gly
 225           230           235           240

Arg Tyr Ala Arg Arg Leu Arg Pro Ser Val Phe Arg Ala Phe Val Val
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Ile Val Gly Ile Thr Thr Val Ile Val Met Thr Ile Gly
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<220>

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<222> (101)..(646)

<223> RXC02789

<400> 511

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                                         Met Lys Val Ser Ala
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gat aca ccc ggt cac gat gat cca ggc cca ggc cgg cgc ctt ggc tta 163
Asp Thr Pro Gly His Asp Asp Pro Gly Pro Gly Arg Arg Leu Gly Leu
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gat gtc ggc acc gtg cgc atc gga gtg gca gcc tct gac cgc gat gcc 211
Asp Val Gly Thr Val Arg Ile Gly Val Ala Ala Ser Asp Arg Asp Ala
                               25                               30                               35

aag ctt gcc atg cct gtg gaa acc gtt ccg cgg gaa act gga ttc aaa 259
Lys Leu Ala Met Pro Val Glu Thr Val Pro Arg Glu Thr Gly Phe Lys
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ggg cca gac ctg gcc gat att gat cgg ttg gtc gcc atc gtt gag gaa 307
Gly Pro Asp Leu Ala Asp Ile Asp Arg Leu Val Ala Ile Val Glu Glu
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Tyr Asn Ala Val Glu Val Ile Val Gly Leu Pro Thr Asp Leu Gln Gly
                               70                               75                               80                               85

aat ggc tcc gcc agt gtg aag cat gca aag gaa att gct ttc cgc gtc 403
Asn Gly Ser Ala Ser Val Lys His Ala Lys Glu Ile Ala Phe Arg Val
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cgt cgg cgc ctc acc aat gct gga aag aac att ccg gta cgg ctt ggc 451
Arg Arg Arg Leu Thr Asn Ala Gly Lys Asn Ile Pro Val Arg Leu Gly
                               105                               110                               115

gac gaa cgc ctc acc acc gtc gtg gcc acc caa gcc ttg cgg gcc tca 499
Asp Glu Arg Leu Thr Thr Val Val Ala Thr Gln Ala Leu Arg Ala Ser
                               120                               125                               130

gga gtc agc gaa aaa gcg gga cgt aaa gtt att gat -caa gct gcc gca 547
Gly Val Ser Glu Lys Ala Gly Arg Lys Val Ile Asp Gln Ala Ala Ala
                               135                               140                               145

gta gaa atc ctt caa acc tgg ttg gat gct cgc acc cga gcc ctt gaa 595
Val Glu Ile Leu Gln Thr Trp Leu Asp Ala Arg Thr Arg Ala Leu Glu
                               150                               155                               160                               165

cca caa tcc aca gac acc caa gat ttc gac gag aag gga aat ttc cca 643
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Gly

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                               1       5

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tgg atc gac gca gta atc ggc ggt ggc gga ctc gtc ctc atc ccg ctg	211
Trp Ile Asp Ala Val Ile Gly Gly Gly Gly Leu Val Leu Ile Pro Leu	
25 30 35	
atc ctc gcg gtc atg ccg caa ctc gca cct gtg aca gcg ctg gcc tcc	259
Ile Leu Ala Val Met Pro Gln Leu Ala Pro Val Thr Ala Leu Ala Ser	
40 45 50	
aac aaa ctg gca gcc gtc acc ggc acg gca tcg gcg gca ttc acc ctg	307
Asn Lys Leu Ala Ala Val Thr Gly Thr Ala Ser Ala Ala Phe Thr Leu	
55 60 65	
gtc agg cgc gtc aaa ccc gac aaa aaa ctg ctt gcg ctc tac gtt ctg	355
Val Arg Arg Val Lys Pro Asp Lys Lys Leu Leu Ala Leu Tyr Val Leu	
70 75 80 85	
gtg gca gct gtg tgc tcc ggt gca ggc gcc ctg gct gcg agt ctc att	403
Val Ala Ala Val Cys Ser Gly Ala Gly Ala Leu Ala Ala Ser Leu Ile	
90 95 100	
gac aaa caa atc atg cga ccg ctg atc atc gtg ttg atg ctg gtc gtt	451
Asp Lys Gln Ile Met Arg Pro Leu Ile Ile Val Leu Met Leu Val Val	
105 110 115	
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Gly Leu Ile Val Val Phe Lys Pro Asn Phe Gly Thr Gly Glu Ser Lys	
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gcc ctg ccc acc gga tgg aaa cgc tgg gcc gcc atc gtt gca gtc gga	547
Ala Leu Pro Thr Gly Trp Lys Arg Trp Ala Ala Ile Val Ala Val Gly	
135 140 145	
ctc atc gca gcc tac gac ggc atc ttc gga ccc gga acc ggc atg ttc	595
Leu Ile Ala Ala Tyr Asp Gly Ile Phe Gly Pro Gly Thr Gly Met Phe	
150 155 160 165	
ctc atc atg gcg ttc acc gca ctg ctc tcc caa aat ttc ctg tcc tcc	643
Leu Ile Met Ala Phe Thr Ala Leu Leu Ser Gln Asn Phe Leu Ser Ser	
170 175 180	
gca gcc atg gcg aag gtc gta aac acc gca aca aac ctg ggt gcg cta	691
Ala Ala Met Ala Lys Val Val Asn Thr Ala Thr Asn Leu Gly Ala Leu	
185 190 195	
att gta ttc atc atc ggc ggc cac atg tgg tgg acc cta gga ctc gtg	739
Ile Val Phe Ile Ile Gly Gly His Met Trp Trp Thr Leu Gly Leu Val	
200 205 210	
ctg gca gtc gcc aat gtc gca ggc gca caa ctc ggt gcc cga acg gtg	787
Leu Ala Val Ala Asn Val Ala Gly Ala Gln Leu Gly Ala Arg Thr Val	
215 220 225	
ctt ggt ggc ggt acc agg cta att aga tac gca cta cta acc ctg gtt	835
Leu Gly Gly Gly Thr Arg Leu Ile Arg Tyr Ala Leu Leu Thr Leu Val	
230 235 240 245	

gtc gtc atg agc gtc tac ctc acc tgg caa caa atc caa gga atg 880
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<212> PRT

<213> Corynebacterium glutamicum

<400> 514

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 35 40 45
 Thr Ala Leu Ala Ser Asn Lys Leu Ala Ala Val Thr Gly Thr Ala Ser
 50 55 60
 Ala Ala Phe Thr Leu Val Arg Arg Val Lys Pro Asp Lys Lys Leu Leu
 65 70 75 80
 Ala Leu Tyr Val Leu Val Ala Ala Val Cys Ser Gly Ala Gly Ala Leu
 85 90 95
 Ala Ala Ser Leu Ile Asp Lys Gln Ile Met Arg Pro Leu Ile Ile Val
 100 105 110
 Leu Met Leu Val Val Gly Leu Ile Val Val Phe Lys Pro Asn Phe Gly
 115 120 125
 Thr Gly Glu Ser Lys Ala Leu Pro Thr Gly Trp Lys Arg Trp Ala Ala
 130 135 140
 Ile Val Ala Val Gly Leu Ile Ala Ala Tyr Asp Gly Ile Phe Gly Pro
 145 150 155 160
 Gly Thr Gly Met Phe Leu Ile Met Ala Phe Thr Ala Leu Leu Ser Gln
 165 170 175
 Asn Phe Leu Ser Ser Ala Ala Met Ala Lys Val Val Asn Thr Ala Thr
 180 185 190
 Asn Leu Gly Ala Leu Ile Val Phe Ile Ile Gly Gly His Met Trp Trp
 195 200 205
 Thr Leu Gly Leu Val Leu Ala Val Ala Asn Val Ala Gly Ala Gln Leu
 210 215 220
 Gly Ala Arg Thr Val Leu Gly Gly Gly Thr Arg Leu Ile Arg Tyr Ala
 225 230 235 240
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 245 250 255

Ile Gln Gly Met
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<213> Corynebacterium glutamicum

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<222> (101)..(1132)
<223> RXN03063

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Val Glu Asp Leu Ser
1 5
tac cgc atc ccg cag tcg cgc acc gtg gcc gag cag gtg cca ggg ccg 163
Tyr Arg Ile Pro Gln Ser Arg Thr Val Ala Glu Gln Val Pro Gly Pro
10 15 20
aag tcg aaa gcg ctg gat gag cgt cga caa gca gca gta gca cga gca 211
Lys Ser Lys Ala Leu Asp Glu Arg Arg Gln Ala Ala Val Ala Arg Ala
25 30 35
ctt gca ccg ggt ctg cct gga tac gtg gtg gac gca gac ggt ggc atc 259
Leu Ala Pro Gly Leu Pro Gly Tyr Val Val Asp Ala Asp Gly Gly Ile
40 45 50
ttg gct gac gcg gac ggc aac cgt ttc atc gac ctg gcc tcc ggc atc 307
Leu Ala Asp Ala Asp Gly Asn Arg Phe Ile Asp Leu Ala Ser Gly Ile
55 60 65
gcc gtg acc acg gtc ggc gga tcc aac gcg gcc gtc gcg aaa gcc gtc 355
Ala Val Thr Thr Val Gly Gly Ser Asn Ala Ala Val Ala Lys Ala Val
70 75 80 85
ggc gcc gca gct gcc cgc ttc acc cac acc tgc ttc atg gtc tca cct 403
Gly Ala Ala Ala Arg Phe Thr His Thr Cys Phe Met Val Ser Pro
90 95 100
tat gaa act tac gtg gcc atg gcg gag aga ctc aac gcc ttg act cca 451
Tyr Glu Thr Tyr Val Ala Met Ala Glu Arg Leu Asn Ala Leu Thr Pro
105 110 115
ggc gat cac gac aag aag agc gcg ctg ttt aac tct ggc gcc gaa gcc 499
Gly Asp His Asp Lys Lys Ser Ala Leu Phe Asn Ser Gly Ala Glu Ala
120 125 130
gtg gaa aac gcc gtc aag gtg gca cgc gcc tac acc ggc aag ggc gcg 547
Val Glu Asn Ala Val Lys Val Ala Arg Ala Tyr Thr Gly Lys Gly Ala
135 140 145
gtc gtg gtg ttc gac aac gcg tac cac gga cgg acc aac ctc acc atg 595
Val Val Val Phe Asp Asn Ala Tyr His Gly Arg Thr Asn Leu Thr Met
150 155 160 165

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 Ala Met Thr Ala Lys Asn Arg Pro Tyr Lys Ser Gly Phe Gly Pro Leu
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gcc gca gac gtc tac cgt gca cca atg tct tac cca ctg cgc gac gga 691
 Ala Ala Asp Val Tyr Arg Ala Pro Met Ser Tyr Pro Leu Arg Asp Gly
 185 190 195

ctg tcc ggc ccg gaa gcc gca gag cgc gcg atc tcc gtg atc gaa tcc 739
 Leu Ser Gly Pro Glu Ala Ala Glu Arg Ala Ile Ser Val Ile Glu Ser
 200 205 210

cag gtc gga gcc gaa aac ctc gcc tgc gtg gtc att gaa ccg atc cag 787
 Gln Val Gly Ala Glu Asn Leu Ala Cys Val Val Ile Glu Pro Ile Gln
 215 220 225

ggc gaa ggc gga ttc atc gtc ccc gca cca gga ttc ctc gca gcc att 835
 Gly Glu Gly Gly Phe Ile Val Pro Ala Pro Gly Phe Leu Ala Ala Ile
 230 235 240 245

tcc acc tgg tgc cgc gag aac gac gtg gtg ttc atc gcc gat gaa atc 883
 Ser Thr Trp Cys Arg Glu Asn Asp Val Val Phe Ile Ala Asp Glu Ile
 250 255 260

caa tct ggc ttc ctg cgc acc ggc gac tgg ttc gcc agc gac gca gaa 931
 Gln Ser Gly Phe Leu Arg Thr Gly Asp Trp Phe Ala Ser Asp Ala Glu
 265 270 275

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 Gly Val Ile Pro Asp Val Ile Thr Thr Ala Lys Gly Ile Ala Gly Gly
 280 285 290

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 1027
 Met Pro Leu Ser Ala Val Thr Gly Arg Ala Glu Ile Met Asp Ala Pro
 295 300 305

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 1075
 Gly Pro Gly Ala Leu Gly Gly Thr Tyr Gly Gly Asn Pro Val Ala Cys
 310 315 320 325

gcc gcg gca ctt gca gcc att gaa gtg atg gaa caa gcc gac ctt aag
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<212> PRT

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<400> 516

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 35 40 45
 Ala Asp Gly Gly Ile Leu Ala Asp Ala Asp Gly Asn Arg Phe Ile Asp
 50 55 60
 Leu Ala Ser Gly Ile Ala Val Thr Thr Val Gly Gly Ser Asn Ala Ala
 65 70 75 80
 Val Ala Lys Ala Val Gly Ala Ala Ala Ala Arg Phe Thr His Thr Cys
 85 90 95
 Phe Met Val Ser Pro Tyr Glu Thr Tyr Val Ala Met Ala Glu Arg Leu
 100 105 110
 Asn Ala Leu Thr Pro Gly Asp His Asp Lys Lys Ser Ala Leu Phe Asn
 115 120 125
 Ser Gly Ala Glu Ala Val Glu Asn Ala Val Lys Val Ala Arg Ala Tyr
 130 135 140
 Thr Gly Lys Gly Ala Val Val Val Phe Asp Asn Ala Tyr His Gly Arg
 145 150 155 160
 Thr Asn Leu Thr Met Ala Met Thr Ala Lys Asn Arg Pro Tyr Lys Ser
 165 170 175
 Gly Phe Gly Pro Leu Ala Ala Asp Val Tyr Arg Ala Pro Met Ser Tyr
 180 185 190
 Pro Leu Arg Asp Gly Leu Ser Gly Pro Glu Ala Ala Glu Arg Ala Ile
 195 200 205
 Ser Val Ile Glu Ser Gln Val Gly Ala Glu Asn Leu Ala Cys Val Val
 210 215 220
 Ile Glu Pro Ile Gln Gly Glu Gly Gly Phe Ile Val Pro Ala Pro Gly
 225 230 235 240
 Phe Leu Ala Ala Ile Ser Thr Trp Cys Arg Glu Asn Asp Val Val Phe
 245 250 255
 Ile Ala Asp Glu Ile Gln Ser Gly Phe Leu Arg Thr Gly Asp Trp Phe
 260 265 270
 Ala Ser Asp Ala Glu Gly Val Ile Pro Asp Val Ile Thr Thr Ala Lys
 275 280 285
 Gly Ile Ala Gly Gly Met Pro Leu Ser Ala Val Thr Gly Arg Ala Glu
 290 295 300
 Ile Met Asp Ala Pro Gly Pro Gly Ala Leu Gly Gly Thr Tyr Gly Gly
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Gln Ala Asp Leu Lys Thr Arg Ala
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<211> 1491

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(1468)

<223> RXN02970

<400> 517

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                                   Leu Ala Leu Lys Gly
                                   1          5

tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca      163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
              10              15              20

aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc      211
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
              25              30              35

cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct      259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
              40              45              50

gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac      307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
              55              60              65

atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga      355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
              70              75              80              85

tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac      403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
              90              95              100

ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg      451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
              105              110              115

tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc      499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
              120              125              130

gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga      547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
              135              140              145

cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga      595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
              150              155              160              165

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Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr	
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Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser	
185 190 195	
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag	739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys	
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His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala	
215 220 225	
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Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro	
230 235 240 245	
gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc	883
Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile	
250 255 260	
ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa	931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys	
265 270 275	
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Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile	
280 285 290	
acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc	1027
Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile	
295 300 305	
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Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser	
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Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys	
330 335 340	
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Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala	
345 350 355	
cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa	1219
Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu	
360 365 370	
gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca	1267
Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala	
375 380 385	

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 1315
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 1363
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 425 430 435

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 35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
 50 55 60

Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
 65 70 75 80

His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
 85 90 95

Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
 100 105 110

Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
 115 120 125

Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
 130 135 140

Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr

145					150					155				160	
His	Gly	Ala	Thr	Gly	Ser	Ala	Met	Met	Leu	Thr	Gly	Glu	His	Arg	Arg
				165					170					175	
Leu	Gly	Asn	Pro	Thr	Thr	Asp	Pro	Asp	Ile	Tyr	His	Phe	Trp	Ala	Pro
			180					185					190		
Phe	Leu	His	His	Ser	Ser	Phe	Phe	Ala	Thr	Thr	Gln	Glu	Glu	Glu	Cys
		195					200					205			
Glu	Arg	Ala	Leu	Lys	His	Leu	Glu	Asp	Val	Ile	Ala	Phe	Glu	Gly	Ala
	210					215					220				
Gly	Met	Ile	Ala	Ala	Ile	Val	Leu	Glu	Pro	Val	Val	Gly	Ser	Ser	Gly
225					230					235					240
Ile	Ile	Leu	Pro	Pro	Ala	Gly	Tyr	Leu	Asn	Gly	Val	Arg	Glu	Leu	Cys
				245					250					255	
Asn	Lys	His	Gly	Ile	Leu	Phe	Ile	Ala	Asp	Glu	Val	Met	Val	Gly	Phe
			260					265					270		
Gly	Arg	Thr	Gly	Lys	Leu	Phe	Ala	Tyr	Glu	His	Ala	Gly	Asp	Asp	Phe
		275					280					285			
Gln	Pro	Asp	Met	Ile	Thr	Phe	Ala	Lys	Gly	Val	Asn	Ala	Gly	Tyr	Ala
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Pro	Leu	Gly	Gly	Ile	Val	Met	Thr	Gln	Ser	Ile	Arg	Asp	Thr	Phe	Gly
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Ser	Glu	Ala	Tyr	Ser	Gly	Gly	Leu	Thr	Tyr	Ser	Gly	His	Pro	Leu	Ala
				325					330					335	
Val	Ala	Pro	Ala	Lys	Ala	Ala	Leu	Glu	Ile	Tyr	Ala	Glu	Gly	Glu	Ile
			340					345					350		
Ile	Pro	Arg	Val	Ala	Arg	Leu	Gly	Ala	Glu	Leu	Ile	Glu	Pro	Arg	Leu
		355					360					365			
Arg	Glu	Leu	Ala	Glu	Glu	Asn	Val	Ala	Ile	Ala	Asp	Val	Arg	Gly	Ile
	370					375					380				
Gly	Phe	Phe	Trp	Ala	Val	Glu	Phe	Asn	Ala	Asp	Ala	Thr	Ala	Met	Ala
385					390					395					400
Ala	Gly	Ala	Ala	Glu	Phe	Lys	Glu	Arg	Gly	Val	Trp	Pro	Met	Ile	Ser
				405					410					415	
Gly	Asn	Arg	Phe	His	Ile	Ala	Pro	Pro	Leu	Thr	Thr	Thr	Asp	Asp	Glu
			420					425					430		
Leu	Val	Ala	Leu	Leu	Asp	Ala	Val	Glu	Ala	Ala	Ala	Gln	Ala	Val	Glu
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 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1330)
 <223> FRXA01009

<400> 519

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Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
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aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
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cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
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gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
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Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
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tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
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ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
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tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
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gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
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cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
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tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc 643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr
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 Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys
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 cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg 787
 His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala
 215 220 225
 atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca 835
 Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro
 230 235 240 245
 gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc 883
 Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile
 250 255 260
 ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa 931
 Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys
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 Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile
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 1027
 Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile
 295 300 305
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 345 350 355
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 1219
 Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu
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 1267
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 375 380 385
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 <213> Corynebacterium glutamicum

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Arg	Ala	His	Val	Phe	His	Ser	Trp	Ser	Ala	Gln	Asp	Lys	Ile	Ser	Pro
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Lys	Val	Trp	Ala	Ala	Ala	Glu	Gly	Ser	Thr	Leu	Tyr	Asp	Phe	Asp	Gly
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Asn	Ala	Phe	Ile	Asp	Met	Gly	Ser	Gln	Leu	Val	Ser	Ala	Asn	Leu	Gly
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His	Asn	Asn	Pro	Arg	Leu	Val	Glu	Ala	Ile	Gln	Arg	Gln	Ala	Ala	Arg
				85					90					95	
Leu	Thr	Asn	Ile	Asn	Pro	Ala	Phe	Gly	Asn	Asp	Val	Arg	Ser	Asp	Val
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Ala	Ala	Lys	Ile	Val	Ser	Met	Ala	Arg	Gly	Glu	Phe	Ser	His	Val	Phe
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Phe	Thr	Asn	Gly	Gly	Ala	Asp	Ala	Ile	Glu	His	Ser	Ile	Arg	Met	Ala
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His	Gly	Ala	Thr	Gly	Ser	Ala	Met	Met	Leu	Thr	Gly	Glu	His	Arg	Arg
			165						170					175	
Leu	Gly	Asn	Pro	Thr	Thr	Asp	Pro	Asp	Ile	Tyr	His	Phe	Trp	Ala	Pro
			180					185					190		
Phe	Leu	His	His	Ser	Ser	Phe	Phe	Ala	Thr	Thr	Gln	Glu	Glu	Glu	Cys
		195					200					205			
Glu	Arg	Ala	Leu	Lys	His	Leu	Glu	Asp	Val	Ile	Ala	Phe	Glu	Gly	Ala
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Gly	Met	Ile	Ala	Ala	Ile	Val	Leu	Glu	Pro	Val	Val	Gly	Ser	Ser	Gly
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Ile	Ile	Leu	Pro	Pro	Ala	Gly	Tyr	Leu	Asn	Gly	Val	Arg	Glu	Leu	Cys
			245						250					255	

Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe
 260 265 270
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe
 275 280 285
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala
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 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly
 305 310 315 320
 Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala
 325 330 335
 Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile
 340 345 350
 Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu
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 <223> RXA01551

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 Leu Lys Ala Val Pro
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 Thr Gly Ala Arg Ala Arg Ala Glu Ile Ala Leu Ile Ala Ala Arg Ala
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 Pro Phe Glu Pro Val Arg Leu Ala Pro Ala Lys Glu Glu Arg Asn Gly
 25 30 35
 gca atg acg cct acc caa aat gag atc cac ccg aaa cat agc tac tcc 259
 Ala Met Thr Pro Thr Gln Asn Glu Ile His Pro Lys His Ser Tyr Ser
 40 45 50
 ccc atc cgc aag gac ggt ctc gag gtc ccg gag acc gaa atc cgc ctc 307

Pro Ile Arg Lys Asp Gly Leu Glu Val Pro Glu Thr Glu Ile Arg Leu
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 Asp Asp Ser Pro Ser Gly Pro Asn Glu Pro Phe Arg Ile Tyr Arg Thr
 70 75 80 85
 cgt ggc cca gaa acc aac ccc aag cag gga ctt ccg cgg ctg cgc gag 403
 Arg Gly Pro Glu Thr Asn Pro Lys Gln Gly Leu Pro Arg Leu Arg Glu
 90 95 100
 tca tgg atc acc gcc cgc ggc gac gtt gcc acc tat cag ggg cgc gag 451
 Ser Trp Ile Thr Ala Arg Gly Asp Val Ala Thr Tyr Gln Gly Arg Glu
 105 110 115
 cgt ttg ctt atc gac gac ggc cgc tcg gca atg cgt cga ggt caa gct 499
 Arg Leu Leu Ile Asp Asp Gly Arg Ser Ala Met Arg Arg Gly Gln Ala
 120 125 130
 tcg gct gag tgg aaa ggc caa aaa cca gct cct ttg aag gcg cta cct 547
 Ser Ala Glu Trp Lys Gly Gln Lys Pro Ala Pro Leu Lys Ala Leu Pro
 135 140 145
 ggc aaa aga gtc acc caa atg gcc tat gca cgt gct ggc gtg att act 595
 Gly Lys Arg Val Thr Gln Met Ala Tyr Ala Arg Ala Gly Val Ile Thr
 150 155 160 165
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 Arg Glu Met Glu Phe Val Ala Leu Arg Glu His Val Asp Ala Glu Phe
 170 175 180
 gtg cgc tct gag gtg gcg cgc ggt cgg gcc att att ccc aac aac gtc 691
 Val Arg Ser Glu Val Ala Arg Gly Arg Ala Ile Ile Pro Asn Asn Val
 185 190 195
 aac cac ccc gaa tct gaa ccg atg att att ggt cgc aaa ttt ttg acc 739
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 215 220 225
 gaa gag gtg tcc aag ctg cag tgg gcc acg cgc tgg ggt gcc gat acc 835
 Glu Glu Val Ser Lys Leu Gln Trp Ala Thr Arg Trp Gly Ala Asp Thr
 230 235 240 245
 gtg atg gat cta tcc acc ggc gat gat att cac acc acc cgc gaa tgg 883
 Val Met Asp Leu Ser Thr Gly Asp Asp Ile His Thr Thr Arg Glu Trp
 250 255 260
 att atc cgc aac tcc ccc gtt cct atc ggc acc gtc ccg atc tac caa 931
 Ile Ile Arg Asn Ser Pro Val Pro Ile Gly Thr Val Pro Ile Tyr Gln
 265 270 275
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 1027

Phe Arg Asp Thr Ile Ile Glu Gln Cys Glu Gln Gly Val Asp Tyr Met
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 1123
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 330 335 340
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 1267
 Gly Leu Arg Pro Gly Ser Leu Ala Asp Ala Asn Asp Ala Ala Gln Phe
 375 380 385
 gcc gag ctg aaa acc att ggt gag ctc acc caa cgc gcc tgg gaa tac
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 Ala Glu Leu Lys Thr Ile Gly Glu Leu Thr Gln Arg Ala Trp Glu Tyr
 390 395 400 405
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 1363
 Asp Val Gln Val Met Val Glu Gly Pro Gly His Val Pro Leu Asn Met
 410 415 420
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 1411
 Ile Gln Glu Asn Asn Glu Leu Glu Gln Lys Trp Ala Ala Asp Ala Pro
 425 430 435
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 1459
 Phe Tyr Thr Leu Gly Pro Leu Val Thr Asp Ile Ala Pro Gly Tyr Asp
 440 445 450
 cac atc act tct gcc att ggt gca gct cac atc gcc atg ggt ggc acc
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 His Ile Thr Ser Ala Ile Gly Ala Ala His Ile Ala Met Gly Gly Thr
 455 460 465
 gcc atg ctg tgt tat gtc acc ccg aaa gaa cac ctt ggc ctg ccc aac
 1555
 Ala Met Leu Cys Tyr Val Thr Pro Lys Glu His Leu Gly Leu Pro Asn
 470 475 480 485
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 1603
 Arg Asp Asp Val Lys Thr Gly Val Ile Thr Tyr Lys Leu Ala Ala His

490 495 500
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 1651
 Ala Ala Asp Val Ala Lys Gly His Pro Gly Ala Arg Ala Trp Asp Asp
 505 510 515
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 1699
 Ala Met Ser Lys Ala Arg Phe Glu Phe Arg Trp Asn Asp Gln Phe Ala
 520 525 530
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 1747
 Leu Ser Leu Asp Pro Asp Thr Ala Ile Ala Tyr His Asp Glu Thr Leu
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 1795
 Pro Ala Glu Pro Ala Lys Thr Ala His Phe Cys Ser Met Cys Gly Pro
 550 555 560 565
 aag ttc tgc tcc atg cga att agc cag gac att cgc gat atg ttt ggc
 1843
 Lys Phe Cys Ser Met Arg Ile Ser Gln Asp Ile Arg Asp Met Phe Gly
 570 575 580
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 1891
 Asp Gln Ile Ala Glu Leu Gly Met Pro Gly Val Gly Asp Ser Ser Ser
 585 590 595
 gct gtt gct tct agt ggg gca cgg gag ggg atg gct gag aaa tcc cgg
 1939
 Ala Val Ala Ser Ser Gly Ala Arg Glu Gly Met Ala Glu Lys Ser Arg
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 1998

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<211> 625

<212> PRT

<213> Corynebacterium glutamicum

<400> 522

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 35 40 45

Lys His Ser Tyr Ser Pro Ile Arg Lys Asp Gly Leu Glu Val Pro Glu
 50 55 60
 Thr Glu Ile Arg Leu Asp Ser Pro Ser Gly Pro Asn Glu Pro Phe
 65 70 75 80
 Arg Ile Tyr Arg Thr Arg Gly Pro Glu Thr Asn Pro Lys Gln Gly Leu
 85 90 95
 Pro Arg Leu Arg Glu Ser Trp Ile Thr Ala Arg Gly Asp Val Ala Thr
 100 105 110
 Tyr Gln Gly Arg Glu Arg Leu Leu Ile Asp Asp Gly Arg Ser Ala Met
 115 120 125
 Arg Arg Gly Gln Ala Ser Ala Glu Trp Lys Gly Gln Lys Pro Ala Pro
 130 135 140
 Leu Lys Ala Leu Pro Gly Lys Arg Val Thr Gln Met Ala Tyr Ala Arg
 145 150 155 160
 Ala Gly Val Ile Thr Arg Glu Met Glu Phe Val Ala Leu Arg Glu His
 165 170 175
 Val Asp Ala Glu Phe Val Arg Ser Glu Val Ala Arg Gly Arg Ala Ile
 180 185 190
 Ile Pro Asn Asn Val Asn His Pro Glu Ser Glu Pro Met Ile Ile Gly
 195 200 205
 Arg Lys Phe Leu Thr Lys Ile Asn Ala Asn Ile Gly Asn Ser Ala Val
 210 215 220
 Thr Ser Ser Ile Glu Glu Glu Val Ser Lys Leu Gln Trp Ala Thr Arg
 225 230 235 240
 Trp Gly Ala Asp Thr Val Met Asp Leu Ser Thr Gly Asp Asp Ile His
 245 250 255
 Thr Thr Arg Glu Trp Ile Ile Arg Asn Ser Pro Val Pro Ile Gly Thr
 260 265 270
 Val Pro Ile Tyr Gln Ala Leu Glu Lys Val Asn Gly Val Ala Ala Asp
 275 280 285
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 Gly Val Asp Tyr Met Thr Ile His Ala Gly Val Leu Leu Ala Tyr Ile
 305 310 315 320
 Pro Leu Thr Thr Arg Arg Val Thr Gly Ile Val Ser Arg Gly Gly Ser
 325 330 335
 Ile Met Ala Gly Trp Cys Leu Ala His His Arg Glu Ser Phe Leu Tyr
 340 345 350
 Glu His Phe Asp Glu Leu Cys Glu Ile Phe Ala Gln Tyr Asp Val Ala
 355 360 365
 Phe Ser Leu Gly Asp Gly Leu Arg Pro Gly Ser Leu Ala Asp Ala Asn

370	375	380
Asp Ala Ala Gln Phe	Ala Glu Leu Lys Thr	Ile Gly Glu Leu Thr Gln
385	390	395 400
Arg Ala Trp Glu Tyr	Asp Val Gln Val Met	Val Glu Gly Pro Gly His
	405	410 415
Val Pro Leu Asn Met	Ile Gln Glu Asn Asn	Glu Leu Glu Gln Lys Trp
	420	425 430
Ala Ala Asp Ala Pro	Phe Tyr Thr Leu Gly	Pro Leu Val Thr Asp Ile
	435	440 445
Ala Pro Gly Tyr Asp	His Ile Thr Ser Ala	Ile Gly Ala Ala His Ile
	450	455 460
Ala Met Gly Gly Thr	Ala Met Leu Cys Tyr	Val Thr Pro Lys Glu His
	465	470 475 480
Leu Gly Leu Pro Asn	Arg Asp Asp Val Lys	Thr Gly Val Ile Thr Tyr
	485	490 495
Lys Leu Ala Ala His	Ala Ala Asp Val Ala	Lys Gly His Pro Gly Ala
	500	505 510
Arg Ala Trp Asp Asp	Ala Met Ser Lys Ala	Arg Phe Glu Phe Arg Trp
	515	520 525
Asn Asp Gln Phe Ala	Leu Ser Leu Asp Pro	Asp Thr Ala Ile Ala Tyr
	530	535 540
His Asp Glu Thr Leu	Pro Ala Glu Pro Ala	Lys Thr Ala His Phe Cys
	545	550 555 560
Ser Met Cys Gly Pro	Lys Phe Cys Ser Met	Arg Ile Ser Gln Asp Ile
	565	570 575
Arg Asp Met Phe Gly	Asp Gln Ile Ala Glu	Leu Gly Met Pro Gly Val
	580	585 590
Gly Asp Ser Ser Ser	Ala Val Ala Ser Ser	Gly Ala Arg Glu Gly Met
	595	600 605
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Arg		
625		

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<213> Corynebacterium glutamicum

<220>

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<222> (1)..(990)

<223> RXA01019

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acc gtt gga gac ctc ggg gaa ttt gaa gtg att cgg gta atc acg gag 96
 Thr Val Gly Asp Leu Gly Glu Phe Glu Val Ile Arg Val Ile Thr Glu
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caa gct gga tca tct ctc aac ggc gat gac gca gct gtg ctt cgg cat 144
 Gln Ala Gly Ser Ser Leu Asn Gly Asp Asp Ala Ala Val Leu Arg His
 35 40 45

gca tca ccc aat tcc agg gct gtt gtc acc acc gac atg ttg gtt gcg 192
 Ala Ser Pro Asn Ser Arg Ala Val Val Thr Thr Asp Met Leu Val Ala
 50 55 60

ggg agg cat ttc caa ttg gat tgg tcc acc ccg gaa caa ata ggg cag 240
 Gly Arg His Phe Gln Leu Asp Trp Ser Thr Pro Glu Gln Ile Gly Gln
 65 70 75 80

aag gcg att gtg cag aac ttt gct gat att gag gcg atg ggt gca cgt 288
 Lys Ala Ile Val Gln Asn Phe Ala Asp Ile Glu Ala Met Gly Ala Arg
 85 90 95

cca gta gcc gca ttg ttg gcg att tcc gcc ccc aca cac acc ccc gtg 336
 Pro Val Ala Ala Leu Leu Ala Ile Ser Ala Pro Thr His Thr Pro Val
 100 105 110

gag ttt gtc cga ggc tta gcc cgt ggc atg aat caa cgc ttg gag gag 384
 Glu Phe Val Arg Gly Leu Ala Arg Gly Met Asn Gln Arg Leu Glu Glu
 115 120 125

tac tcc gcg gaa ctt gtt ggc gga gac atc acc agc ggg gac tcc ttg 432
 Tyr Ser Ala Glu Leu Val Gly Gly Asp Ile Thr Ser Gly Asp Ser Leu
 130 135 140

gtt att gct gta act gca att ggt caa ctg ggt gga tcc ttg cca gag 480
 Val Ile Ala Val Thr Ala Ile Gly Gln Leu Gly Gly Ser Leu Pro Glu
 145 150 155 160

ctg acg ttg gga cgt gcc cga cca gga cag acc ctg gtg gcc cac gga 528
 Leu Thr Leu Gly Arg Ala Arg Pro Gly Gln Thr Leu Val Ala His Gly
 165 170 175

aag atc ggt tac tcc gca gca ggc ctt gct cta ctg cag cac ttt ggt 576
 Lys Ile Gly Tyr Ser Ala Ala Gly Leu Ala Leu Leu Gln His Phe Gly
 180 185 190

cca gac aac gtt cca gag cac ctt cgc ccc ttg gtg gat gca cac tgc 624
 Pro Asp Asn Val Pro Glu His Leu Arg Pro Leu Val Asp Ala His Cys
 195 200 205

gca cca gtt ctc acc cca ggc cga ggc atg gtg gca cgc gct gct gga 672
 Ala Pro Val Leu Thr Pro Gly Arg Gly Met Val Ala Arg Ala Ala Gly
 210 215 220

gcg acc gcc atg act gat aac tcg gac gga ctg att gtg gat ctt aac 720
 Ala Thr Ala Met Thr Asp Asn Ser Asp Gly Leu Ile Val Asp Leu Asn
 225 230 235 240

caa atg gcc atg aag tct ggt gtg cgc atc gat gtg gat tcc tgt agc 768
 Gln Met Ala Met Lys Ser Gly Val Arg Ile Asp Val Asp Ser Cys Ser
 245 250 255

atc agc ccc gat gaa ctc ctt agc gaa gcc gct tcc gta ctc gga aca 816
 Ile Ser Pro Asp Glu Leu Leu Ser Glu Ala Ala Ser Val Leu Gly Thr
 260 265 270

gac gcc tgg cga tgg atc tta agc ggc ggg gaa gac cac acc ctg ctc 864
 Asp Ala Trp Arg Trp Ile Leu Ser Gly Gly Glu Asp His Thr Leu Leu
 275 280 285

tct acg acg ttt ggc gat gcc ccc tct gga ttc cgc acc atc ggc caa 912
 Ser Thr Thr Phe Gly Asp Ala Pro Ser Gly Phe Arg Thr Ile Gly Gln
 290 295 300

gtc acc aaa aca cgc cac gaa gac ctc gtc acc gta gat aag aaa acc 960
 Val Thr Lys Thr Arg His Glu Asp Leu Val Thr Val Asp Lys Lys Thr
 305 310 315 320

ccc gca ttt tcc gat gga tgg aga agc ttc taatgaccaa caccctatgg
 1010
 Pro Ala Phe Ser Asp Gly Trp Arg Ser Phe
 325 330

aat
 1013

<210> 524

<211> 330

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 524

Thr Leu Ala His Ser Leu Ser Phe Pro Asp Ser Leu Arg Asp Gly Pro
 1 5 10 15

Thr Val Gly Asp Leu Gly Glu Phe Glu Val Ile Arg Val Ile Thr Glu
 20 25 30

Gln Ala Gly Ser Ser Leu Asn Gly Asp Asp Ala Ala Val Leu Arg His
 35 40 45

Ala Ser Pro Asn Ser Arg Ala Val Val Thr Thr Asp Met Leu Val Ala
 50 55 60

Gly Arg His Phe Gln Leu Asp Trp Ser Thr Pro Glu Gln Ile Gly Gln
 65 70 75 80

Lys Ala Ile Val Gln Asn Phe Ala Asp Ile Glu Ala Met Gly Ala Arg
 85 90 95

Pro Val Ala Ala Leu Leu Ala Ile Ser Ala Pro Thr His Thr Pro Val
 100 105 110

Glu Phe Val Arg Gly Leu Ala Arg Gly Met Asn Gln Arg Leu Glu Glu
 115 120 125

Tyr Ser Ala Glu Leu Val Gly Gly Asp Ile Thr Ser Gly Asp Ser Leu
 130 135 140

Val Ile Ala Val Thr Ala Ile Gly Gln Leu Gly Gly Ser Leu Pro Glu
 145 150 155 160
 Leu Thr Leu Gly Arg Ala Arg Pro Gly Gln Thr Leu Val Ala His Gly
 165 170 175
 Lys Ile Gly Tyr Ser Ala Ala Gly Leu Ala Leu Leu Gln His Phe Gly
 180 185 190
 Pro Asp Asn Val Pro Glu His Leu Arg Pro Leu Val Asp Ala His Cys
 195 200 205
 Ala Pro Val Leu Thr Pro Gly Arg Gly Met Val Ala Arg Ala Ala Gly
 210 215 220
 Ala Thr Ala Met Thr Asp Asn Ser Asp Gly Leu Ile Val Asp Leu Asn
 225 230 235 240
 Gln Met Ala Met Lys Ser Gly Val Arg Ile Asp Val Asp Ser Cys Ser
 245 250 255
 Ile Ser Pro Asp Glu Leu Leu Ser Glu Ala Ala Ser Val Leu Gly Thr
 260 265 270
 Asp Ala Trp Arg Trp Ile Leu Ser Gly Gly Glu Asp His Thr Leu Leu
 275 280 285
 Ser Thr Thr Phe Gly Asp Ala Pro Ser Gly Phe Arg Thr Ile Gly Gln
 290 295 300
 Val Thr Lys Thr Arg His Glu Asp Leu Val Thr Val Asp Lys Lys Thr
 305 310 315 320
 Pro Ala Phe Ser Asp Gly Trp Arg Ser Phe
 325 330

<210> 525

<211> 706

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(706)

<223> RXA01352

<400> 525

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ctgggttaaca ccagcgaagg aagcgaggat tgattgtccc gtg ttt gaa aat cgt 115
 Val Phe Glu Asn Arg
 1 5

ttt gac ctg cgt tgt tat gtt gtg act ggt gcg ggc tcg gtg gat gag 163
 Phe Asp Leu Arg Cys Tyr Val Val Thr Gly Ala Gly Ser Val Asp Glu
 10 15 20

gtt gtg cac act gcg tct gct gcg gct cgt ggt ggc gcg ggt gtg gtg 211
 Val Val His Thr Ala Ser Ala Ala Ala Arg Gly Gly Ala Gly Val Val

25	30	35	
cag gtg cgt tca aag cct att tcg cca gaa gcg atg agg gag ttg gca			259
Gln Val Arg Ser Lys Pro Ile Ser Pro Glu Ala Met Arg Glu Leu Ala			
40	45	50	
tca aag gtt gcg ctt gag gtt gcg cgg tgc agc cca aca acg agg gtg			307
Ser Lys Val Ala Leu Glu Val Ala Arg Cys Ser Pro Thr Thr Arg Val			
55	60	65	
ctt atc gac gac cac ctc cac gtt gct tct tcc tta atg cgc gaa gga			355
Leu Ile Asp Asp His Leu His Val Ala Ser Ser Leu Met Arg Glu Gly			
70	75	80	85
ctc ccg att cac ggt gtg cat ctt ggg cag gat gat atg tcg gtg ctt			403
Leu Pro Ile His Gly Val His Leu Gly Gln Asp Asp Met Ser Val Leu			
90	95	100	
gag gct cgt gag ttg ttg ggg cct gag gcg atc att ggg ttg act act			451
Glu Ala Arg Glu Leu Leu Gly Pro Glu Ala Ile Ile Gly Leu Thr Thr			
105	110	115	
gga acc cta gaa ctt gtg gcg gcg gcg aat gag ctg tcc gat gtg ttg			499
Gly Thr Leu Glu Leu Val Ala Ala Asn Glu Leu Ser Asp Val Leu			
120	125	130	
gat tac atc ggt gct ggg ccg ttt cgg aag act ccc acc aag gat tca			547
Asp Tyr Ile Gly Ala Gly Pro Phe Arg Lys Thr Pro Thr Lys Asp Ser			
135	140	145	
ggt cgg cca ccg att ggc ctt gcg ggt tat ccc cct ttg gtg gaa ttg			595
Gly Arg Pro Pro Ile Gly Leu Ala Gly Tyr Pro Pro Leu Val Glu Leu			
150	155	160	165
tcc aag gtg ccg atc gtt gcg att ggt gat gtc acc cct gcc gat gtg			643
Ser Lys Val Pro Ile Val Ala Ile Gly Asp Val Thr Pro Ala Asp Val			
170	175	180	
cgc gct ctc agc gca acc ggt gtg gct ggc gtt gcc atg gtg cgg gct			691
Arg Ala Leu Ser Ala Thr Gly Val Ala Gly Val Ala Met Val Arg Ala			
185	190	195	
ttt tct gaa tct gat			706
Phe Ser Glu Ser Asp			
200			

<210> 526

<211> 202

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 526

Val	Phe	Glu	Asn	Arg	Phe	Asp	Leu	Arg	Cys	Tyr	Val	Val	Thr	Gly	Ala
1				5				10						15	

Gly	Ser	Val	Asp	Glu	Val	Val	His	Thr	Ala	Ser	Ala	Ala	Ala	Arg	Gly
			20					25					30		

Gly	Ala	Gly	Val	Val	Gln	Val	Arg	Ser	Lys	Pro	Ile	Ser	Pro	Glu	Ala
		35					40							45	

Met Arg Glu Leu Ala Ser Lys Val Ala Leu Glu Val Ala Arg Cys Ser
 50 55 60
 Pro Thr Thr Arg Val Leu Ile Asp Asp His Leu His Val Ala Ser Ser
 65 70 75 80
 Leu Met Arg Glu Gly Leu Pro Ile His Gly Val His Leu Gly Gln Asp
 85 90 95
 Asp Met Ser Val Leu Glu Ala Arg Glu Leu Leu Gly Pro Glu Ala Ile
 100 105 110
 Ile Gly Leu Thr Thr Gly Thr Leu Glu Leu Val Ala Ala Asn Glu
 115 120 125
 Leu Ser Asp Val Leu Asp Tyr Ile Gly Ala Gly Pro Phe Arg Lys Thr
 130 135 140
 Pro Thr Lys Asp Ser Gly Arg Pro Pro Ile Gly Leu Ala Gly Tyr Pro
 145 150 155 160
 Pro Leu Val Glu Leu Ser Lys Val Pro Ile Val Ala Ile Gly Asp Val
 165 170 175
 Thr Pro Ala Asp Val Arg Ala Leu Ser Ala Thr Gly Val Ala Gly Val
 180 185 190
 Ala Met Val Arg Ala Phe Ser Glu Ser Asp
 195 200

<210> 527
 <211> 944
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (1)..(921)
 <223> RXA01381

<400> 527
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 Ser Ala Gly Val Gly Thr Ile Thr Val Ile Asp Asp Asp Thr Val Asp
 1 5 10 15
 att tcc aac att cac cgc caa atc ctc ttc ggc gca agc gat gtc ggt 96
 Ile Ser Asn Ile His Arg Gln Ile Leu Phe Gly Ala Ser Asp Val Gly
 20 25 30
 cga ccc aag gtc gag gtt gcc gcc gag cgc ctc aaa gaa ctc caa cca 144
 Arg Pro Lys Val Glu Val Ala Ala Glu Arg Leu Lys Glu Leu Gln Pro
 35 40 45
 gac atc acc gtc aac gcg ttg cac gaa cgg atc act cca gaa aac gcc 192
 Asp Ile Thr Val Asn Ala Leu His Glu Arg Ile Thr Pro Glu Asn Ala
 50 55 60
 tgc gag ctg ctc aat tcc gtg gac ctc gtc tta gac ggc tcc gat tct 240
 Cys Glu Leu Leu Asn Ser Val Asp Leu Val Leu Asp Gly Ser Asp Ser

65	70	75	80	
ttc tcc aca aaa tac tta gtg tct gat gcc gcc gaa atc acc gga act	288			
Phe Ser Thr Lys Tyr Leu Val Ser Asp Ala Ala Glu Ile Thr Gly Thr				
85 90 95				
ccc ctc atc tgg gca acg gta ctg cgc ttt cac ggc gaa ctg gca ctc	336			
Pro Leu Ile Trp Ala Thr Val Leu Arg Phe His Gly Glu Leu Ala Leu				
100 105 110				
ttc aac tct ggc ccc gac cac cgc gga gtc ggc ctg cgc gac gtc ttc	384			
Phe Asn Ser Gly Pro Asp His Arg Gly Val Gly Leu Arg Asp Val Phe				
115 120 125				
ccc gaa caa ccc tcc gcc gat ttc gtc cct gac tgc gcc acc gct ggt	432			
Pro Glu Gln Pro Ser Ala Asp Phe Val Pro Asp Cys Ala Thr Ala Gly				
130 135 140				
gtt ctt ggc gcc acc aca gcc acc atc ggc gca ctc atg gcc act cac	480			
Val Leu Gly Ala Thr Thr Ala Thr Ile Gly Ala Leu Met Ala Thr His				
145 150 155 160				
gcc atc gga ttt ctc aca gaa atc ggc gac gtc caa cca ggc aca atc	528			
Ala Ile Gly Phe Leu Thr Glu Ile Gly Asp Val Gln Pro Gly Thr Ile				
165 170 175				
ctc tcc tac gac gca ttc ccc gcc gcc acg cgc agc ttc cgc gtc tcc	576			
Leu Ser Tyr Asp Ala Phe Pro Ala Ala Thr Arg Ser Phe Arg Val Ser				
180 185 190				
gcc gac ccg gcg cgc cca ctg gtc acc cgc ctc cgc gcc tcc tac gag	624			
Ala Asp Pro Ala Arg Pro Leu Val Thr Arg Leu Arg Ala Ser Tyr Glu				
195 200 205				
gca gcg cgc acc gat aca act tcg ctt atc gac gcc acc ctc aac ggc	672			
Ala Ala Arg Thr Asp Thr Thr Ser Leu Ile Asp Ala Thr Leu Asn Gly				
210 215 220				
tcc ctc acc gcc ctc gat atc cga gag cca cat gaa gtt ctg ctc aaa	720			
Ser Leu Thr Ala Leu Asp Ile Arg Glu Pro His Glu Val Leu Leu Lys				
225 230 235 240				
gac ctc ccc gag ggc gca acg tca ctg aag ctc ccc tta agc cag atc	768			
Asp Leu Pro Glu Gly Ala Thr Ser Leu Lys Leu Pro Leu Ser Gln Ile				
245 250 255				
acc tcg gac agc gac att tta gag gca ctg tct gga atc gac ggc gac	816			
Thr Ser Asp Ser Asp Ile Leu Glu Ala Leu Ser Gly Ile Asp Gly Asp				
260 265 270				
att ttg gtc tac tgc gct tcg gga atc cgc agt tcc gac ttc atc gac	864			
Ile Leu Val Tyr Cys Ala Ser Gly Ile Arg Ser Ser Asp Phe Ile Asp				
275 280 285				
aac tac tcc cac ctc ggc cac aaa ttt gtg aat ctt ccc ggt ggg gtc	912			
Asn Tyr Ser His Leu Gly His Lys Phe Val Asn Leu Pro Gly Gly Val				
290 295 300				
aac gcg ctg tagctgtcaa tttaagaggc cag	944			
Asn Ala Leu				
305				

<210> 528

<211> 307

<212> PRT

<213> Corynebacterium glutamicum

<400> 528

Ser Ala Gly Val Gly Thr Ile Thr Val Ile Asp Asp Asp Thr Val Asp
 1 5 10 15

Ile Ser Asn Ile His Arg Gln Ile Leu Phe Gly Ala Ser Asp Val Gly
 20 25 30

Arg Pro Lys Val Glu Val Ala Ala Glu Arg Leu Lys Glu Leu Gln Pro
 35 40 45

Asp Ile Thr Val Asn Ala Leu His Glu Arg Ile Thr Pro Glu Asn Ala
 50 55 60

Cys Glu Leu Leu Asn Ser Val Asp Leu Val Leu Asp Gly Ser Asp Ser
 65 70 75 80

Phe Ser Thr Lys Tyr Leu Val Ser Asp Ala Ala Glu Ile Thr Gly Thr
 85 90 95

Pro Leu Ile Trp Ala Thr Val Leu Arg Phe His Gly Glu Leu Ala Leu
 100 105 110

Phe Asn Ser Gly Pro Asp His Arg Gly Val Gly Leu Arg Asp Val Phe
 115 120 125

Pro Glu Gln Pro Ser Ala Asp Phe Val Pro Asp Cys Ala Thr Ala Gly
 130 135 140

Val Leu Gly Ala Thr Thr Ala Thr Ile Gly Ala Leu Met Ala Thr His
 145 150 155 160

Ala Ile Gly Phe Leu Thr Glu Ile Gly Asp Val Gln Pro Gly Thr Ile
 165 170 175

Leu Ser Tyr Asp Ala Phe Pro Ala Ala Thr Arg Ser Phe Arg Val Ser
 180 185 190

Ala Asp Pro Ala Arg Pro Leu Val Thr Arg Leu Arg Ala Ser Tyr Glu
 195 200 205

Ala Ala Arg Thr Asp Thr Thr Ser Leu Ile Asp Ala Thr Leu Asn Gly
 210 215 220

Ser Leu Thr Ala Leu Asp Ile Arg Glu Pro His Glu Val Leu Leu Lys
 225 230 235 240

Asp Leu Pro Glu Gly Ala Thr Ser Leu Lys Leu Pro Leu Ser Gln Ile
 245 250 255

Thr Ser Asp Ser Asp Ile Leu Glu Ala Leu Ser Gly Ile Asp Gly Asp
 260 265 270

Ile Leu Val Tyr Cys Ala Ser Gly Ile Arg Ser Ser Asp Phe Ile Asp
 275 280 285

Asn Tyr Ser His Leu Gly His Lys Phe Val Asn Leu Pro Gly Gly Val
 290 295 300

Asn Ala Leu
 305

<210> 529
 <211> 259
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(259)
 <223> RXA01360

<400> 529
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 gattccgtag aagttctcac cgcaattcag ggaggttaaa atg ctg cat att gct 115
 Met Leu His Ile Ala
 1 5
 gat aaa act ttc gat tcc cac ctc atc atg ggc acc ggc gga gcc acc 163
 Asp Lys Thr Phe Asp Ser His Leu Ile Met Gly Thr Gly Gly Ala Thr
 10 15 20
 tct cag gcg ttg ctg gag gaa tcc ctt gtc gcc agt gga act caa ttg 211
 Ser Gln Ala Leu Leu Glu Glu Ser Leu Val Ala Ser Gly Thr Gln Leu
 25 30 35
 acc acc gtg gcg atg cgt cga cac caa gca acc acc tct agc gga gaa 259
 Thr Thr Val Ala Met Arg Arg His Gln Ala Thr Thr Ser Ser Gly Glu
 40 45 50

<210> 530
 <211> 53
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 530
 Met Leu His Ile Ala Asp Lys Thr Phe Asp Ser His Leu Ile Met Gly
 1 5 10 15
 Thr Gly Gly Ala Thr Ser Gln Ala Leu Leu Glu Glu Ser Leu Val Ala
 20 25 30
 Ser Gly Thr Gln Leu Thr Thr Val Ala Met Arg Arg His Gln Ala Thr
 35 40 45
 Thr Ser Ser Gly Glu
 50

<210> 531
 <211> 629
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(606)

<223> RXA01361

<400> 531

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gcc gac gct gtg atc tct att gat ggc cac gat ccg tgt ttg acc gtg   48
Ala Asp Ala Val Ile Ser Ile Asp Gly His Asp Pro Cys Leu Thr Val
  1             5             10             15

acg atg aat tcg ggg gtg agg gtt gcg tcg aaa agc gtt gtt gtt ttg   96
Thr Met Asn Ser Gly Val Arg Val Ala Ser Lys Ser Val Val Val Leu
             20             25             30

gcg gcg ggc ctg ggc gcc gca agc att ccc ggc tgg ttt gag ggc gcg   144
Ala Ala Gly Leu Gly Ala Ala Ser Ile Pro Gly Trp Phe Glu Gly Ala
             35             40             45

aac cca ttg cag ttg agg ccg gtg tac ggc gat att gtg cgc gtg cgc   192
Asn Pro Leu Gln Leu Arg Pro Val Tyr Gly Asp Ile Val Arg Val Arg
             50             55             60

gtg ccg gag cga ctg cag ccg atg gtc acc aag gtg gtg cgc ggg ttt   240
Val Pro Glu Arg Leu Gln Pro Met Val Thr Lys Val Val Arg Gly Phe
             65             70             75             80

gtg gaa gat cgt cag att tat atc att ccg cgt acc gat ggc acc ctc   288
Val Glu Asp Arg Gln Ile Tyr Ile Ile Pro Arg Thr Asp Gly Thr Leu
             85             90             95

gcg atc ggc gcg aca agc cgt gag gat cac ccg caa cct cga acg ggc   336
Ala Ile Gly Ala Thr Ser Arg Glu Asp His Pro Gln Pro Arg Thr Gly
             100            105            110

gca gtg cat gat ttg cta cgc gat gct atc cgt ttg att ccg ggc att   384
Ala Val His Asp Leu Leu Arg Asp Ala Ile Arg Leu Ile Pro Gly Ile
             115            120            125

gaa gaa acc gaa ttt atc gaa gtc acc tgc ggc gcc cgc ccc ggc acc   432
Glu Glu Thr Glu Phe Ile Glu Val Thr Cys Gly Ala Arg Pro Gly Thr
             130            135            140

ccg gat gac ctg ccg tac ctg gga tgg gtt gga tcc aat gtg att gcg   480
Pro Asp Asp Leu Pro Tyr Leu Gly Trp Val Gly Ser Asn Val Ile Ala
             145            150            155            160

tcc aca gga tat ttc cgc cat gga att ttg ctg tca gcc ctt ggt gca   528
Ser Thr Gly Tyr Phe Arg His Gly Ile Leu Leu Ser Ala Leu Gly Ala
             165            170            175

cgc gct gcc gtt gat atg gca acc aac cag cca ctg ttc ccc act ctt   576
Arg Ala Ala Val Asp Met Ala Thr Asn Gln Pro Leu Phe Pro Thr Leu
             180            185            190

gat gtg tgc gat ccg ttt cgc cac caa att taaggatttt tcacaagtga   626
Asp Val Cys Asp Pro Phe Arg His Gln Ile
             195            200

tta                                                                    629

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<210> 532
 <211> 202
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 532
 Ala Asp Ala Val Ile Ser Ile Asp Gly His Asp Pro Cys Leu Thr Val
 1 5 10 15
 Thr Met Asn Ser Gly Val Arg Val Ala Ser Lys Ser Val Val Val Leu
 20 25 30
 Ala Ala Gly Leu Gly Ala Ala Ser Ile Pro Gly Trp Phe Glu Gly Ala
 35 40 45
 Asn Pro Leu Gln Leu Arg Pro Val Tyr Gly Asp Ile Val Arg Val Arg
 50 55 60
 Val Pro Glu Arg Leu Gln Pro Met Val Thr Lys Val Val Arg Gly Phe
 65 70 75 80
 Val Glu Asp Arg Gln Ile Tyr Ile Ile Pro Arg Thr Asp Gly Thr Leu
 85 90 95
 Ala Ile Gly Ala Thr Ser Arg Glu Asp His Pro Gln Pro Arg Thr Gly
 100 105 110
 Ala Val His Asp Leu Leu Arg Asp Ala Ile Arg Leu Ile Pro Gly Ile
 115 120 125
 Glu Glu Thr Glu Phe Ile Glu Val Thr Cys Gly Ala Arg Pro Gly Thr
 130 135 140
 Pro Asp Asp Leu Pro Tyr Leu Gly Trp Val Gly Ser Asn Val Ile Ala
 145 150 155 160
 Ser Thr Gly Tyr Phe Arg His Gly Ile Leu Leu Ser Ala Leu Gly Ala
 165 170 175
 Arg Ala Ala Val Asp Met Ala Thr Asn Gln Pro Leu Phe Pro Thr Leu
 180 185 190
 Asp Val Cys Asp Pro Phe Arg His Gln Ile
 195 200

<210> 533
 <211> 927
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(904)
 <223> RXA01208

<400> 533
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 aacctgctct agctcgtact agcgaaggga tggccttaac gtg gct aac tcg ttt 115

768

230	235	240	245	
gcg ttt att gat	gcg ctt tat gac	gtg gat gcc	cag gct gtg gcc	tcg 883
Ala Phe Ile Asp	Ala Leu Tyr Asp	Val Asp Ala	Gln Ala Val Ala	Ser
	250	255	260	
ttg gtt gat gtg	cga gag gcc	tgaaaagtac	gtgactgatt	ttt 927
Leu Val Asp Val	Arg Glu Ala			
	265			

<210> 534

<211> 268

<212> PRT

<213> Corynebacterium glutamicum

<400> 534

Val Ala Asn Ser	Phe Leu Asp Ser	Leu Thr Leu Val	Arg Gln Asn Thr
1	5	10	15
Pro Leu Val Gln	Cys Leu Thr Asn	Ser Val Val Met	Gln Phe Thr Ala
	20	25	30
Asn Val Leu Leu	Ala Ala Gly Ala	Thr Pro Ala Met	Val Asp Thr Pro
	35	40	45
Ala Glu Ser Ala	Glu Phe Ala Ala	Val Ala Asn Gly	Val Leu Ile Asn
	50	55	60
Ala Gly Thr Pro	Ser Ala Glu Gln	Tyr Gln Gly Met	Thr Lys Ala Ile
	65	70	75
Glu Gly Ala Arg	Lys Ala Gly Thr	Pro Trp Val Leu	Asp Pro Val Ala
	85	90	95
Val Gly Gly Leu	Ser Glu Arg Thr	Lys Tyr Ala Glu	Gly Ile Val Asp
	100	105	110
Lys Gln Pro Ala	Ala Ile Arg Gly	Asn Ala Ser Glu	Val Val Ala Leu
	115	120	125
Ala Gly Leu Gly	Ala Gly Gly Arg	Gly Val Asp Ala	Thr Asp Ser Val
	130	135	140
Glu Val Ala Leu	Glu Ala Ala Gln	Leu Leu Ala Lys	Arg Thr Gly Gly
	145	150	155
Val Val Ala Val	Ser Gly Ala Glu	Asp Leu Ile Val	Ser Ala Asp Arg
	165	170	175
Val Thr Trp Leu	Arg Ser Gly Asp	Pro Met Leu Gln	Leu Val Ile Gly
	180	185	190
Thr Gly Cys Ser	Leu Gly Ala Leu	Thr Ala Ala Tyr	Leu Gly Ala Thr
	195	200	205
Val Asp Ser Asp	Ile Ser Ala His	Asp Ala Val Leu	Ala Ala His Ala
	210	215	220
His Val Gly Ala	Ala Gly Gln Ile	Ala Ala Gln Lys	Ala Ser Ala Pro
	225	230	235
			240

[illegible]

tct ggt gaa ctt tct agg caa ttc gca agc act ctt gaa cag gcc ggt 595
 Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr Leu Glu Gln Ala Gly
 150 155 160 165

att gac gga gtt ctg cat ccc gat att ttg gtg gat gtg tgg gag aaa 643
 Ile Asp Gly Val Leu His Pro Asp Ile Leu Val Asp Val Trp Glu Lys
 170 175 180

gcc atg ttc gta gag gtt ttc ggc ggg ttg ggg gct ttc gtc gaa aag 691
 Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly Ala Phe Val Glu Lys
 185 190 195

caa tta ggt acc ttg cgt acg cat ttt agg gct tcc ctg gaa gcc ttg 739
 Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala Ser Leu Glu Ala Leu
 200 205 210

atg gaa gag gtg gct gag gtg gct cgc gcg gca ggt gtt gcg ttg ccg 787
 Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala Gly Val Ala Leu Pro
 215 220 225

agc gat gcg gtg gag cgc acc atg aat ttt gcg gat cgg atg cct gag 835
 Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala Asp Arg Met Pro Glu
 230 235 240 245

aat tcg acg agt tcg atg cag cgt gat ttg gcc gcg gga gtg gct agt 883
 Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala Ala Gly Val Ala Ser
 250 255 260

gag ctt gag gct cag aca ggt gca att gtg cgg gca gcg cac aaa gtg 931
 Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg Ala Ala His Lys Val
 265 270 275

ggt gtg aaa act ccg ctt cat gac ctt att tat gct ggt ctt aag ctg 979
 Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr Ala Gly Leu Lys Leu
 280 285 290

aaa gaa gag gaa aat tca ctt tagggataga atcaagatcc atg
 1023
 Lys Glu Glu Glu Asn Ser Leu
 295 300

<210> 536

<211> 300

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 536

Met Lys Ile Ala Ile Val Gly Ala Gly Ala Val Gly Gly Tyr Phe Gly
 1 5 10 15

Ala Leu Leu Gln Glu Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly
 20 25 30

Arg Thr Leu Glu Ala Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala
 35 40 45

Arg Gly Glu Arg Tyr Val Pro Ile Pro Ala Val Ala Ser Val Gln Glu
 50 55 60

Leu Lys Asp Ala Asp Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg

65	70	75	80
Ser Leu Asp Leu Ala Glu Leu Leu Gly Gly Ile Pro Ala Asn Ser Val	85	90	95
Val Ala Ile Thr Gln Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys	100	105	110
Ser Ile Gly Ala Asp Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe	115	120	125
Val His Glu Gly Pro Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser	130	135	140
Tyr Thr Phe Gly Asp Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr	145	150	155
Leu Glu Gln Ala Gly Ile Asp Gly Val Leu His Pro Asp Ile Leu Val	165	170	175
Asp Val Trp Glu Lys Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly	180	185	190
Ala Phe Val Glu Lys Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala	195	200	205
Ser Leu Glu Ala Leu Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala	210	215	220
Gly Val Ala Leu Pro Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala	225	230	235
Asp Arg Met Pro Glu Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala	245	250	255
Ala Gly Val Ala Ser Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg	260	265	270
Ala Ala His Lys Val Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr	275	280	285
Ala Gly Leu Lys Leu Lys Glu Glu Glu Asn Ser Leu	290	295	300

<210> 537

<211> 693

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(670)

<223> RXA02400

<400> 537

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tttaagtcgc cagattaaag tegtcaatga aaggacatac atg tct att tcc cgc	115
Met Ser Ile Ser Arg	
1 5	

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acc gtc ttc ggc atc gca gcc acc gca gcc ctg tct gca gct ctc gtt 163
Thr Val Phe Gly Ile Ala Ala Thr Ala Ala Leu Ser Ala Ala Leu Val
          10                      15                      20

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Ala Cys Ser Pro Pro His Gln Gln Asp Ser Pro Val Gln Arg Thr Asn
          25                      30                      35

gag atc ttg act act tct cag aac cca act tct gcg agc agc acc tca 259
Glu Ile Leu Thr Thr Ser Gln Asn Pro Thr Ser Ala Ser Ser Thr Ser
          40                      45                      50

acc tct tcc gca acg act act tcc tca gct cct gtg gaa gag gac gta 307
Thr Ser Ser Ala Thr Thr Thr Ser Ser Ala Pro Val Glu Glu Asp Val
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gag atc gtt gtt tca cca gca gcg ttg gtg gac ggt gag cag gtt acc 355
Glu Ile Val Val Ser Pro Ala Ala Leu Val Asp Gly Glu Gln Val Thr
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ttc gaa atc tct gga ctt gat cca gag ggc ggc tac tac gca gcg atc 403
Phe Glu Ile Ser Gly Leu Asp Pro Glu Gly Gly Tyr Tyr Ala Ala Ile
          90                      95                      100

tgc gat tcc gta gcg aac cct ggt aac cca gtt cct tct tgc acc ggc 451
Cys Asp Ser Val Ala Asn Pro Gly Asn Pro Val Pro Ser Cys Thr Gly
          105                      110                      115

gaa atg gct gat ttc acg tcc cag gca tgg ttg agc aac tcc cag ccc 499
Glu Met Ala Asp Phe Thr Ser Gln Ala Trp Leu Ser Asn Ser Gln Pro
          120                      125                      130

ggc gcg act gta gag atc gca gaa gac ggc acc gca act gtg gag ctt 547
Gly Ala Thr Val Glu Ile Ala Glu Asp Gly Thr Ala Thr Val Glu Leu
          135                      140                      145

gaa gct acc gca acc ggc act ggc ttg gac tgc acc act cag gct tgt 595
Glu Ala Thr Ala Thr Gly Thr Gly Leu Asp Cys Thr Thr Gln Ala Cys
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gta gcg aag gtc ttc ggc gat cat acc gaa ggt ttc cgc gat gtt gct 643
Val Ala Lys Val Phe Gly Asp His Thr Glu Gly Phe Arg Asp Val Ala
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tca 693

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<213> Corynebacterium glutamicum

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 Val Gln Arg Thr Asn Glu Ile Leu Thr Thr Ser Gln Asn Pro Thr Ser
 35 40 45
 Ala Ser Ser Thr Ser Thr Ser Ser Ala Thr Thr Thr Ser Ser Ala Pro
 50 55 60
 Val Glu Glu Asp Val Glu Ile Val Val Ser Pro Ala Ala Leu Val Asp
 65 70 75 80
 Gly Glu Gln Val Thr Phe Glu Ile Ser Gly Leu Asp Pro Glu Gly Gly
 85 90 95
 Tyr Tyr Ala Ala Ile Cys Asp Ser Val Ala Asn Pro Gly Asn Pro Val
 100 105 110
 Pro Ser Cys Thr Gly Glu Met Ala Asp Phe Thr Ser Gln Ala Trp Leu
 115 120 125
 Ser Asn Ser Gln Pro Gly Ala Thr Val Glu Ile Ala Glu Asp Gly Thr
 130 135 140
 Ala Thr Val Glu Leu Glu Ala Thr Ala Thr Gly Thr Gly Leu Asp Cys
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<210> 539
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 <222> (101)..(1528)
 <223> RXN01209

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 Met Cys Glu Arg Pro
 1 5
 gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt 163
 Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val
 10 15 20
 ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att 211
 Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile
 25 30 35
 tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg 259
 Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val

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gaa gat gtt cgt gcg gca gca aag gag ctg aaa gaa ctc tgc gat gct Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala 55 60 65			307
cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu 70 75 80 85			355
ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln 90 95 100			403
gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu Gly Leu Ser Ile Glu 105 110 115			451
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gtg gca ttg ccc gat gtg att ggc att ggt ccg gtg gcc tct act gcg Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala 135 140 145			547
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atc gcc gct gta gct caa gac cac ggc atc gca tca gta gct att gga Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly 170 175 180			643
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act caa act gaa ctc tct caa aca gaa ctc caa gga gcc ttc gtg aat Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln Gly Ala Phe Val Asn 230 235 240 245			835
tcg cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr 250 255 260			883
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 Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln
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 1075
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 310 315 320 325

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 1123
 Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly
 330 335 340

tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc
 1171
 Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr
 345 350 355

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 1219
 Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg
 360 365 370

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 1267
 Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala
 375 380 385

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 1315
 Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala
 390 395 400 405

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 1363
 Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys
 410 415 420

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 1411
 Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro
 425 430 435

gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac
 1459
 Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn
 440 445 450

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      35              40              45

Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Lys Glu Leu Lys
      50              55              60

Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu
      65              70              75              80

Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp
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Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu
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Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln
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Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro
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Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val
      145             150             155             160

Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala
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Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala
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Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala
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Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro
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Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln
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Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala
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Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser
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Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val
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Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr
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Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp
 305 310 315 320

Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val
 325 330 335

Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro
 340 345 350

Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu
 355 360 365

Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn
 370 375 380

Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met
 385 390 395 400

Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr
 405 410 415

Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn
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Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg
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<211> 1528

<212> DNA

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<220>

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<222> (101)..(1528)

<223> FRXA01209

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 Met Cys Glu Arg Pro
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 Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val
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ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att 211
 Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile
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tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg	259
Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val	
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Glu Asp Val Arg Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	
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cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag	355
Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu	
70 75 80 85	
ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa	403
Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln	
90 95 100	
gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa	451
Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu Gly Leu Ser Ile Glu	
105 110 115	
aac ctg gat caa ttg cat gct gtg atc gcg cag tgc gcc gag act ggt	499
Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly	
120 125 130	
gtg gca ttg ccc gat gtg att ggc att ggt ccg gtg gcc tct act gcg	547
Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala	
135 140 145	
acc aaa cca gat gcg gca ccc gca ttg ggt gtg gag ggc atc gct gag	595
Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu	
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atc gcc gct gta gct caa gac cac ggc atc gca tca gta gct att gga	643
Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly	
170 175 180	
ggc gtt ggt cta cgc aac gcg gcc gaa ctc gct gct acg ccc atc gac	691
Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala Ala Thr Pro Ile Asp	
185 190 195	
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Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu	
215 220 225	
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Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln Gly Ala Phe Val Asn	
230 235 240 245	
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Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr	
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Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly	
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 Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His
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ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag
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 Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln
 295 300 305

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 1075
 Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly
 310 315 320 325

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 Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly
 330 335 340

tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc
 1171
 Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr
 345 350 355

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 1219
 Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg
 360 365 370

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 1267
 Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala
 375 380 385

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 1315
 Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala
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 1363
 Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys
 410 415 420

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 Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro
 425 430 435

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 Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn
 440 445 450

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35 40 45

Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys
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Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu
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Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp
85 90 95

Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu
100 105 110

Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln
115 120 125

Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro
130 135 140

Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val
145 150 155 160

Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala
165 170 175

Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala
180 185 190

Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala
195 200 205

Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro
210 215 220

Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln
225 230 235 240

Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala
245 250 255

Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser
260 265 270

Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val
 275 280 285
 Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr
 290 295 300
 Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp
 305 310 315 320
 Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val
 325 330 335
 Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro
 340 345 350
 Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu
 355 360 365
 Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn
 370 375 380
 Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met
 385 390 395 400
 Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr
 405 410 415
 Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn
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 Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg
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 <223> RXN01413

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 Leu Thr His Leu Phe
 1 5

 tta gaa ctc gat gag cgt tta gta ctg ggt gtt cag caa gat ggt tac 163
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783

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				Leu	Ile	Leu	Lys	Thr										
				1				5										
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Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala Gln Val Ile Ala Asn																		
	10						15						20					
cag att gag gcc gcc acc gca gcg cac gat ctt gat gtg gtg aag atc													211					
Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val Lys Ile																		
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Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr Ala Leu																		

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Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala Leu Arg			
70	75	80	85
gcg aag gtg ctg cca cag gca acc gtg gtt act cca aac aac ttc gag			403
Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn Phe Glu			
	90	95	100
gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac gac ctg			451
Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp Asp Leu			
	105	110	115
aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac gtc gtt			499
Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr Val Val			
	120	125	130
gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac gta ctt			547
Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp Val Leu			
	135	140	145
ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc ggc gac			595
Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile Gly Asp			
150	155	160	165
gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc acc gca			643
Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile Thr Ala			
	170	175	180
gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc gct aag			691
Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr Ala Lys			
	185	190	195
cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac gca ccg			739
Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn Ala Pro			
	200	205	210
ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt aaacaagctc			792
Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys			
215	220		
cct			795
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Gln Val Ile Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu			
20	25	30	

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<210> 547
<211> 638
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (1) .. (615)  
<223> FRXA01617
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<400> 547																
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Ala	Asn	Gln	Ile	Glu	Ala	Ala	Thr	Ala	Ala	His	Asp	Leu	Asp	Val	Val	
1				5					10					15		
aag	atc	ggt	atg	ttg	ggt	act	cct	gca	acg	atc	gat	act	gtg	gca	acc	96
Lys	Ile	Gly	Met	Leu	Gly	Thr	Pro	Ala	Thr	Ile	Asp	Thr	Val	Ala	Thr	
			20					25					30			
gct	ttg	gag	gaa	aac	agc	ttc	aag	cac	gtt	gtc	cta	gac	ccg	gta	ctg	144
Ala	Leu	Glu	Glu	Asn	Ser	Phe	Lys	His	Val	Val	Leu	Asp	Pro	Val	Leu	

35	40	45	
atc tgc aag ggc cag gag ccc ggc gcg gca ctt gat act gac act gcc			192
Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala			
50	55	60	
ctt cgc gcg aag gtg ctg cca cag gca acc gtg gtt act cca aac aac			240
Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn			
65	70	75	80
ttc gag gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac			288
Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp			
85	90	95	
gac ctg aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac			336
Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr			
100	105	110	
gtc gtt gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac			384
Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp			
115	120	125	
gta ctt ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc			432
Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile			
130	135	140	
ggc gac gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc			480
Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile			
145	150	155	160
acc gca gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc			528
Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr			
165	170	175	
gct aag cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac			576
Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn			
180	185	190	
gca ccg ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt			625
Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys			
195	200	205	
aaacaagctc cct			638

<210> 548

<211> 205

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 548

Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val
 1 5 10 15

Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr
 20 25 30

Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu
 35 40 45

Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala

50	55	60
Leu Arg Ala Lys Val	Leu Pro Gln Ala Thr Val Val Thr	Pro Asn Asn
65	70	75 80
Phe Glu Ala Thr Thr	Leu Ser Gly Leu Asp Lys Leu Glu Thr	Ile Asp
	85	90 95
Asp Leu Lys Glu Ala Ala Arg	Leu Ile His Glu Gln Gly	Pro Gln Tyr
	100	105 110
Val Val Val Lys Gly Gly	Ile Asp Phe Pro Gly Asp	Asn Ala Val Asp
	115	120 125
Val Leu Phe Asp Gly Thr	Asp Tyr His Val Phe Ser	Glu Pro Lys Ile
	130	135 140
Gly Asp Glu Arg Val	Ser Gly Ala Gly Cys Thr	Phe Ala Ala Val Ile
	145	150 155 160
Thr Ala Glu Leu Ala	Lys Gly Asn Ser Ala Val Asp	Ala Val Thr Thr
	165	170 175
Ala Lys Arg Val Val	Thr Arg Ala Val Lys Asp	Ala Val Ala Ser Asn
	180	185 190
Ala Pro Phe Thr Ser	Val Trp Leu Ala Glu Asp	Asn Lys
	195	200 205

<210> 549
 <211> 915
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(892)
 <223> RXS01807

<400> 549
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 gcagtggtcg gaactcggcg aggaaatcga gggctagttc atg ccg tcg gca ggc 115
 Met Pro Ser Ala Gly
 1 5
 gag gag att tta gag cag cgc gca cag ctg gag ttt gat cag cgc cgc 163
 Glu Glu Ile Leu Glu Gln Arg Ala Gln Leu Glu Phe Asp Gln Arg Arg
 10 15 20
 gcc gat gtg gtg atg atc ggc agc cag gtg gtt tat ggt tcc gtg ggg 211
 Ala Asp Val Val Met Ile Gly Ser Gln Val Val Tyr Gly Ser Val Gly
 25 30 35
 ctc agt gct gcc att ccg gtg atg cac aac gaa ggc ctc cgc gtg gtc 259
 Leu Ser Ala Ala Ile Pro Val Met His Asn Glu Gly Leu Arg Val Val
 40 45 50
 gct gtc ccc acc gtg gtg tta agt tcc atg ccg cgt tat gca agt tct 307
 Ala Val Pro Thr Val Val Leu Ser Ser Met Pro Arg Tyr Ala Ser Ser

55	60	65	
cac cgc cag ccg atg tcg gac caa tgg ctc gcc gac gcg ctg caa gac			355
His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala Asp Ala Leu Gln Asp			
70	75	80	85
ctg gtg gat ctg ggg att atc gat gag gtt tcc acc att tcc acc ggc			403
Leu Val Asp Leu Gly Ile Ile Asp Glu Val Ser Thr Ile Ser Thr Gly			
	90	95	100
tat ttt acc tcc gct tct cag gtg cgt gtg gtc gct gcg tgg ctg cag			451
Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val Ala Ala Trp Leu Gln			
	105	110	115
aaa atc cgc gaa acc cat ccg cat gtg cgc atc gtg gtg gat ccc atc			499
Lys Ile Arg Glu Thr His Pro His Val Arg Ile Val Val Asp Pro Ile			
	120	125	130
atg ggg gac agt gac gtg gga att tat gtc gcc gac gag atc gca acc			547
Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala Asp Glu Ile Ala Thr			
	135	140	145
gcc atc tgc cag gac tta tgc cct ctg gct acc gga atc att ccc aat			595
Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr Gly Ile Ile Pro Asn			
	150	155	160
gct ttc gag ctc tcc cac atg gtt ggc tcc ggc gat ccg cgc tcg ctg			643
Ala Phe Glu Leu Ser His Met Val Gly Ser Gly Asp Pro Arg Ser Leu			
	170	175	180
ctc ggc ccg ttt ggc gag tgg atc atc atc acc agc gcc act gaa act			691
Leu Gly Pro Phe Gly Glu Trp Ile Ile Ile Thr Ser Ala Thr Glu Thr			
	185	190	195
gtg ggc acc acc gtc acc cgc atc gtc acc cgt gac agc gtc cag gaa			739
Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg Asp Ser Val Gln Glu			
	200	205	210
atc gcc tcc gcc acc gtc gat acc acg gcc aaa ggg gca ggc gac gtc			787
Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys Gly Ala Gly Asp Val			
	215	220	225
tac gcc gca gca tta atc gcc gcc ctg cat aaa gat ttt tcg ctt atc			835
Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys Asp Phe Ser Leu Ile			
	230	235	240
gac gcc gcc agc cac gca tcc aac acc gtc tgc gcc ggc ctg cag acc			883
Asp Ala Ala Ser His Ala Ser Asn Thr Val Cys Ala Gly Leu Gln Thr			
	250	255	260
aaa gcg ctt taggtttcgt ccgtctctga cag			915
Lys Ala Leu			

<210> 550

<211> 264

<212> PRT

<213> Corynebacterium glutamicum

<400> 550

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Met  Pro  Ser  Ala  Gly  Glu  Glu  Ile  Leu  Glu  Gln  Arg  Ala  Gln  Leu  Glu
 1              5              10              15
Phe  Asp  Gln  Arg  Arg  Ala  Asp  Val  Val  Met  Ile  Gly  Ser  Gln  Val  Val
              20              25              30
Tyr  Gly  Ser  Val  Gly  Leu  Ser  Ala  Ala  Ile  Pro  Val  Met  His  Asn  Glu
      35              40              45
Gly  Leu  Arg  Val  Val  Ala  Val  Pro  Thr  Val  Val  Leu  Ser  Ser  Met  Pro
      50              55              60
Arg  Tyr  Ala  Ser  Ser  His  Arg  Gln  Pro  Met  Ser  Asp  Gln  Trp  Leu  Ala
65              70              75              80
Asp  Ala  Leu  Gln  Asp  Leu  Val  Asp  Leu  Gly  Ile  Ile  Asp  Glu  Val  Ser
              85              90              95
Thr  Ile  Ser  Thr  Gly  Tyr  Phe  Thr  Ser  Ala  Ser  Gln  Val  Arg  Val  Val
      100              105              110
Ala  Ala  Trp  Leu  Gln  Lys  Ile  Arg  Glu  Thr  His  Pro  His  Val  Arg  Ile
      115              120              125
Val  Val  Asp  Pro  Ile  Met  Gly  Asp  Ser  Asp  Val  Gly  Ile  Tyr  Val  Ala
      130              135              140
Asp  Glu  Ile  Ala  Thr  Ala  Ile  Cys  Gln  Asp  Leu  Cys  Pro  Leu  Ala  Thr
145              150              155              160
Gly  Ile  Ile  Pro  Asn  Ala  Phe  Glu  Leu  Ser  His  Met  Val  Gly  Ser  Gly
              165              170              175
Asp  Pro  Arg  Ser  Leu  Leu  Gly  Pro  Phe  Gly  Glu  Trp  Ile  Ile  Ile  Thr
              180              185              190
Ser  Ala  Thr  Glu  Thr  Val  Gly  Thr  Thr  Val  Thr  Arg  Ile  Val  Thr  Arg
      195              200              205
Asp  Ser  Val  Gln  Glu  Ile  Ala  Ser  Ala  Thr  Val  Asp  Thr  Thr  Ala  Lys
      210              215              220
Gly  Ala  Gly  Asp  Val  Tyr  Ala  Ala  Ala  Leu  Ile  Ala  Ala  Leu  His  Lys
225              230              235              240
Asp  Phe  Ser  Leu  Ile  Asp  Ala  Ala  Ser  His  Ala  Ser  Asn  Thr  Val  Cys
              245              250              255
Ala  Gly  Leu  Gln  Thr  Lys  Ala  Leu
      260

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<210> 551
<211> 622
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (101)..(622)
<223> RXC01021

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<210> 552
<211> 174
<212> PRT
<213> Corynebacterium glutamicum
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<400> 552
Met Ser Ser Ser Glu Ser Ser Arg Ser Glu Gly Ser Gln Pro Ala Pro
  1             5             10             15
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<400> 553
tgccgacgcgt ggcgtgggatg ccttcgttgc aggttccgcgt gtgtacggcg ctgaggatcc 60

caacaaggcgt atccaggagt tgcgagcact cgcgcagtaa atg gat gtt gcg cac      115
               Met Asp Val Ala His
                        1                               5

gcg tta gat ctg gcc cac cac gtg tca gat caa gtc cga ggc acc acc      163
Ala Leu Asp Leu Ala His His Val Ser Asp Gln Val Arg Gly Thr Thr
                10                          15                      20

agc cct aat ccg cca gtc ggc gct gtc att ttg gac gcc gac ggc gag      211
Ser Pro Asn Pro Pro Val Gly Ala Val Ile Leu Asp Ala Asp Gly Glu
                25                          30                      35

gtc gtt ggc gtt ggc gcc acg gca cct cct ggt ggc ccg cac gcc gaa      259
Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly Gly Pro His Ala Glu
                40                          45                      50
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gtg	gtg	gcg	ctt	gca	gct	gcc	gga	gtg	cgt	gcc	aac	ggg	ggc	acg	gcg	307
Val	Val	Ala	Leu	Ala	Ala	Ala	Gly	Val	Arg	Ala	Asn	Gly	Gly	Thr	Ala	
	55					60					65					
gtg	gtc	acc	ctc	gag	ccg	tgc	aac	cat	tac	ggc	cgc	acg	ggt	cca	tgt	355
Val	Val	Thr	Leu	Glu	Pro	Cys	Asn	His	Tyr	Gly	Arg	Thr	Gly	Pro	Cys	
	70				75					80					85	
tcc	aag	gcg	ctt	ctc	gac	gcc	ggg	atc	gca	cac	gtg	ttt	tac	gcc	aat	403
Ser	Lys	Ala	Leu	Leu	Asp	Ala	Gly	Ile	Ala	His	Val	Phe	Tyr	Ala	Asn	
			90						95					100		
gcg	gat	ccc	ttc	ccg	tca	gcc	gct	ggg	ggc	ggt	gcc	ttt	ttg	gcg	gag	451
Ala	Asp	Pro	Phe	Pro	Ser	Ala	Ala	Gly	Gly	Gly	Ala	Phe	Leu	Ala	Glu	
			105					110					115			
gcg	ggc	gtc	gat	acg	cat	ttt	tta	gat	gag	cgg	atc	agg	gca	ctg	gag	499
Ala	Gly	Val	Asp	Thr	His	Phe	Leu	Asp	Glu	Arg	Ile	Arg	Ala	Leu	Glu	
		120					125					130				
ccc	tgg	ctg	gtt	gcg	acg	cgt	ctg	ggc	agg	ccc	cat	gtc	acg	ttg	aag	547
Pro	Trp	Leu	Val	Ala	Thr	Arg	Leu	Gly	Arg	Pro	His	Val	Thr	Leu	Lys	
	135					140					145					
ttt	gcg	tcc	acc	gtg	gac	ggg	ttt	gct	ggg	gcc	acc	gat	ggc	acc	agc	595
Phe	Ala	Ser	Thr	Val	Asp	Gly	Phe	Ala	Gly	Ala	Thr	Asp	Gly	Thr	Ser	
150					155					160					165	
cag	tgg	att	acc	ggg	ccg	gat	gcg	cgg	gcg	ttt	gtg	cac	gaa	gat	cga	643
Gln	Trp	Ile	Thr	Gly	Pro	Asp	Ala	Arg	Ala	Phe	Val	His	Glu	Asp	Arg	
			170					175					180			
agt	aaa	aga	gat	gcg	atc	atc	gtg	ggg	acc	ggg	act	gcg	ttg	act	gat	691
Ser	Lys	Arg	Asp	Ala	Ile	Ile	Val	Gly	Thr	Gly	Thr	Ala	Leu	Thr	Asp	
			185					190					195			
aat	ccc	tcc	ttg	acg	gcg	cgg	acc	gat	acg	ggg	ctt	tat	gaa	aat	caa	739
Asn	Pro	Ser	Leu	Thr	Ala	Arg	Thr	Asp	Thr	Gly	Leu	Tyr	Glu	Asn	Gln	
		200					205					210				
ccc	agg	cgc	gtt	gtt	att	ggc	tcc	cgc	gag	gtt	cca	gca	gat	tcc	aac	787
Pro	Arg	Arg	Val	Val	Ile	Gly	Ser	Arg	Glu	Val	Pro	Ala	Asp	Ser	Asn	
	215					220					225					
ttg	gct	cgc	ttg	gga	tat	gag	cag	tac	gcg	gga	ata	cca	gag	gct	tta	835
Leu	Ala	Arg	Leu	Gly	Tyr	Glu	Gln	Tyr	Ala	Gly	Ile	Pro	Glu	Ala	Leu	
230					235					240					245	
tca	gcg	ctg	tgg	gat	aaa	ggg	tgc	cga	gac	att	tta	atc	gaa	ggg	ggc	883
Ser	Ala	Leu	Trp	Asp	Lys	Gly	Cys	Arg	Asp	Ile	Leu	Ile	Glu	Gly	Gly	
			250					255					260			
cca	acg	tta	gct	ggg	gca	gcg	ctg	cgc	tta	ggc	att	gtt	gat	cag	gtg	931
Pro	Thr	Leu	Ala	Gly	Ala	Ala	Leu	Arg	Leu	Gly	Ile	Val	Asp	Gln	Val	
			265					270					275			
cag	gcc	tat	gtt	gcc	ccc	gct	ttg	ttg	ggc	gct	gga	cga	tca	gtg	att	979
Gln	Ala	Tyr	Val	Ala	Pro	Ala	Leu	Leu	Gly	Ala	Gly	Arg	Ser	Val	Ile	
	280						285					290				

aac tgg cca caa gaa acc acg atg gat cag att atg cgt ttt gac acc
1027

Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile Met Arg Phe Asp Thr
295 300 305

acg tcc gtg aga cag ttg ggt tca gat gta ttg ata gaa atg atg aga
1075

Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu Ile Glu Met Met Arg
310 315 320 325

aag gaa cac taaatgttca caggtattgt cga
1107

Lys Glu His

<210> 554

<211> 328

<212> PRT

<213> Corynebacterium glutamicum

<400> 554

Met Asp Val Ala His Ala Leu Asp Leu Ala His His Val Ser Asp Gln
1 5 10 15

Val Arg Gly Thr Thr Ser Pro Asn Pro Pro Val Gly Ala Val Ile Leu
20 25 30

Asp Ala Asp Gly Glu Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly
35 40 45

Gly Pro His Ala Glu Val Val Ala Leu Ala Ala Ala Gly Val Arg Ala
50 55 60

Asn Gly Gly Thr Ala Val Val Thr Leu Glu Pro Cys Asn His Tyr Gly
65 70 75 80

Arg Thr Gly Pro Cys Ser Lys Ala Leu Leu Asp Ala Gly Ile Ala His
85 90 95

Val Phe Tyr Ala Asn Ala Asp Pro Phe Pro Ser Ala Ala Gly Gly Gly
100 105 110

Ala Phe Leu Ala Glu Ala Gly Val Asp Thr His Phe Leu Asp Glu Arg
115 120 125

Ile Arg Ala Leu Glu Pro Trp Leu Val Ala Thr Arg Leu Gly Arg Pro
130 135 140

His Val Thr Leu Lys Phe Ala Ser Thr Val Asp Gly Phe Ala Gly Ala
145 150 155 160

Thr Asp Gly Thr Ser Gln Trp Ile Thr Gly Pro Asp Ala Arg Ala Phe
165 170 175

Val His Glu Asp Arg Ser Lys Arg Asp Ala Ile Ile Val Gly Thr Gly
180 185 190

Thr Ala Leu Thr Asp Asn Pro Ser Leu Thr Ala Arg Thr Asp Thr Gly
195 200 205

Leu Tyr Glu Asn Gln Pro Arg Arg Val Val Ile Gly Ser Arg Glu Val
 210 215 220
 Pro Ala Asp Ser Asn Leu Ala Arg Leu Gly Tyr Glu Gln Tyr Ala Gly
 225 230 235 240
 Ile Pro Glu Ala Leu Ser Ala Leu Trp Asp Lys Gly Cys Arg Asp Ile
 245 250 255
 Leu Ile Glu Gly Gly Pro Thr Leu Ala Gly Ala Ala Leu Arg Leu Gly
 260 265 270
 Ile Val Asp Gln Val Gln Ala Tyr Val Ala Pro Ala Leu Leu Gly Ala
 275 280 285
 Gly Arg Ser Val Ile Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile
 290 295 300
 Met Arg Phe Asp Thr Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu
 305 310 315 320
 Ile Glu Met Met Arg Lys Glu His
 325

<210> 555
 <211> 1107
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1084)
 <223> FRXA02246

<400> 555
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 caacaaggcg atccaggagt tgcgagcact cgcgacagtaa atg gat gtt gcg cac 115
 Met Asp Val Ala His
 1 5
 gcg tta gat ctg gcc cac cac gtg tca gat caa gtc cga ggc acc acc 163
 Ala Leu Asp Leu Ala His His Val Ser Asp Gln Val Arg Gly Thr Thr
 10 15 20
 agc cct aat ccg cca gtc ggc gct gtc att ttg gac gcc gac ggc gag 211
 Ser Pro Asn Pro Pro Val Gly Ala Val Ile Leu Asp Ala Asp Gly Glu
 25 30 35
 gtc gtt ggc gtt ggc gcc acg gca cct cct ggt ggc ccg cac gcc gaa 259
 Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly Gly Pro His Ala Glu
 40 45 50
 gtg gtg gcg ctt gca gct gcc gga gtg cgt gcc aac ggg ggc acg gcg 307
 Val Val Ala Leu Ala Ala Ala Gly Val Arg Ala Asn Gly Gly Thr Ala
 55 60 65
 gtg gtc acc ctc gag ccg tgc aac cat tac ggc cgc acg ggt cca tgt 355
 Val Val Thr Leu Glu Pro Cys Asn His Tyr Gly Arg Thr Gly Pro Cys
 70 75 80 85

tcc aag gcg ctt ctc gac gcc ggg atc gca cac gtg ttt tac gcc aat 403
 Ser Lys Ala Leu Leu Asp Ala Gly Ile Ala His Val Phe Tyr Ala Asn
 90 95 100

gcg gat ccc ttc ccg tca gcc gct ggg ggc ggt gcc ttt ttg gcg gag 451
 Ala Asp Pro Phe Pro Ser Ala Ala Gly Gly Gly Ala Phe Leu Ala Glu
 105 110 115

gcg ggc gtc gat acg cat ttt tta gat gag cgg atc agg gca ctg gag 499
 Ala Gly Val Asp Thr His Phe Leu Asp Glu Arg Ile Arg Ala Leu Glu
 120 125 130

ccc tgg ctg gtt gcg acg cgt ctg ggc agg ccc cat gtc acg ttg aag 547
 Pro Trp Leu Val Ala Thr Arg Leu Gly Arg Pro His Val Thr Leu Lys
 135 140 145

ttt gcg tcc acc gtg gac ggt ttt gct ggt gcc acc gat ggc acc agc 595
 Phe Ala Ser Thr Val Asp Gly Phe Ala Gly Ala Thr Asp Gly Thr Ser
 150 155 160 165

cag tgg att acc ggg ccg gat gcg cgg gcg ttt gtg cac gaa gat cga 643
 Gln Trp Ile Thr Gly Pro Asp Ala Arg Ala Phe Val His Glu Asp Arg
 170 175 180

agt aaa aga gat gcg atc atc gtg ggt acc ggt act gcg ttg act gat 691
 Ser Lys Arg Asp Ala Ile Ile Val Gly Thr Gly Thr Ala Leu Thr Asp
 185 190 195

aat ccc tcc ttg acg gcg cgg acc gat acg ggt ctt tat gaa aat caa 739
 Asn Pro Ser Leu Thr Ala Arg Thr Asp Thr Gly Leu Tyr Glu Asn Gln
 200 205 210

ccc agg cgc gtt gtt att ggc tcc cgc gag gtt cca gca gat tcc aac 787
 Pro Arg Arg Val Val Ile Gly Ser Arg Glu Val Pro Ala Asp Ser Asn
 215 220 225

ttg gct cgc ttg gga tat gag cag tac gcg gga ata cca gag gct tta 835
 Leu Ala Arg Leu Gly Tyr Glu Gln Tyr Ala Gly Ile Pro Glu Ala Leu
 230 235 240 245

tca gcg ctg tgg gat aaa ggg tgc cga gac att tta atc gaa ggt ggc 883
 Ser Ala Leu Trp Asp Lys Gly Cys Arg Asp Ile Leu Ile Glu Gly Gly
 250 255 260

cca acg tta gct ggg gca gcg ctg cgc tta ggc att gtt gat cag gtg 931
 Pro Thr Leu Ala Gly Ala Ala Leu Arg Leu Gly Ile Val Asp Gln Val
 265 270 275

cag gcc tat gtt gcc ccc gct ttg ttg ggc gct gga cga tca gtg att 979
 Gln Ala Tyr Val Ala Pro Ala Leu Leu Gly Ala Gly Arg Ser Val Ile
 280 285 290

aac tgg cca caa gaa acc acg atg gat cag att atg cgt ttt gac acc
 1027
 Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile Met Arg Phe Asp Thr
 295 300 305

acg tcc gtg aga cag ttg ggt tca gat gta ttg ata gaa atg atg aga
 1075
 Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu Ile Glu Met Met Arg

310

315

320

325

aag gaa cac taaatgttca caggtattgt cga

1107

Lys Glu His

<210> 556

<211> 328

<212> PRT

<213> Corynebacterium glutamicum

<400> 556

Met	Asp	Val	Ala	His	Ala	Leu	Asp	Leu	Ala	His	His	Val	Ser	Asp	Gln
1				5					10					15	

Val	Arg	Gly	Thr	Thr	Ser	Pro	Asn	Pro	Pro	Val	Gly	Ala	Val	Ile	Leu
			20					25						30	

Asp	Ala	Asp	Gly	Glu	Val	Val	Gly	Val	Gly	Ala	Thr	Ala	Pro	Pro	Gly
		35					40					45			

Gly	Pro	His	Ala	Glu	Val	Val	Ala	Leu	Ala	Ala	Ala	Gly	Val	Arg	Ala
	50						55				60				

Asn	Gly	Gly	Thr	Ala	Val	Val	Thr	Leu	Glu	Pro	Cys	Asn	His	Tyr	Gly
65					70					75					80

Arg	Thr	Gly	Pro	Cys	Ser	Lys	Ala	Leu	Leu	Asp	Ala	Gly	Ile	Ala	His
				85					90					95	

Val	Phe	Tyr	Ala	Asn	Ala	Asp	Pro	Phe	Pro	Ser	Ala	Ala	Gly	Gly	Gly
			100					105					110		

Ala	Phe	Leu	Ala	Glu	Ala	Gly	Val	Asp	Thr	His	Phe	Leu	Asp	Glu	Arg
		115					120					125			

Ile	Arg	Ala	Leu	Glu	Pro	Trp	Leu	Val	Ala	Thr	Arg	Leu	Gly	Arg	Pro
	130					135					140				

His	Val	Thr	Leu	Lys	Phe	Ala	Ser	Thr	Val	Asp	Gly	Phe	Ala	Gly	Ala
145					150					155					160

Thr	Asp	Gly	Thr	Ser	Gln	Trp	Ile	Thr	Gly	Pro	Asp	Ala	Arg	Ala	Phe
				165					170					175	

Val	His	Glu	Asp	Arg	Ser	Lys	Arg	Asp	Ala	Ile	Ile	Val	Gly	Thr	Gly
			180					185					190		

Thr	Ala	Leu	Thr	Asp	Asn	Pro	Ser	Leu	Thr	Ala	Arg	Thr	Asp	Thr	Gly
		195				200						205			

Leu	Tyr	Glu	Asn	Gln	Pro	Arg	Arg	Val	Val	Ile	Gly	Ser	Arg	Glu	Val
	210					215					220				

Pro	Ala	Asp	Ser	Asn	Leu	Ala	Arg	Leu	Gly	Tyr	Glu	Gln	Tyr	Ala	Gly
225					230					235					240

Ile	Pro	Glu	Ala	Leu	Ser	Ala	Leu	Trp	Asp	Lys	Gly	Cys	Arg	Asp	Ile
				245					250					255	

Leu Ile Glu Gly Gly Pro Thr Leu Ala Gly Ala Ala Leu Arg Leu Gly
 260 265 270

Ile Val Asp Gln Val Gln Ala Tyr Val Ala Pro Ala Leu Leu Gly Ala
 275 280 285

Gly Arg Ser Val Ile Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile
 290 295 300

Met Arg Phe Asp Thr Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu
 305 310 315 320

Ile Glu Met Met Arg Lys Glu His
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<211> 756

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<213> Corynebacterium glutamicum

<220>

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<222> (101)..(733)

<223> RXA02247

<400> 557

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 Met Phe Thr Gly Ile
 1 5
 gtc gag gag ctt ggc tcc gtt gca ggc gtg gaa cat ctg gga gat tcc 163
 Val Glu Glu Leu Gly Ser Val Ala Gly Val Glu His Leu Gly Asp Ser
 10 15 20
 atc cgg atg cag att tcc gcg tcc acc gtt tta gag ggt gtg cat ttg 211
 Ile Arg Met Gln Ile Ser Ala Ser Thr Val Leu Glu Gly Val His Leu
 25 30 35
 ggg gat tcc att tct gtc aat ggt gtg tgc ttg aca gtg gcg tcc ttt 259
 Gly Asp Ser Ile Ser Val Asn Gly Val Cys Leu Thr Val Ala Ser Phe
 40 45 50
 ggc gag gga cat ttc act gca gac ctc atg cag gaa acc tta gat cgc 307
 Gly Glu Gly His Phe Thr Ala Asp Leu Met Gln Glu Thr Leu Asp Arg
 55 60 65
 agc tcc ctg ggc gca tta tcc acc ggt agc aaa gtc aac ctt gag cgc 355
 Ser Ser Leu Gly Ala Leu Ser Thr Gly Ser Lys Val Asn Leu Glu Arg
 70 75 80 85
 gcc atg gca gcc gat ggc cgt ctg ggt gga cac atc atg caa ggc cat 403
 Ala Met Ala Ala Asp Gly Arg Leu Gly Gly His Ile Met Gln Gly His
 90 95 100
 gtt gat gcc acc acc tcg ctg atc aag cgc acc agc tca gag aac tgg 451
 Val Asp Ala Thr Thr Ser Leu Ile Lys Arg Thr Ser Ser Glu Asn Trp
 105 110 115

gat gtt ctg cgt ttt gag ctg cca gct gat ttg gct cgc tat gtg gtg 499
 Asp Val Leu Arg Phe Glu Leu Pro Ala Asp Leu Ala Arg Tyr Val Val
 120 125 130
 gaa aaa ggc tcc atc gca ctc aat ggc aca tcc ttg act gta tcg tct 547
 Glu Lys Gly Ser Ile Ala Leu Asn Gly Thr Ser Leu Thr Val Ser Ser
 135 140 145
 ttg ggt gat gat tgg ttt gag gtt tcc ctg att ccc acc acc ttg cgc 595
 Leu Gly Asp Asp Trp Phe Glu Val Ser Leu Ile Pro Thr Thr Leu Arg
 150 155 160 165
 gac acc acc cac ggc gaa ctg gcg gta ggg gat atc gta aac att gag 643
 Asp Thr Thr His Gly Glu Leu Ala Val Gly Asp Ile Val Asn Ile Glu
 170 175 180
 gtt gat gtg atc gct aag tac gtc gaa cgc atg atg acg cgc ggc gtg 691
 Val Asp Val Ile Ala Lys Tyr Val Glu Arg Met Met Thr Arg Gly Val
 185 190 195
 gct gga aac act ccc aat gac tac acc gat ttc acg aga gac 733
 Ala Gly Asn Thr Pro Asn Asp Tyr Thr Asp Phe Thr Arg Asp
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 taggttagac aacgtgagtg aac 756

<210> 558
 <211> 211
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 558
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 20 25 30
 Glu Gly Val His Leu Gly Asp Ser Ile Ser Val Asn Gly Val Cys Leu
 35 40 45
 Thr Val Ala Ser Phe Gly Glu Gly His Phe Thr Ala Asp Leu Met Gln
 50 55 60
 Glu Thr Leu Asp Arg Ser Ser Leu Gly Ala Leu Ser Thr Gly Ser Lys
 65 70 75 80
 Val Asn Leu Glu Arg Ala Met Ala Ala Asp Gly Arg Leu Gly Gly His
 85 90 95
 Ile Met Gln Gly His Val Asp Ala Thr Thr Ser Leu Ile Lys Arg Thr
 100 105 110
 Ser Ser Glu Asn Trp Asp Val Leu Arg Phe Glu Leu Pro Ala Asp Leu
 115 120 125
 Ala Arg Tyr Val Val Glu Lys Gly Ser Ile Ala Leu Asn Gly Thr Ser
 130 135 140

Leu Thr Val Ser Ser Leu Gly Asp Asp Trp Phe Glu Val Ser Leu Ile
 145 150 155 160

Pro Thr Thr Leu Arg Asp Thr Thr His Gly Glu Leu Ala Val Gly Asp
 165 170 175

Ile Val Asn Ile Glu Val Asp Val Ile Ala Lys Tyr Val Glu Arg Met
 180 185 190

Met Thr Arg Gly Val Ala Gly Asn Thr Pro Asn Asp Tyr Thr Asp Phe
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Thr Arg Asp
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<210> 559

<211> 1389

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1366)

<223> RXN02248

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aatgactaca ccgatttcac gagagactag gttagacaac gtg agt gaa cat gag 115
 Val Ser Glu His Glu
 1 5

cag gca cac agc caa tta gat tct gtt gaa gag gcc atc gct gac atc 163
 Gln Ala His Ser Gln Leu Asp Ser Val Glu Glu Ala Ile Ala Asp Ile
 10 15 20

gct gcg ggt aaa gcc gtc gtg gtg gta gat gat gaa gat cgt gaa aat 211
 Ala Ala Gly Lys Ala Val Val Val Val Asp Asp Glu Asp Arg Glu Asn
 25 30 35

gaa ggc gac atc atc ttt gcc gcc gaa tta gcc act cca gaa tta gtc 259
 Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala Thr Pro Glu Leu Val
 40 45 50

gct ttc atg gtg cgt tat tcc tcg gga tac atc tgt gcg cca tta acc 307
 Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile Cys Ala Pro Leu Thr
 55 60 65

gca aag gat gca gat cgt ctt gat ctg cct ccg atg acc gcg cac aat 355
 Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro Met Thr Ala His Asn
 70 75 80 85

cag gat gcc cgc ggc acc gct tac acc gtg acc gtt gat gcc aac acc 403
 Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr Val Asp Ala Asn Thr
 90 95 100

ggc acc aca ggc att tct gca aca gac cgc gcc cac act ttg cgc ttg 451
 Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala His Thr Leu Arg Leu
 105 110 115

ctt gct gat cca gaa gcc gac cgc acg gat ttc acc cgt ccc gga cac 499
 Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe Thr Arg Pro Gly His
 120 125 130

gtt gtg cca ctg cgt gct cgt gaa ggt ggc gtc ttg gtg cgc gct gga 547
 Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val Leu Val Arg Ala Gly
 135 140 145

cac acc gaa gca gct gtc gat ttg gct cgc gct gca ggc ctg cgc cca 595
 His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala Ala Gly Leu Arg Pro
 150 155 160 165

gca ggt gtt atc tgc gaa gtg gtc agt gaa gag gac ccc acc ggc atg 643
 Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu Asp Pro Thr Gly Met
 170 175 180

gct cgg gtt cct gag ctg cgc cgc ttc tgc gat gag cac gat ctg aag 691
 Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp Glu His Asp Leu Lys
 185 190 195

ctg atc tct att gag cag ctc att gag tgg cgt cgc aag aat gaa att 739
 Leu Ile Ser Ile Glu Gln Leu Ile Glu Trp Arg Arg Lys Asn Glu Ile
 200 205 210

ttg gtg gag cgc cag gtg gaa act gtg ctg cct acc gat ttc ggc acg 787
 Leu Val Glu Arg Gln Val Glu Thr Val Leu Pro Thr Asp Phe Gly Thr
 215 220 225

ttc aag gct gtt ggt tac cgt tcc atc atc gat ggc acc gag ctt gtt 835
 Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp Gly Thr Glu Leu Val
 230 235 240 245

gcc att gtt gcc ggc gac gtg gca tcc gac ggt ggc gaa aac gtc ctg 883
 Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly Gly Glu Asn Val Leu
 250 255 260

gtt cga gtc cac tct gag tgc ttg act ggt gat gtt ttt gga tcc cgg 931
 Val Arg Val His Ser Glu Cys Leu Thr Gly Asp Val Phe Gly Ser Arg
 265 270 275

cgc tgc gac tgt gga cag cag ctg cac gag tct ttg cgc ctg atc cag 979
 Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser Leu Arg Leu Ile Gln
 280 285 290

gaa gct ggt cgg gga gta gtg gtg tac atg cgt ggg cat gag gga cga
 1027
 Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg Gly His Glu Gly Arg
 295 300 305

ggc att ggt ctg ctc gcc aag cta cgc gcc tac caa ctc cag gat gaa
 1075
 Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr Gln Leu Gln Asp Glu
 310 315 320 325

ggt gcc gac acc gtc gat gcc aac ctc gca ctt ggt ctt cca gcc gat
 1123
 Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu Gly Leu Pro Ala Asp
 330 335 340

gcc cgc gaa ttt ggc acc agc gcc cag att ctc tac gac ttg ggt gtg
 1171

Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu Tyr Asp Leu Gly Val
 345 350 355

cgc tcg ctc aac ttg atc agc aac aac cca gcc aag aag gtg gga ctt
 1219

Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala Lys Lys Val Gly Leu
 360 365 370

gaa ggc cac ggc att tcc att gcc agc cga acc ccc atc cct gtt gct
 1267

Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr Pro Ile Pro Val Ala
 375 380 385

gtt cat gaa gac aat gtt cga tac ctg aaa acc aag cgt gac cgc atg
 1315

Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr Lys Arg Asp Arg Met
 390 395 400 405

gga cat gac ctc cca gat gtc gca ctg tgg gaa caa gag cac cca gaa
 1363

Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu Gln Glu His Pro Glu
 410 415 420

aac taaggagcac aacaatggct aaa
 1389

Asn

<210> 560
 <211> 422
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 560
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Glu Asp Arg Glu Asn Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala
 35 40 45

Thr Pro Glu Leu Val Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile
 50 55 60

Cys Ala Pro Leu Thr Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro
 65 70 75 80

Met Thr Ala His Asn Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr
 85 90 95

Val Asp Ala Asn Thr Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala
 100 105 110

His Thr Leu Arg Leu Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe
 115 120 125

Thr Arg Pro Gly His Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val
 130 135 140

Leu Val Arg Ala Gly His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala
 145 150 155 160
 Ala Gly Leu Arg Pro Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu
 165 170 175
 Asp Pro Thr Gly Met Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp
 180 185 190
 Glu His Asp Leu Lys Leu Ile Ser Ile Glu Gln Leu Ile Glu Trp Arg
 195 200 205
 Arg Lys Asn Glu Ile Leu Val Glu Arg Gln Val Glu Thr Val Leu Pro
 210 215 220
 Thr Asp Phe Gly Thr Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp
 225 230 235 240
 Gly Thr Glu Leu Val Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly
 245 250 255
 Gly Glu Asn Val Leu Val Arg Val His Ser Glu Cys Leu Thr Gly Asp
 260 265 270
 Val Phe Gly Ser Arg Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser
 275 280 285
 Leu Arg Leu Ile Gln Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg
 290 295 300
 Gly His Glu Gly Arg Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr
 305 310 315 320
 Gln Leu Gln Asp Glu Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu
 325 330 335
 Gly Leu Pro Ala Asp Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu
 340 345 350
 Tyr Asp Leu Gly Val Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala
 355 360 365
 Lys Lys Val Gly Leu Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr
 370 375 380
 Pro Ile Pro Val Ala Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr
 385 390 395 400
 Lys Arg Asp Arg Met Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu
 405 410 415
 Gln Glu His Pro Glu Asn
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<210> 561

<211> 1389

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(1366)
<223> FRXA02248

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aatgactaca ccgatttcac gagagactag gttagacaac gtg agt gaa cat gag      115
                                   Val Ser Glu His Glu
                                   1          5

cag gca cac agc caa tta gat tct gtt gaa gag gcc atc gct gac atc      163
Gln Ala His Ser Gln Leu Asp Ser Val Glu Glu Ala Ile Ala Asp Ile
              10              15              20

gct gcg ggt aaa gcc gtc gtg gtg gta gat gat gaa gat cgt gaa aat      211
Ala Ala Gly Lys Ala Val Val Val Val Asp Asp Glu Asp Arg Glu Asn
              25              30              35

gaa ggc gac atc atc ttt gcc gcc gaa tta gcc act cca gaa tta gtc      259
Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala Thr Pro Glu Leu Val
              40              45              50

gct ttc atg gtg cgt tat tcc tcg gga tac atc tgt gcg cca tta acc      307
Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile Cys Ala Pro Leu Thr
              55              60              65

gca aag gat gca gat cgt ctt gat ctg cct ccg atg acc gcg cac aat      355
Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro Met Thr Ala His Asn
              70              75              80              85

cag gat gcc cgc ggc acc gct tac acc gtg acc gtt gat gcc aac acc      403
Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr Val Asp Ala Asn Thr
              90              95              100

ggc acc aca ggc att tct gca aca gac cgc gcc cac act ttg cgc ttg      451
Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala His Thr Leu Arg Leu
              105              110              115

ctt gct gat cca gaa gcc gac cgc acg gat ttc acc cgt ccc gga cac      499
Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe Thr Arg Pro Gly His
              120              125              130

gtt gtg cca ctg cgt gct cgt gaa ggt ggc gtc ttg gtg cgc gct gga      547
Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val Leu Val Arg Ala Gly
              135              140              145

cac acc gaa gca gct gtc gat ttg gct cgc gct gca ggc ctg cgc cca      595
His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala Ala Gly Leu Arg Pro
              150              155              160              165

gca ggt gtt atc tgc gaa gtg gtc agt gaa gag gac ccc acc ggc atg      643
Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu Asp Pro Thr Gly Met
              170              175              180

gct cgg gtt cct gag ctg cgc cgc ttc tgc gat gag cac gat ctg aag      691
Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp Glu His Asp Leu Lys
              185              190              195

ctg atc tct att gag cag ctc att gag tgg cgt cgc aag aat gaa att      739

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Leu Ile Ser Ile Glu Gln Leu Ile Glu Trp Arg Arg Lys Asn Glu Ile
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 ttg gtg gag cgc cag gtg gaa act gtg ctg cct acc gat ttc ggc acg 787
 Leu Val Glu Arg Gln Val Glu Thr Val Leu Pro Thr Asp Phe Gly Thr
 215 220 225
 ttc aag gct gtt ggt tac cgt tcc atc atc gat ggc acc gag ctt gtt 835
 Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp Gly Thr Glu Leu Val
 230 235 240 245
 gcc att gtt gcc ggc gac gtg gca tcc gac ggt ggc gaa aac gtc ctg 883
 Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly Gly Glu Asn Val Leu
 250 255 260
 gtt cga gtc cac tct gag tgc ttg act ggt gat gtt ttt gga tcc cgg 931
 Val Arg Val His Ser Glu Cys Leu Thr Gly Asp Val Phe Gly Ser Arg
 265 270 275
 cgc tgc gac tgt gga cag cag ctg cac gag tct ttg cgc ctg atc cag 979
 Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser Leu Arg Leu Ile Gln
 280 285 290
 gaa gct ggt cgg gga gta gtg gtg tac atg cgt ggg cat gag gga cga
 1027
 Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg Gly His Glu Gly Arg
 295 300 305
 ggc att ggt ctg ctc gcc aag cta cgc gcc tac caa ctc cag gat gaa
 1075
 Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr Gln Leu Gln Asp Glu
 310 315 320 325
 ggt gcc gac acc gtc gat gcc aac ctc gca ctt ggt ctt cca gcc gat
 1123
 Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu Gly Leu Pro Ala Asp
 330 335 340
 gcc cgc gaa ttt ggc acc agc gcc cag att ctc tac gac ttg ggt gtg
 1171
 Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu Tyr Asp Leu Gly Val
 345 350 355
 cgc tcg ctc aac ttg atc agc aac aac cca gcc aag aag gtg gga ctt
 1219
 Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala Lys Lys Val Gly Leu
 360 365 370
 gaa ggc cac ggc att tcc att gcc agc cga acc ccc atc cct gtt gct
 1267
 Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr Pro Ile Pro Val Ala
 375 380 385
 gtt cat gaa gac aat gtt cga tac ctg aaa acc aag cgt gac cgc atg
 1315
 Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr Lys Arg Asp Arg Met
 390 395 400 405
 gga cat gac ctc cca gat gtc gca ctg tgg gaa caa gag cac cca gaa
 1363
 Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu Gln Glu His Pro Glu

410

415

420

aac taaggagcac aacaatggct aaa
1389
Asn

<210> 562

<211> 422

<212> PRT

<213> Corynebacterium glutamicum

<400> 562

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Ala	Ile	Ala	Asp	Ile	Ala	Ala	Gly	Lys	Ala	Val	Val	Val	Val	Asp	Asp
			20					25						30	
Glu	Asp	Arg	Glu	Asn	Glu	Gly	Asp	Ile	Ile	Phe	Ala	Ala	Glu	Leu	Ala
	35						40					45			
Thr	Pro	Glu	Leu	Val	Ala	Phe	Met	Val	Arg	Tyr	Ser	Ser	Gly	Tyr	Ile
	50					55					60				
Cys	Ala	Pro	Leu	Thr	Ala	Lys	Asp	Ala	Asp	Arg	Leu	Asp	Leu	Pro	Pro
65					70				75					80	
Met	Thr	Ala	His	Asn	Gln	Asp	Ala	Arg	Gly	Thr	Ala	Tyr	Thr	Val	Thr
				85					90					95	
Val	Asp	Ala	Asn	Thr	Gly	Thr	Thr	Gly	Ile	Ser	Ala	Thr	Asp	Arg	Ala
			100					105					110		
His	Thr	Leu	Arg	Leu	Leu	Ala	Asp	Pro	Glu	Ala	Asp	Arg	Thr	Asp	Phe
		115					120					125			
Thr	Arg	Pro	Gly	His	Val	Val	Pro	Leu	Arg	Ala	Arg	Glu	Gly	Gly	Val
	130					135					140				
Leu	Val	Arg	Ala	Gly	His	Thr	Glu	Ala	Ala	Val	Asp	Leu	Ala	Arg	Ala
145					150					155				160	
Ala	Gly	Leu	Arg	Pro	Ala	Gly	Val	Ile	Cys	Glu	Val	Val	Ser	Glu	Glu
				165					170					175	
Asp	Pro	Thr	Gly	Met	Ala	Arg	Val	Pro	Glu	Leu	Arg	Arg	Phe	Cys	Asp
			180					185					190		
Glu	His	Asp	Leu	Lys	Leu	Ile	Ser	Ile	Glu	Gln	Leu	Ile	Glu	Trp	Arg
		195					200					205			
Arg	Lys	Asn	Glu	Ile	Leu	Val	Glu	Arg	Gln	Val	Glu	Thr	Val	Leu	Pro
		210				215					220				
Thr	Asp	Phe	Gly	Thr	Phe	Lys	Ala	Val	Gly	Tyr	Arg	Ser	Ile	Ile	Asp
225					230					235				240	
Gly	Thr	Glu	Leu	Val	Ala	Ile	Val	Ala	Gly	Asp	Val	Ala	Ser	Asp	Gly
			245						250					255	

807

Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr Val Ser Glu Tyr Arg
40 45 50

gtc atc ggc gcc ctg gaa ctt cca gtc gta gtg caa gaa ctg gca cgc 307
Val Ile Gly Ala Leu Glu Leu Pro Val Val Val Gln Glu Leu Ala Arg
55 60 65

acc cat gac gca gta gtt gcc ttg ggc tgt gtc gtt cgt ggc ggc acc 355
Thr His Asp Ala Val Val Ala Leu Gly Cys Val Val Arg Gly Gly Thr
70 75 80 85

cca cac ttt gat tac gtg tgc gac tct gtc acc gaa ggc ctc acc cgc 403
Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr Glu Gly Leu Thr Arg
90 95 100

att gct ctt gat act tcc acc cca atc ggc aac ggt gtg ttg act acc 451
Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn Gly Val Leu Thr Thr
105 110 115

aac acc gaa gag caa gcc gtg gaa cgc tcc ggt gga gaa ggc tct gta 499
Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly Gly Glu Gly Ser Val
120 125 130

gag gac aaa ggc gca gag gca atg gtc gct gca ctc gat act gcc ctc 547
Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala Leu Asp Thr Ala Leu
135 140 145

gtg ctt tct caa att cgt gca act gag ggt tagactgttc tttaaaaggt 597
Val Leu Ser Gln Ile Arg Ala Thr Glu Gly
150 155

ttg 600

<210> 564

<211> 159

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 564

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Leu Lys Val Ala Val Val Thr Ala Arg Trp Asn Ala Glu Ile Cys Asp
20 25 30

Arg Leu His Lys His Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr
35 40 45

Val Ser Glu Tyr Arg Val Ile Gly Ala Leu Glu Leu Pro Val Val Val
50 55 60

Gln Glu Leu Ala Arg Thr His Asp Ala Val Val Ala Leu Gly Cys Val
65 70 75 80

Val Arg Gly Gly Thr Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr
85 90 95

Glu Gly Leu Thr Arg Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn
100 105 110

Gly Val Leu Thr Thr Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly
 115 120 125

Gly Glu Gly Ser Val Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala
 130 135 140

Leu Asp Thr Ala Leu Val Leu Ser Gln Ile Arg Ala Thr Glu Gly
 145 150 155

<210> 565

<211> 600

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(577)

<223> FRXA02249

<400> 565

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 Met Ala Lys Glu Gly
 1 5

ttg ccg gca gtc gaa ctc ccc gac gcc agc gga tta aaa gtc gcc gta 163
 Leu Pro Ala Val Glu Leu Pro Asp Ala Ser Gly Leu Lys Val Ala Val
 10 15 20

gtc acc gca cgg tgg aac gca gaa atc tgc gac cgc ctg cac aag cac 211
 Val Thr Ala Arg Trp Asn Ala Glu Ile Cys Asp Arg Leu His Lys His
 25 30 35

gca gta gat gcg gga cgt gca gca gga gca acg gtg agc gaa tac cgc 259
 Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr Val Ser Glu Tyr Arg
 40 45 50

gtc atc ggc gcc ctg gaa ctt cca gtc gta gtg caa gaa ctg gca cgc 307
 Val Ile Gly Ala Leu Glu Leu Pro Val Val Val Gln Glu Leu Ala Arg
 55 60 65

acc cat gac gca gta gtt gcc ttg ggc tgt gtc gtt cgt ggc ggc acc 355
 Thr His Asp Ala Val Val Ala Leu Gly Cys Val Val Arg Gly Gly Thr
 70 75 80 85

cca cac ttt gat tac gtg tgc gac tct gtc acc gaa ggc ctc acc cgc 403
 Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr Glu Gly Leu Thr Arg
 90 95 100

att gct ctt gat act tcc acc cca atc ggc aac ggt gtg ttg act acc 451
 Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn Gly Val Leu Thr Thr
 105 110 115

aac acc gaa gag caa gcc gtg gaa cgc tcc ggt gga gaa ggc tct gta 499
 Asn Thr Glu Gln Ala Val Glu Arg Ser Gly Gly Glu Gly Ser Val
 120 125 130

gag gac aaa ggc gca gag gca atg gtc gct gca ctc gat act gcc ctc 547
 Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala Leu Asp Thr Ala Leu

135 140 145

gtg ctt tct caa att cgt gca act gag ggt tagactgttc tttaaaaggt 597
 Val Leu Ser Gln Ile Arg Ala Thr Glu Gly
 150 155

ttg 600

<210> 566
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 <212> PRT
 <213> Corynebacterium glutamicum

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Arg Leu His Lys His Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr
 35 40 45

Val Ser Glu Tyr Arg Val Ile Gly Ala Leu Glu Leu Pro Val Val Val
 50 55 60

Gln Glu Leu Ala Arg Thr His Asp Ala Val Val Ala Leu Gly Cys Val
 65 70 75 80

Val Arg Gly Gly Thr Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr
 85 90 95

Glu Gly Leu Thr Arg Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn
 100 105 110

Gly Val Leu Thr Thr Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly
 115 120 125

Gly Glu Gly Ser Val Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala
 130 135 140

Leu Asp Thr Ala Leu Val Leu Ser Gln Ile Arg Ala Thr Glu Gly
 145 150 155

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(679)
 <223> RXA02250

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tgcgcgccac cgctaattag ttctaaggat ttgtgaaatc gtg aca acc aac gcc 115
 Val Thr Thr Asn Ala

	1	5	
ccc gac gga gca acg aac aac atc aac aac gca cat tcg ggc gct gtc			163
Pro Asp Gly Ala Thr Asn Asn Ile Asn Asn Ala His Ser Gly Ala Val			
	10	15	20
ggg aag cca aag gta cag ctc agc gat gcg gaa att cag gaa tac acc			211
Gly Lys Pro Lys Val Gln Leu Ser Asp Ala Glu Ile Gln Glu Tyr Thr			
	25	30	35
gca gct ttc gct ggc acc acc aca acc aag cca tgg gag ctg gag gtg			259
Ala Ala Phe Ala Gly Thr Thr Thr Thr Lys Pro Trp Glu Leu Glu Val			
	40	45	50
acc aca aag ttt ctg aaa aag atc gcg tgg gta gcc gtg gtt gtc atc			307
Thr Thr Lys Phe Leu Lys Lys Ile Ala Trp Val Ala Val Val Val Ile			
	55	60	65
atg gcc gtt cac atc ttc atg ggt gcc gtg gtg gac gtc gat ttc acc			355
Met Ala Val His Ile Phe Met Gly Ala Val Val Asp Val Asp Phe Thr			
	70	75	80
ggg gca gcg gtc acc ttt gtt gac act ctg gca ttc cca gcg ttg ggc			403
Gly Ala Ala Val Thr Phe Val Asp Thr Leu Ala Phe Pro Ala Leu Gly			
	90	95	100
atc atc ttc tcc gtt ctt gtg ttc ttg gga ctg act cgc cct cgc gtg			451
Ile Ile Phe Ser Val Leu Val Phe Leu Gly Leu Thr Arg Pro Arg Val			
	105	110	115
cgt gcc aac gaa gac ggc gtt gag gtg cgt aac ttc atc gga act cgt			499
Arg Ala Asn Glu Asp Gly Val Glu Val Arg Asn Phe Ile Gly Thr Arg			
	120	125	130
ttc tac cca tgg gtt gtc atc tac ggc atg tct ttc ccc aag ggc agc			547
Phe Tyr Pro Trp Val Val Ile Tyr Gly Met Ser Phe Pro Lys Gly Ser			
	135	140	145
agc gtg gca cgt ttg gag ctt cca gac ttt gaa ttc gtt ccc atg tgg			595
Ser Val Ala Arg Leu Glu Leu Pro Asp Phe Glu Phe Val Pro Met Trp			
	150	155	160
gct ttc cag tcc cgc gat gga gaa gat gtg gtg cgc gcg gtt gcg acc			643
Ala Phe Gln Ser Arg Asp Gly Glu Asp Val Val Arg Ala Val Ala Thr			
	170	175	180
ttc cgc gac ctc gaa aac aag tac atg cca gag gac taattaagct			689
Phe Arg Asp Leu Glu Asn Lys Tyr Met Pro Glu Asp			
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gtggctgac caa			702
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<213> Corynebacterium glutamicum			
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Asp

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<222> (101)..(1123)
<223> RXA01489
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agcattcatg tctgttgagt ctatgccgta gtctaaaaca gtg gat att tgg agt 115
Val Asp Ile Trp Ser
1 5

gga cta gac agc gtt ccg gct gat ctt caa gga tca gta gtc acc att 163
Gly Leu Asp Ser Val Pro Ala Asp Leu Gln Gly Ser Val Val Thr Ile
10 15 20

ggt gtg ttt gat ggg ctc cac cgg ggg cat caa agt tta atc ggc gag 211
Gly Val Phe Asp Gly Leu His Arg Gly His Gln Ser Leu Ile Gly Glu

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25	30	35	
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ttt gac ccg cat ccg atc gct gtg ttt ttg cca ggt aaa gag cca acc Phe Asp Pro His Pro Ile Ala Val Phe Leu Pro Gly Lys Glu Pro Thr 55 60 65			307
cgt ttg gct cct ttg gat tat cgc ctt aat ttg gct gcg gaa tgt ggc Arg Leu Ala Pro Leu Asp Tyr Arg Leu Asn Leu Ala Ala Glu Cys Gly 70 75 80 85			355
gtc gat gct gcg ttg gtt att gat ttc act aaa gaa ctc gca ggt ctg Val Asp Ala Ala Leu Val Ile Asp Phe Thr Lys Glu Leu Ala Gly Leu 90 95 100			403
agc gct gaa gag tat ttc aca acc atg atc gtg gat acg ctg cat gcg Ser Ala Glu Glu Tyr Phe Thr Thr Met Ile Val Asp Thr Leu His Ala 105 110 115			451
cgt tca gtt gtg gtg ggg gag aac ttc acc ttc ggt gtc aat ggc gct Arg Ser Val Val Val Gly Glu Asn Phe Thr Phe Gly Val Asn Gly Ala 120 125 130			499
ggc act gag tcc acg atg cgg gaa ttg gga caa aag ttt ggc gtg aat Gly Thr Glu Ser Thr Met Arg Glu Leu Gly Gln Lys Phe Gly Val Asn 135 140 145			547
gtc acg att gct ccg ctg ctg cat gat gat gac cag cgt att tgc tcc Val Thr Ile Ala Pro Leu Leu His Asp Asp Gln Arg Ile Cys Ser 150 155 160 165			595
acc ttg gtg cgc gat tac ttg gat cag ggc gag gtt gag cgc gcg aac Thr Leu Val Arg Asp Tyr Leu Asp Gln Gly Glu Val Glu Arg Ala Asn 170 175 180			643
tgg gcg ctt ggt cga cgc tat gcc gtg cgc ggc gaa gtt gtc cgt ggt Trp Ala Leu Gly Arg Arg Tyr Ala Val Arg Gly Glu Val Val Arg Gly 185 190 195			691
gct ggc cgt ggc ggc aaa gaa ttg ggc tat ccc acc gcg aat ctc tac Ala Gly Arg Gly Gly Lys Glu Leu Gly Tyr Pro Thr Ala Asn Leu Tyr 200 205 210			739
ctg ccg acc tct gtg gcg ctg ccc gcc gat ggc gtg tat gca ggc tgg Leu Pro Thr Ser Val Ala Leu Pro Ala Asp Gly Val Tyr Ala Gly Trp 215 220 225			787
ttc acc atc acc gat gac cgc gaa atc gac aag gaa atc tcc cgc gat Phe Thr Ile Thr Asp Asp Arg Glu Ile Asp Lys Glu Ile Ser Arg Asp 230 235 240 245			835
atc gac ggc acc atg gtt cca ggc gtg cgt tac caa act gcc att tcc Ile Asp Gly Thr Met Val Pro Gly Val Arg Tyr Gln Thr Ala Ile Ser 250 255 260			883
gtg ggc acc aat ccc acc ttc ggc gat gag cga cgc agc gtc gag gca Val Gly Thr Asn Pro Thr Phe Gly Asp Glu Arg Arg Ser Val Glu Ala 265 270 275			931

ttc atc ctc gac cag gaa gcc gac ctg tac ggt cac cat gtc atg gtg 979
 Phe Ile Leu Asp Gln Glu Ala Asp Leu Tyr Gly His His Val Met Val
 280 285 290

gaa ttc gtg gga cac ttg cgc gac atg gtc aaa ttc aac ggc gtc gac
 1027
 Glu Phe Val Gly His Leu Arg Asp Met Val Lys Phe Asn Gly Val Asp
 295 300 305

gag cta cta gac gcc atg gcc cga gat gtc acc aac gcc cgc gac atc
 1075
 Glu Leu Leu Asp Ala Met Ala Arg Asp Val Thr Asn Ala Arg Asp Ile
 310 315 320 325

ctt gcc aaa gac aaa ttg ctt ctc gac gcc gac acc cag ccc agc gct
 1123
 Leu Ala Lys Asp Lys Leu Leu Leu Asp Ala Asp Thr Gln Pro Ser Ala
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 1146

<210> 570
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 570
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Ser Val Val Thr Ile Gly Val Phe Asp Gly Leu His Arg Gly His Gln
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Ser Leu Ile Gly Glu Ala Lys Lys Gln Ala Glu Glu Leu Gly Val Pro
 35 40 45

Cys Val Met Val Thr Phe Asp Pro His Pro Ile Ala Val Phe Leu Pro
 50 55 60

Gly Lys Glu Pro Thr Arg Leu Ala Pro Leu Asp Tyr Arg Leu Asn Leu
 65 70 75 80

Ala Ala Glu Cys Gly Val Asp Ala Ala Leu Val Ile Asp Phe Thr Lys
 85 90 95

Glu Leu Ala Gly Leu Ser Ala Glu Glu Tyr Phe Thr Thr Met Ile Val
 100 105 110

Asp Thr Leu His Ala Arg Ser Val Val Val Gly Glu Asn Phe Thr Phe
 115 120 125

Gly Val Asn Gly Ala Gly Thr Glu Ser Thr Met Arg Glu Leu Gly Gln
 130 135 140

Lys Phe Gly Val Asn Val Thr Ile Ala Pro Leu Leu His Asp Asp Asp
 145 150 155 160

Gln Arg Ile Cys Ser Thr Leu Val Arg Asp Tyr Leu Asp Gln Gly Glu

165 170 175
 Val Glu Arg Ala Asn Trp Ala Leu Gly Arg Arg Tyr Ala Val Arg Gly
 180 185 190
 Glu Val Val Arg Gly Ala Gly Arg Gly Gly Lys Glu Leu Gly Tyr Pro
 195 200 205
 Thr Ala Asn Leu Tyr Leu Pro Thr Ser Val Ala Leu Pro Ala Asp Gly
 210 215 220
 Val Tyr Ala Gly Trp Phe Thr Ile Thr Asp Asp Arg Glu Ile Asp Lys
 225 230 235 240
 Glu Ile Ser Arg Asp Ile Asp Gly Thr Met Val Pro Gly Val Arg Tyr
 245 250 255
 Gln Thr Ala Ile Ser Val Gly Thr Asn Pro Thr Phe Gly Asp Glu Arg
 260 265 270
 Arg Ser Val Glu Ala Phe Ile Leu Asp Gln Glu Ala Asp Leu Tyr Gly
 275 280 285
 His His Val Met Val Glu Phe Val Gly His Leu Arg Asp Met Val Lys
 290 295 300
 Phe Asn Gly Val Asp Glu Leu Leu Asp Ala Met Ala Arg Asp Val Thr
 305 310 315 320
 Asn Ala Arg Asp Ile Leu Ala Lys Asp Lys Leu Leu Leu Asp Ala Asp
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 Thr Gln Pro Ser Ala
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 <211> 1197
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1174)
 <223> RXA02135

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 aaaacgtttt aagaaaacag tcggtttgaa ggagttgtta atg gtt cca gca gag 115
 Met Val Pro Ala Glu
 1 5
 ctt ttt gcg cgt gtg gaa ttt ccg gat cat aaa atc ctg gct cag acg 163
 Leu Phe Ala Arg Val Glu Phe Pro Asp His Lys Ile Leu Ala Gln Thr
 10 15 20
 aag gat ttc cat gac tcc ctc acc aag cca ccc gga tct ttg ggc aag 211
 Lys Asp Phe His Asp Ser Leu Thr Lys Pro Pro Gly Ser Leu Gly Lys
 25 30 35

ttg gag cag atc ggc tgt ttc att tcc gca tgc cag ggc cag att ccg	259
Leu Glu Gln Ile Gly Cys Phe Ile Ser Ala Cys Gln Gly Gln Ile Pro	
40 45 50	
cca cgt cca ctc aac aac tca aag atc gtt gtt ttc gct ggc gat cac	307
Pro Arg Pro Leu Asn Asn Ser Lys Ile Val Val Phe Ala Gly Asp His	
55 60 65	
ggc gtt gca act aaa ggc gtg tcc gcg tac cca tcc tca gta agc ttg	355
Gly Val Ala Thr Lys Gly Val Ser Ala Tyr Pro Ser Ser Val Ser Leu	
70 75 80 85	
cag atg gct gaa aac att aca aac ggt ggc gcc gcc atc aac gtg att	403
Gln Met Ala Glu Asn Ile Thr Asn Gly Gly Ala Ala Ile Asn Val Ile	
90 95 100	
gca cgc acc acc ggc acg tcc gtc cga ctt att gat acc tcc ctc gac	451
Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile Asp Thr Ser Leu Asp	
105 110 115	
cac gaa gca tgg ggc gac gag cgc gta tct agg tcc tgc gga tcc atc	499
His Glu Ala Trp Gly Asp Glu Arg Val Ser Arg Ser Cys Gly Ser Ile	
120 125 130	
gat gtt gaa gac gcc atg acc caa gaa cag gtc gaa cgc gca ctg aag	547
Asp Val Glu Asp Ala Met Thr Gln Glu Gln Val Glu Arg Ala Leu Lys	
135 140 145	
atc ggt aag cgc att gcg gat caa gaa gtg gac gca ggc gcc gac att	595
Ile Gly Lys Arg Ile Ala Asp Gln Glu Val Asp Ala Gly Ala Asp Ile	
150 155 160 165	
tta atc ccc ggc gat tta gga att ggc aac acc acc acc gcc gct gcc	643
Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr Thr Thr Ala Ala Ala	
170 175 180	
ctc gtt gga acg ttc acc ctc gca gag cct gtt gtt gtc gta ggc cgc	691
Leu Val Gly Thr Phe Thr Leu Ala Glu Pro Val Val Val Val Gly Arg	
185 190 195	
ggc acc gga atc gac gat gaa gcc tgg aaa ctc aaa gtc tcc gcg atc	739
Gly Thr Gly Ile Asp Asp Glu Ala Trp Lys Leu Lys Val Ser Ala Ile	
200 205 210	
cgc gac gcc atg ttc cgc gcc cgc gac ctg cgc caa gac ccc atc gcc	787
Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg Gln Asp Pro Ile Ala	
215 220 225	
atc gcc cgg aaa atc tct tcc cca gac ctt gca gcc atg gca gca ttc	835
Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala Ala Met Ala Ala Phe	
230 235 240 245	
att gcc caa gca gca gtt cga cgc acc ccc gtg ctt ctc gac ggc gtt	883
Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val Leu Leu Asp Gly Val	
250 255 260	
gta gtc acc gcc gca gcc ctc cta gcc aac aaa ctg gcc cca ggt gcc	931
Val Val Thr Ala Ala Ala Leu Leu Ala Asn Lys Leu Ala Pro Gly Ala	
265 270 275	
agg cgt tgg ttc atc gca gga cac cgc tcc acc gaa cca gcg cat tcc	979

Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr Glu Pro Ala His Ser
280 285 290

gta gct cta aac gca ctg gcc ctt gat ccc atc ctg gaa ctt gga atg
1027

Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile Leu Glu Leu Gly Met
295 300 305

tcc ctt ggc gaa ggc tcc ggc gca gcc acc gca ctc ccc ctg gtc aag
1075

Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala Leu Pro Leu Val Lys
310 315 320 325

att gcc gtt gac ctg atg aac gac atg tcg aca ttt tct tcc gcc ggc
1123

Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr Phe Ser Ser Ala Gly
330 335 340

gtc gat gga ccc cta aac gcc tct tcc gaa gcg ccc gag caa aac acg
1171

Val Asp Gly Pro Leu Asn Ala Ser Ser Glu Ala Pro Glu Gln Asn Thr
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gag taacttttcta agcgatgtcc ggc
1197
Glu

<210> 572

<211> 358

<212> PRT

<213> Corynebacterium glutamicum

<400> 572

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Ile Leu Ala Gln Thr Lys Asp Phe His Asp Ser Leu Thr Lys Pro Pro
20 25 30

Gly Ser Leu Gly Lys Leu Glu Gln Ile Gly Cys Phe Ile Ser Ala Cys
35 40 45

Gln Gly Gln Ile Pro Pro Arg Pro Leu Asn Asn Ser Lys Ile Val Val
50 55 60

Phe Ala Gly Asp His Gly Val Ala Thr Lys Gly Val Ser Ala Tyr Pro
65 70 75 80

Ser Ser Val Ser Leu Gln Met Ala Glu Asn Ile Thr Asn Gly Gly Ala
85 90 95

Ala Ile Asn Val Ile Ala Arg Thr Thr Gly Thr Ser Val Arg Leu Ile
100 105 110

Asp Thr Ser Leu Asp His Glu Ala Trp Gly Asp Glu Arg Val Ser Arg
115 120 125

Ser Cys Gly Ser Ile Asp Val Glu Asp Ala Met Thr Gln Glu Gln Val
130 135 140

Glu Arg Ala Leu Lys Ile Gly Lys Arg Ile Ala Asp Gln Glu Val Asp
 145 150 155 160
 Ala Gly Ala Asp Ile Leu Ile Pro Gly Asp Leu Gly Ile Gly Asn Thr
 165 170 175
 Thr Thr Ala Ala Ala Leu Val Gly Thr Phe Thr Leu Ala Glu Pro Val
 180 185 190
 Val Val Val Gly Arg Gly Thr Gly Ile Asp Asp Glu Ala Trp Lys Leu
 195 200 205
 Lys Val Ser Ala Ile Arg Asp Ala Met Phe Arg Ala Arg Asp Leu Arg
 210 215 220
 Gln Asp Pro Ile Ala Ile Ala Arg Lys Ile Ser Ser Pro Asp Leu Ala
 225 230 235 240
 Ala Met Ala Ala Phe Ile Ala Gln Ala Ala Val Arg Arg Thr Pro Val
 245 250 255
 Leu Leu Asp Gly Val Val Val Thr Ala Ala Ala Leu Leu Ala Asn Lys
 260 265 270
 Leu Ala Pro Gly Ala Arg Arg Trp Phe Ile Ala Gly His Arg Ser Thr
 275 280 285
 Glu Pro Ala His Ser Val Ala Leu Asn Ala Leu Ala Leu Asp Pro Ile
 290 295 300
 Leu Glu Leu Gly Met Ser Leu Gly Glu Gly Ser Gly Ala Ala Thr Ala
 305 310 315 320
 Leu Pro Leu Val Lys Ile Ala Val Asp Leu Met Asn Asp Met Ser Thr
 325 330 335
 Phe Ser Ser Ala Gly Val Asp Gly Pro Leu Asn Ala Ser Ser Glu Ala
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 Pro Glu Gln Asn Thr Glu
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<210> 573
 <211> 1146
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1123)
 <223> RXA01489

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 Val Asp Ile Trp Ser
 1 5

gga cta gac agc gtt ccg gct gat ctt caa gga tca gta gtc acc att	163
Gly Leu Asp Ser Val Pro Ala Asp Leu Gln Gly Ser Val Val Thr Ile	
10 15 20	
ggt gtg ttt gat ggg ctc cac cgg ggg cat caa agt tta atc ggc gag	211
Gly Val Phe Asp Gly Leu His Arg Gly His Gln Ser Leu Ile Gly Glu	
25 30 35	
gcc aag aag cag gcc gag gag ctg ggt gtg cct tgt gtc atg gtg acc	259
Ala Lys Lys Gln Ala Glu Glu Leu Gly Val Pro Cys Val Met Val Thr	
40 45 50	
ttt gac ccg cat ccg atc gct gtg ttt ttg cca ggt aaa gag cca acc	307
Phe Asp Pro His Pro Ile Ala Val Phe Leu Pro Gly Lys Glu Pro Thr	
55 60 65	
cgt ttg gct cct ttg gat tat cgc ctt aat ttg gct gcg gaa tgt ggc	355
Arg Leu Ala Pro Leu Asp Tyr Arg Leu Asn Leu Ala Ala Glu Cys Gly	
70 75 80 85	
gtc gat gct gcg ttg gtt att gat ttc act aaa gaa ctc gca ggt ctg	403
Val Asp Ala Ala Leu Val Ile Asp Phe Thr Lys Glu Leu Ala Gly Leu	
90 95 100	
agc gct gaa gag tat ttc aca acc atg atc gtg gat acg ctg cat gcg	451
Ser Ala Glu Glu Tyr Phe Thr Thr Met Ile Val Asp Thr Leu His Ala	
105 110 115	
cgt tca gtt gtg gtg ggg gag aac ttc acc ttc ggt gtc aat ggc gct	499
Arg Ser Val Val Val Gly Glu Asn Phe Thr Phe Gly Val Asn Gly Ala	
120 125 130	
ggc act gag tcc acg atg cgg gaa ttg gga caa aag ttt ggc gtg aat	547
Gly Thr Glu Ser Thr Met Arg Glu Leu Gly Gln Lys Phe Gly Val Asn	
135 140 145	
gtc acg att gct ccg ctg ctg cat gat gat gac cag cgt att tgc tcc	595
Val Thr Ile Ala Pro Leu Leu His Asp Asp Gln Arg Ile Cys Ser	
150 155 160 165	
acc ttg gtg cgc gat tac ttg gat cag ggc gag gtt gag cgc gcg aac	643
Thr Leu Val Arg Asp Tyr Leu Asp Gln Gly Glu Val Glu Arg Ala Asn	
170 175 180	
tgg gcg ctt ggt cga cgc tat gcc gtg cgc ggc gaa gtt gtc cgt ggt	691
Trp Ala Leu Gly Arg Arg Tyr Ala Val Arg Gly Glu Val Val Arg Gly	
185 190 195	
gct ggc cgt ggc ggc aaa gaa ttg ggc tat ccc acc gcg aat ctc tac	739
Ala Gly Arg Gly Gly Lys Glu Leu Gly Tyr Pro Thr Ala Asn Leu Tyr	
200 205 210	
ctg ccg acc tct gtg gcg ctg ccc gcc gat ggc gtg tat gca ggc tgg	787
Leu Pro Thr Ser Val Ala Leu Pro Ala Asp Gly Val Tyr Ala Gly Trp	
215 220 225	
ttc acc atc acc gat gac cgc gaa atc gac aag gaa atc tcc cgc gat	835
Phe Thr Ile Thr Asp Asp Arg Glu Ile Asp Lys Glu Ile Ser Arg Asp	
230 235 240 245	
atc gac ggc acc atg gtt cca ggc gtg cgt tac caa act gcc att tcc	883

820

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Ala Ile Asn Gly Ser Thr Thr Ile Asn Gly Thr Ser Gly Gln Leu Gly				
	30	35	40	
aat tcc acg gat acg gaa ctt ctg ttg gcg ctt cgc agg tgg tcg gac				257
Asn Ser Thr Asp Thr Glu Leu Leu Leu Ala Leu Arg Arg Trp Ser Asp				
	45	50	55	
gtg gtg ttg gtt ggg tcg agc acg gtg aag gct gaa aat tat ggt ggc				305
Val Val Leu Val Gly Ser Ser Thr Val Lys Ala Glu Asn Tyr Gly Gly				
	60	65	70	
gtg gag gtt tcg cct gaa atc cag aag caa cgc cag gag ttg ggt cag				353
Val Glu Val Ser Pro Glu Ile Gln Lys Gln Arg Gln Glu Leu Gly Gln				
	75	80	85	
gaa gcg att ccg ccg att gcg gtg atg tca ggg tcg ttg aat ttt gat				401
Glu Ala Ile Pro Pro Ile Ala Val Met Ser Gly Ser Leu Asn Phe Asp				
	90	95	100	105
gtg gat act cgc ttt ttc ctt gag gcc gaa gtg ccg ccg atc atc atc				449
Val Asp Thr Arg Phe Phe Leu Glu Ala Glu Val Pro Pro Ile Ile Ile				
	110	115	120	
acg gat aat tcc gat caa gca aag cag cag cgg ctt gtg gat gct ggg				497
Thr Asp Asn Ser Asp Gln Ala Lys Gln Gln Arg Leu Val Asp Ala Gly				
	125	130	135	
gct cag gtt att gag gtg gag acg ttg acg gcg gag gtt ggc gtc gaa				545
Ala Gln Val Ile Glu Val Glu Thr Leu Thr Ala Glu Val Gly Val Glu				
	140	145	150	
aag ctt agg tct ttg ggt tac gcc cgc att gat tgt gag ggc ggt gca				593
Lys Leu Arg Ser Leu Gly Tyr Ala Arg Ile Asp Cys Glu Gly Gly Ala				
	155	160	165	
acg ttg tat ggg cag atg ttg gcc gcc gat ctt gtt gat gtg tgg cat				641
Thr Leu Tyr Gly Gln Met Leu Ala Ala Asp Leu Val Asp Val Trp His				
	170	175	180	185
cac acg att gat ccg acg ttg tcg ggc agc gtg gag cgc ccc acg gtg				689
His Thr Ile Asp Pro Thr Leu Ser Gly Ser Val Glu Arg Pro Thr Val				
	190	195	200	
aag ggc ggc gat gat gcg ccg cgc cga ttc gcg ttg gag cac gtc ttt				737
Lys Gly Gly Asp Asp Ala Pro Arg Arg Phe Ala Leu Glu His Val Phe				
	205	210	215	
gtc gat gat gac agc acc cta ttc ttg cgg tat aag cgc gcc aag				782
Val Asp Asp Asp Ser Thr Leu Phe Leu Arg Tyr Lys Arg Ala Lys				
	220	225	230	
tgagtgttgg actctccgga tct				805

<210> 576

<211> 232

<212> PRT

<213> Corynebacterium glutamicum

<400> 576
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 20 25 30
 Ile Asn Gly Thr Ser Gly Gln Leu Gly Asn Ser Thr Asp Thr Glu Leu
 35 40 45
 Leu Leu Ala Leu Arg Arg Trp Ser Asp Val Val Leu Val Gly Ser Ser
 50 55 60
 Thr Val Lys Ala Glu Asn Tyr Gly Gly Val Glu Val Ser Pro Glu Ile
 65 70 75 80
 Gln Lys Gln Arg Gln Glu Leu Gly Gln Glu Ala Ile Pro Pro Ile Ala
 85 90 95
 Val Met Ser Gly Ser Leu Asn Phe Asp Val Asp Thr Arg Phe Phe Leu
 100 105 110
 Glu Ala Glu Val Pro Pro Ile Ile Ile Thr Asp Asn Ser Asp Gln Ala
 115 120 125
 Lys Gln Gln Arg Leu Val Asp Ala Gly Ala Gln Val Ile Glu Val Glu
 130 135 140
 Thr Leu Thr Ala Glu Val Gly Val Glu Lys Leu Arg Ser Leu Gly Tyr
 145 150 155 160
 Ala Arg Ile Asp Cys Glu Gly Gly Ala Thr Leu Tyr Gly Gln Met Leu
 165 170 175
 Ala Ala Asp Leu Val Asp Val Trp His His Thr Ile Asp Pro Thr Leu
 180 185 190
 Ser Gly Ser Val Glu Arg Pro Thr Val Lys Gly Gly Asp Asp Ala Pro
 195 200 205
 Arg Arg Phe Ala Leu Glu His Val Phe Val Asp Asp Asp Ser Thr Leu
 210 215 220
 Phe Leu Arg Tyr Lys Arg Ala Lys
 225 230

<210> 577
 <211> 578
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (55) .. (555)
 <223> FRXA01712

<400> 577
 cttctgttgg cgcttcgcag gtgggtcggac gtggtgttgg ttgggtcgag cacggtg 57
 Val

1

aag gct gaa aat tat ggt ggc gtg gag gtt tcg cct gaa atc cag aag 105
Lys Ala Glu Asn Tyr Gly Gly Val Glu Val Ser Pro Glu Ile Gln Lys
5 10 15

caa cgc cag gag ttg ggt cag gaa gcg att ccg ccg att gcg gtg atg 153
Gln Arg Gln Glu Leu Gly Gln Glu Ala Ile Pro Pro Ile Ala Val Met
20 25 30

tca ggg tcg ttg aat ttt gat gtg gat act cgc ttt ttc ctt gag gcc 201
Ser Gly Ser Leu Asn Phe Asp Val Asp Thr Arg Phe Phe Leu Glu Ala
35 40 45

gaa gtg ccg ccg atc atc atc acg gat aat tcc gat caa gca aag cag 249
Glu Val Pro Pro Ile Ile Ile Thr Asp Asn Ser Asp Gln Ala Lys Gln
50 55 60 65

cag cgg ctt gtg gat gct ggg gct cag gtt att gag gtg gag acg ttg 297
Gln Arg Leu Val Asp Ala Gly Ala Gln Val Ile Glu Val Glu Thr Leu
70 75 80

acg gcg gag gtt ggc gtc gaa aag ctt agg tct ttg ggt tac gcc cgc 345
Thr Ala Glu Val Gly Val Glu Lys Leu Arg Ser Leu Gly Tyr Ala Arg
85 90 95

att gat tgt gag ggc ggt gca acg ttg tat ggg cag atg ttg gcc gcc 393
Ile Asp Cys Glu Gly Gly Ala Thr Leu Tyr Gly Gln Met Leu Ala Ala
100 105 110

gat ctt gtt gat gtg tgg cat cac acg att gat ccg acg ttg tcg ggc 441
Asp Leu Val Asp Val Trp His His Thr Ile Asp Pro Thr Leu Ser Gly
115 120 125

agc gtg gag cgc ccc acg gtg aag ggc ggc gat gat gcg ccg cgc cga 489
Ser Val Glu Arg Pro Thr Val Lys Gly Gly Asp Asp Ala Pro Arg Arg
130 135 140 145

ttc gcg ttg gag cac gtc ttt gtc gat gat gac agc acc cta ttc ttg 537
Phe Ala Leu Glu His Val Phe Val Asp Asp Ser Thr Leu Phe Leu
150 155 160

cgg tat aag cgc gcc aag tgagtgttg actctccgga tct 578
Arg Tyr Lys Arg Ala Lys
165

<210> 578

<211> 167

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 578

Val Lys Ala Glu Asn Tyr Gly Gly Val Glu Val Ser Pro Glu Ile Gln
1 5 10 15

Lys Gln Arg Gln Glu Leu Gly Gln Glu Ala Ile Pro Pro Ile Ala Val
20 25 30

Met Ser Gly Ser Leu Asn Phe Asp Val Asp Thr Arg Phe Phe Leu Glu
35 40 45

Ala Glu Val Pro Pro Ile Ile Ile Thr Asp Asn Ser Asp Gln Ala Lys
 50 55 60

Gln Gln Arg Leu Val Asp Ala Gly Ala Gln Val Ile Glu Val Glu Thr
 65 70 75 80

Leu Thr Ala Glu Val Gly Val Glu Lys Leu Arg Ser Leu Gly Tyr Ala
 85 90 95

Arg Ile Asp Cys Glu Gly Gly Ala Thr Leu Tyr Gly Gln Met Leu Ala
 100 105 110

Ala Asp Leu Val Asp Val Trp His His Thr Ile Asp Pro Thr Leu Ser
 115 120 125

Gly Ser Val Glu Arg Pro Thr Val Lys Gly Gly Asp Asp Ala Pro Arg
 130 135 140

Arg Phe Ala Leu Glu His Val Phe Val Asp Asp Asp Ser Thr Leu Phe
 145 150 155 160

Leu Arg Tyr Lys Arg Ala Lys
 165

<210> 579
 <211> 831
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(808)
 <223> RXN02384

<400> 579
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aatacgagcc tggctacgag gacgattaag aggtagtcct gtg act cgt cgc ctg 115
 Val Thr Arg Arg Leu
 1 5

att ctg ctc cga cac ggg cag act gaa tac aac gcc acg tcc cga atg 163
 Ile Leu Leu Arg His Gly Gln Thr Glu Tyr Asn Ala Thr Ser Arg Met
 10 15 20

cag gga caa ttg gac aca gag ctg tct gac ctg ggc ttt caa cag gcg 211
 Gln Gly Gln Leu Asp Thr Glu Leu Ser Asp Leu Gly Phe Gln Gln Ala
 25 30 35

gcc agc gca gcc tca gtg ctg gtt caa aaa aac atc acc cat gtg ttc 259
 Ala Ser Ala Ala Ser Val Leu Val Gln Lys Asn Ile Thr His Val Phe
 40 45 50

agc tcg gat ctt tcc cgc gcc ttc aac acc gca agc gcg gtt gcg gcg 307
 Ser Ser Asp Leu Ser Arg Ala Phe Asn Thr Ala Ser Ala Val Ala Ala
 55 60 65

ctg att gac gcg gag gtg cgc gtc gat aag cgt ctt cgg gaa acg cat 355
 Leu Ile Asp Ala Glu Val Arg Val Asp Lys Arg Leu Arg Glu Thr His

70	75	80	85	
ttg ggt gag tgg cag gcc aaa acc cac act gag gtg gat tcc gaa tat				403
Leu Gly Glu Trp Gln Ala Lys Thr His Thr Glu Val Asp Ser Glu Tyr				
	90	95	100	
cca ggt gcg cgc gct caa tgg cgc cac gat ccg cag tgg gca cca ccc				451
Pro Gly Ala Arg Ala Gln Trp Arg His Asp Pro Gln Trp Ala Pro Pro				
	105	110	115	
ggc ggc gaa tcg cgc gtg gat gtt gcg cgc cgg gca cgc caa gtt gtc				499
Gly Gly Glu Ser Arg Val Asp Val Ala Arg Arg Ala Arg Gln Val Val				
	120	125	130	
gac gag ttg atg gtg tcg ctt gat gat tgg gat gaa ggc acc gtg ctc				547
Asp Glu Leu Met Val Ser Leu Asp Asp Trp Asp Glu Gly Thr Val Leu				
	135	140	145	
atc gtg gct cac ggt ggc acg att aat gcg ctg acc tcg aat ctt ttg				595
Ile Val Ala His Gly Gly Thr Ile Asn Ala Leu Thr Ser Asn Leu Leu				
	150	155	160	165
gac ctg gcg tat gat cag tac ccc atg ttc tct gga ctt gga aat acc				643
Asp Leu Ala Tyr Asp Gln Tyr Pro Met Phe Ser Gly Leu Gly Asn Thr				
	170	175	180	
tgt tgg gca caa ttg acc gcc cga cct cgc tat tat gca ggt agt gag				691
Cys Trp Ala Gln Leu Thr Ala Arg Pro Arg Tyr Tyr Ala Gly Ser Glu				
	185	190	195	
aac cca gaa gat gac ctc aag att tct tcg gcg gtt tcc aac agc cct				739
Asn Pro Glu Asp Asp Leu Lys Ile Ser Ser Ala Val Ser Asn Ser Pro				
	200	205	210	
cat ttt gag ggc aac aat gtg gaa aac gcc cag tgg tat ctt gac ggc				787
His Phe Glu Gly Asn Asn Val Glu Asn Ala Gln Trp Tyr Leu Asp Gly				
	215	220	225	
tgg aac atg ggt gtt acg cag taaagaagat ggcaataaaaa atg				831
Trp Asn Met Gly Val Thr Gln				
	230	235		
<210> 580				
<211> 236				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 580				
Val Thr Arg Arg Leu Ile Leu Leu Arg His Gly Gln Thr Glu Tyr Asn				
1	5	10	15	
Ala Thr Ser Arg Met Gln Gly Gln Leu Asp Thr Glu Leu Ser Asp Leu				
	20	25	30	
Gly Phe Gln Gln Ala Ala Ser Ala Ala Ser Val Leu Val Gln Lys Asn				
	35	40	45	
Ile Thr His Val Phe Ser Ser Asp Leu Ser Arg Ala Phe Asn Thr Ala				
	50	55	60	

Ser Ala Val Ala Ala Leu Ile Asp Ala Glu Val Arg Val Asp Lys Arg
 65 70 75 80
 Leu Arg Glu Thr His Leu Gly Glu Trp Gln Ala Lys Thr His Thr Glu
 85 90 95
 Val Asp Ser Glu Tyr Pro Gly Ala Arg Ala Gln Trp Arg His Asp Pro
 100 105 110
 Gln Trp Ala Pro Pro Gly Gly Glu Ser Arg Val Asp Val Ala Arg Arg
 115 120 125
 Ala Arg Gln Val Val Asp Glu Leu Met Val Ser Leu Asp Asp Trp Asp
 130 135 140
 Glu Gly Thr Val Leu Ile Val Ala His Gly Gly Thr Ile Asn Ala Leu
 145 150 155 160
 Thr Ser Asn Leu Leu Asp Leu Ala Tyr Asp Gln Tyr Pro Met Phe Ser
 165 170 175
 Gly Leu Gly Asn Thr Cys Trp Ala Gln Leu Thr Ala Arg Pro Arg Tyr
 180 185 190
 Tyr Ala Gly Ser Glu Asn Pro Glu Asp Asp Leu Lys Ile Ser Ser Ala
 195 200 205
 Val Ser Asn Ser Pro His Phe Glu Gly Asn Asn Val Glu Asn Ala Gln
 210 215 220
 Trp Tyr Leu Asp Gly Trp Asn Met Gly Val Thr Gln
 225 230 235

<210> 581
 <211> 453
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(430)
 <223> RXN01560

<400> 581
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 tgcatacagta agcgatgcgt tttaggcaca tctgcgatcc gtg ggc gtg tcc tac 115
 Val Gly Val Ser Tyr
 1 5
 atc atc gcc ggc gat gag cag ctg gat atg gca gaa gcc gtt cgc aaa 163
 Ile Ile Ala Gly Asp Glu Gln Leu Asp Met Ala Glu Ala Val Arg Lys
 10 15 20
 att ggg gag acc ttt aaa act gag gaa att atc ctt ggt ggc gga gga 211
 Ile Gly Glu Thr Phe Lys Thr Glu Glu Ile Ile Leu Gly Gly Gly Gly
 25 30 35
 acc ctg aac tgg tcc atg ctc cgc gac ggt ttg tgc gac gag gtt agc 259
 Thr Leu Asn Trp Ser Met Leu Arg Asp Gly Leu Cys Asp Glu Val Ser

40 45 50
 atc gtg atg atg cca atc gcc gat ggt gaa aag cac acc cac tct ttg 307
 Ile Val Met Met Pro Ile Ala Asp Gly Glu Lys His Thr His Ser Leu
 55 60 65
 ttc gaa gcc gat gaa aaa tac tca gca ccg ttg ccg atc ggt ttt tca 355
 Phe Glu Ala Asp Glu Lys Tyr Ser Ala Pro Leu Pro Ile Gly Phe Ser
 70 75 80 85
 ctc gcc agc gtt gaa cca cta gaa gat gga agc gtt tgg atg cgt tac 403
 Leu Ala Ser Val Glu Pro Leu Glu Asp Gly Ser Val Trp Met Arg Tyr
 90 95 100
 ggg gtc aat ggc cca gtg gac gcg aac taggtagcaa atactcgctc 450
 Gly Val Asn Gly Pro Val Asp Ala Asn
 105 110
 ttt 453

<210> 582
 <211> 110
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 582
 Val Gly Val Ser Tyr Ile Ile Ala Gly Asp Glu Gln Leu Asp Met Ala
 1 5 10 15
 Glu Ala Val Arg Lys Ile Gly Glu Thr Phe Lys Thr Glu Glu Ile Ile
 20 25 30
 Leu Gly Gly Gly Gly Thr Leu Asn Trp Ser Met Leu Arg Asp Gly Leu
 35 40 45
 Cys Asp Glu Val Ser Ile Val Met Met Pro Ile Ala Asp Gly Glu Lys
 50 55 60
 His Thr His Ser Leu Phe Glu Ala Asp Glu Lys Tyr Ser Ala Pro Leu
 65 70 75 80
 Pro Ile Gly Phe Ser Leu Ala Ser Val Glu Pro Leu Glu Asp Gly Ser
 85 90 95
 Val Trp Met Arg Tyr Gly Val Asn Gly Pro Val Asp Ala Asn
 100 105 110

<210> 583
 <211> 1137
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1114)
 <223> RXN00667

<400> 583
 ggcatcagtg tttgaaggga aaagcagggtc aaacaagggtg cggctgattt gagcgatcac 60

ggc ccc gtc aac gca cgc act gaa ctg gtg tca gtc acc cca gtc gaa 835
 Gly Pro Val Asn Ala Arg Thr Glu Leu Val Ser Val Thr Pro Val Glu
 230 235 240 245

gac gcc gaa cag agc atc ctc gaa gaa atg cac ggg cca ctc ccc cgc 883
 Asp Ala Glu Gln Ser Ile Leu Glu Glu Met His Gly Pro Leu Pro Arg
 250 255 260

caa gcg cgc tac gtt cta gcc ccc tca aca ggc aaa acc cac cag ctg 931
 Gln Ala Arg Tyr Val Leu Ala Pro Ser Thr Gly Lys Thr His Gln Leu
 265 270 275

cgc atc cac atg cgc gac ttc gca gcc ccc atc ctc ggc gac ccc ctc 979
 Arg Ile His Met Arg Asp Phe Ala Ala Pro Ile Leu Gly Asp Pro Leu
 280 285 290

tac ccc gtc ctc cac gca gtc gac gat gag gac tac acc acc cca atg
 1027
 Tyr Pro Val Leu His Ala Val Asp Asp Glu Asp Tyr Thr Thr Pro Met
 295 300 305

cac ctc atc gcc cgc acg cta acc ttc gtg gat cct caa acc aac gag
 1075
 His Leu Ile Ala Arg Thr Leu Thr Phe Val Asp Pro Gln Thr Asn Glu
 310 315 320 325

gaa cgt acc ttt gtg agt aat cga cct acg gga agt ttg taggcctcgt
 1124
 Glu Arg Thr Phe Val Ser Asn Arg Pro Thr Gly Ser Leu
 330 335

agacatcacc cag
 1137

<210> 584

<211> 338

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 584

Met Ile Ala Leu Lys Ser Met Ser Asn Arg Val Val Gln Lys Pro Lys
 1 5 10 15

Met Lys Ala Pro Leu Pro Ile Arg Asp Gly Leu Asn Pro Ser Arg Val
 20 25 30

Arg Leu Pro Leu Asp Ala Ala Pro Ile Arg Ala Ile Asp Phe Val Glu
 35 40 45

Tyr Leu Ile Ser Thr Gln Arg His Arg Asn Pro Ala Asp Asn Ala Glu
 50 55 60

Ala Leu Gln Ala Arg Phe Asp Ala Asp Leu Val Val Asn His Tyr Gly
 65 70 75 80

Glu Pro Tyr Ala Pro Asp Thr Met Val Gln Pro Asp Asp Asp Ile Trp
 85 90 95

Phe Tyr Arg Met Pro Ala Ala Glu Arg Pro Ile Pro Tyr Lys Ile His
 100 105 110

Val Ile His Glu Asp Asp Asp Ile Leu Val Ile Asp Lys Pro Pro Tyr
 115 120 125
 Leu Ala Thr Met Pro Arg Gly Arg His Ile Thr Glu Thr Ala Leu Val
 130 135 140
 Lys Met Arg Val Leu Thr Gly Asn Asn Asp Leu Thr Pro Ala His Arg
 145 150 155 160
 Leu Asp Arg Leu Thr Ser Gly Val Leu Val Met Val Lys Lys Pro Glu
 165 170 175
 Leu Arg Gly Ala Tyr Gln Thr Leu Phe Ala Arg Arg Glu Ala Ser Lys
 180 185 190
 Thr Tyr Glu Ala Ile Ala Glu Phe Val Pro Gly Leu Leu Asp Asp Gly
 195 200 205
 Pro Ala Ile Trp Glu Ser Arg Ile Glu Lys Glu Arg Gly Ile Val Gln
 210 215 220
 Ala Phe Val Val Glu Gly Pro Val Asn Ala Arg Thr Glu Leu Val Ser
 225 230 235 240
 Val Thr Pro Val Glu Asp Ala Glu Gln Ser Ile Leu Glu Glu Met His
 245 250 255
 Gly Pro Leu Pro Arg Gln Ala Arg Tyr Val Leu Ala Pro Ser Thr Gly
 260 265 270
 Lys Thr His Gln Leu Arg Ile His Met Arg Asp Phe Ala Ala Pro Ile
 275 280 285
 Leu Gly Asp Pro Leu Tyr Pro Val Leu His Ala Val Asp Asp Glu Asp
 290 295 300
 Tyr Thr Thr Pro Met His Leu Ile Ala Arg Thr Leu Thr Phe Val Asp
 305 310 315 320
 Pro Gln Thr Asn Glu Glu Arg Thr Phe Val Ser Asn Arg Pro Thr Gly
 325 330 335
 Ser Leu

<210> 585

<211> 1281

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1258)

<223> RXC01711

<400> 585

tctcgtgagt ttctccccgg tagcaccttc tatatcagcc cccacgccgc gtcggagcag 60

gtgggatagc atcggcaacg cggttgcatg gccgttgcc atg ttg ttg atg gcg 115

230	235	240	245	
gtc ggc ctc gca gtg ctg gca ctc ctg aga ttc cgt aac acc gag cca				883
Val Gly Leu Ala Val Leu Ala Leu Leu Arg Phe Arg Asn Thr Glu Pro				
	250	255	260	
tac ttc tgg gca gca acc acc acc ggt gta ctc ctg act ggc gta ttc				931
Tyr Phe Trp Ala Ala Thr Thr Thr Gly Val Leu Leu Thr Gly Val Phe				
	265	270	275	
ttc ctg tcc tca ctg gga cag atg tac tac tcc atg atg atc ttc cct				979
Phe Leu Ser Ser Leu Gly Gln Met Tyr Tyr Ser Met Met Ile Phe Pro				
	280	285	290	
atg atc ttc acc ctg ctc gga agc cga tcc gta ttc cac aac tgg gtt				
1027				
Met Ile Phe Thr Leu Leu Gly Ser Arg Ser Val Phe His Asn Trp Val				
	295	300	305	
gcc tgg gtc gcc gcc tac ttc tta cta tcc cct gac act ttc acc tcc				
1075				
Ala Trp Val Ala Ala Tyr Phe Leu Leu Ser Pro Asp Thr Phe Thr Ser				
	310	315	320	325
cag cga cta ccc gat gta gcc cgc tgg atg gaa ttt ttc agc gcg acc				
1123				
Gln Arg Leu Pro Asp Val Ala Arg Trp Met Glu Phe Phe Ser Ala Thr				
	330	335	340	
gtt ggt tgg gga cta ttg ata gtg gtt aca ttt gtc tcg gcg cta atc				
1171				
Val Gly Trp Gly Leu Leu Ile Val Val Thr Phe Val Ser Ala Leu Ile				
	345	350	355	
tgg ttt att ggt gat atc cga gcc aag gga act ccg agc tca ccc att				
1219				
Trp Phe Ile Gly Asp Ile Arg Ala Lys Gly Thr Pro Ser Ser Pro Ile				
	360	365	370	
acc act gat cca acg cac gac cat ctt gag agg aca gca tgacagactt				
1268				
Thr Thr Asp Pro Thr His Asp His Leu Glu Arg Thr Ala				
	375	380	385	
caaactcatc agc				
1281				
<210> 586				
<211> 386				
<212> PRT				
<213> Corynebacterium glutamicum				
<400> 586				
Met Leu Leu Met Ala His Arg Phe Phe Val Leu Ala Ile Asn Gly Ala				
1	5	10	15	
Val Thr Asp Asp Phe Thr Thr Val Tyr Ser Ala Leu Arg Arg Phe Val				
	20	25	30	
Glu Gly Ile Pro Val Tyr Asn Glu Val Tyr His Phe Val Asp Pro His				

35	40	45
Tyr Leu Tyr Asn Pro Gly Ala Thr Leu Leu Leu Ala Pro Leu Gly Tyr 50 55 60		
Ile Thr His Phe Thr Leu Ala Arg Trp Met Phe Ile Ala Val Asn Leu 65 70 75 80		
Leu Ala Ile Val Leu Ala Phe Gly Leu Leu Thr Arg Leu Ser Gly Trp 85 90 95		
Ala Leu Arg Ser Met Val Trp Pro Ile Ala Ile Ala Leu Ala Met Leu 100 105 110		
Thr Glu Thr Val Gln Asn Thr Leu Ile Phe Ser Asn Ile Asn Gly Ile 115 120 125		
Leu Leu Leu Met Leu Ala Ile Phe Leu Trp Cys Val Val His Lys Lys 130 135 140		
Ser Trp Leu Gly Gly Leu Val Ile Gly Leu Ala Ile Leu Ile Lys Pro 145 150 155 160		
Met Phe Leu Pro Leu Leu Phe Leu Pro Leu Val Lys Lys Gln Trp Gly 165 170 175		
Ser Leu Ile Leu Gly Ile Leu Thr Pro Val Ile Phe Asn Ala Val Ala 180 185 190		
Trp Phe Leu Val Pro Gly Ala Ser Glu Tyr Val Thr Arg Thr Met Pro 195 200 205		
Tyr Leu Gly Glu Thr Arg Asp Phe Ala Asn Ser Ser Leu Pro Gly Leu 210 215 220		
Ala Ile Tyr Phe Gly Met Pro Thr Trp Met Glu Ile Thr Trp Phe Leu 225 230 235 240		
Ile Phe Gly Ala Met Val Gly Leu Ala Val Leu Ala Leu Leu Arg Phe 245 250 255		
Arg Asn Thr Glu Pro Tyr Phe Trp Ala Ala Thr Thr Thr Gly Val Leu 260 265 270		
Leu Thr Gly Val Phe Phe Leu Ser Ser Leu Gly Gln Met Tyr Tyr Ser 275 280 285		
Met Met Ile Phe Pro Met Ile Phe Thr Leu Leu Gly Ser Arg Ser Val 290 295 300		
Phe His Asn Trp Val Ala Trp Val Ala Ala Tyr Phe Leu Leu Ser Pro 305 310 315 320		
Asp Thr Phe Thr Ser Gln Arg Leu Pro Asp Val Ala Arg Trp Met Glu 325 330 335		
Phe Phe Ser Ala Thr Val Gly Trp Gly Leu Leu Ile Val Val Thr Phe 340 345 350		
Val Ser Ala Leu Ile Trp Phe Ile Gly Asp Ile Arg Ala Lys Gly Thr 355 360 365		

Pro Ser Ser Pro Ile Thr Thr Asp Pro Thr His Asp His Leu Glu Arg
 370 375 380

Thr Ala
 385

<210> 587

<211> 777

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(754)

<223> RXC02380

<400> 587

gcagattttt gacgaagtcg catcgtggat tgaagctgcc taaaaactcg cgaggacgca 60

tgctcagcaa ggtggtgtgc gaacactata ctgtccactc atg act aca acg gtg 115
 Met Thr Thr Thr Val
 1 5

aaa cgc cgc gct cgc att ggc atc atg ggt ggc aca ttt gac ccc att 163
 Lys Arg Arg Ala Arg Ile Gly Ile Met Gly Gly Thr Phe Asp Pro Ile
 10 15 20

cat aat ggt cac ctt gtg gcg ggc tca gag gta gcg gat cga ttc gat 211
 His Asn Gly His Leu Val Ala Gly Ser Glu Val Ala Asp Arg Phe Asp
 25 30 35

ctt gat ctg gtg gtg tac gtt ccc acc gga cag cca tgg caa aag gcg 259
 Leu Asp Leu Val Val Tyr Val Pro Thr Gly Gln Pro Trp Gln Lys Ala
 40 45 50

aac aag aaa gtc agc cca gcg gaa gat cgt tac ctg atg acg gtg atc 307
 Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr Leu Met Thr Val Ile
 55 60 65

gcc act gcc tct aat cca cgg ttt atg gta tcg cgg gtt gat att gat 355
 Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser Arg Val Asp Ile Asp
 70 75 80 85

cgg gga ggg gat act tac acg atc gat acc ctg caa gat ttg agc aag 403
 Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu Gln Asp Leu Ser Lys
 90 95 100

caa tac ccg gac gcc cag ctg tac ttc atc acc ggt gcc gat gca ctg 451
 Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr Gly Ala Asp Ala Leu
 105 110 115

gca cag atc gtg acg tgg cgc gat tgg gag aaa acc ttc gaa ctt gcc 499
 Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys Thr Phe Glu Leu Ala
 120 125 130

cac ttc gtt gga gtg act cga ccc ggt tat gaa ttg gat gga aac atc 547
 His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu Leu Asp Gly Asn Ile
 135 140 145

att ccg gaa atg cac caa gat cga gtc tca ttg gtg gat atc ccc gcc 595
 Ile Pro Glu Met His Gln Asp Arg Val Ser Leu Val Asp Ile Pro Ala
 150 155 160 165

atg gct att tcc tcc acg gac tgc aga gaa cgc tcc agc gaa gaa cgc 643
 Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg Ser Ser Glu Glu Arg
 170 175 180

cct gtt tgg tat ctt gtc cct gat ggc gtg gtg caa tac att gcc aaa 691
 Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val Gln Tyr Ile Ala Lys
 185 190 195

cgc caa ctc tat cga cct gaa gga tcc gat aag gat atg gat ccc aag 739
 Arg Gln Leu Tyr Arg Pro Glu Gly Ser Asp Lys Asp Met Asp Pro Lys
 200 205 210

ggc caa aac caa gca taaatctagt caaaagtttc aac 777
 Gly Gln Asn Gln Ala
 215

<210> 588

<211> 218

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 588

Met Thr Thr Thr Val Lys Arg Arg Ala Arg Ile Gly Ile Met Gly Gly
 1 5 10 15

Thr Phe Asp Pro Ile His Asn Gly His Leu Val Ala Gly Ser Glu Val
 20 25 30

Ala Asp Arg Phe Asp Leu Asp Leu Val Val Tyr Val Pro Thr Gly Gln
 35 40 45

Pro Trp Gln Lys Ala Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr
 50 55 60

Leu Met Thr Val Ile Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser
 65 70 75 80

Arg Val Asp Ile Asp Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu
 85 90 95

Gln Asp Leu Ser Lys Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr
 100 105 110

Gly Ala Asp Ala Leu Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys
 115 120 125

Thr Phe Glu Leu Ala His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu
 130 135 140

Leu Asp Gly Asn Ile Ile Pro Glu Met His Gln Asp Arg Val Ser Leu
 145 150 155 160

Val Asp Ile Pro Ala Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg
 165 170 175

Ser Ser Glu Glu Arg Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val

180

185

190

Gln Tyr Ile Ala Lys Arg Gln Leu Tyr Arg Pro Glu Gly Ser Asp Lys
 195 200 205

Asp Met Asp Pro Lys Gly Gln Asn Gln Ala
 210 215

<210> 589

<211> 777

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(754)

<223> FRXA02380

<400> 589

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 tgctcagcaa ggtggtgtgc gaacactata ctgtccactc atg act aca acg gtg 115
 Met Thr Thr Thr Val
 1 5
 aaa cgc cgc gct cgc att ggc atc atg ggt ggc aca ttt gac ccc att 163
 Lys Arg Arg Ala Arg Ile Gly Ile Met Gly Gly Thr Phe Asp Pro Ile
 10 15 20
 cat aat ggt cac ctt gtg gcg ggc tca gag gta gcg gat cga ttc gat 211
 His Asn Gly His Leu Val Ala Gly Ser Glu Val Ala Asp Arg Phe Asp
 25 30 35
 ctt gat ctg gtg gtg tac gtt ccc acc gga cag cca tgg caa aag gcg 259
 Leu Asp Leu Val Val Tyr Val Pro Thr Gly Gln Pro Trp Gln Lys Ala
 40 45 50
 aac aag aaa gtc agc cca gcg gaa gat cgt tac ctg atg acg gtg atc 307
 Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr Leu Met Thr Val Ile
 55 60 65
 gcc act gcc tct aat cca cgg ttt atg gta tcg cgg gtt gat att gat 355
 Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser Arg Val Asp Ile Asp
 70 75 80 85
 cgg gga ggg gat act tac acg atc gat acc ctg caa gat ttg agc aag 403
 Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu Gln Asp Leu Ser Lys
 90 95 100
 caa tac ccg gac gcc cag ctg tac ttc atc acc ggt gcc gat gca ctg 451
 Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr Gly Ala Asp Ala Leu
 105 110 115
 gca cag atc gtg acg tgg cgc gat tgg gag aaa acc ttc gaa ctt gcc 499
 Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys Thr Phe Glu Leu Ala
 120 125 130
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 His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu Leu Asp Gly Asn Ile
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 Ile Pro Glu Met His Gln Asp Arg Val Ser Leu Val Asp Ile Pro Ala
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 Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg Ser Ser Glu Glu Arg
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 Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val Gln Tyr Ile Ala Lys
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Pro Trp Gln Lys Ala Asn Lys Lys Val Ser Pro Ala Glu Asp Arg Tyr
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Leu Met Thr Val Ile Ala Thr Ala Ser Asn Pro Arg Phe Met Val Ser
 65 70 75 80

Arg Val Asp Ile Asp Arg Gly Gly Asp Thr Tyr Thr Ile Asp Thr Leu
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Gln Asp Leu Ser Lys Gln Tyr Pro Asp Ala Gln Leu Tyr Phe Ile Thr
 100 105 110

Gly Ala Asp Ala Leu Ala Gln Ile Val Thr Trp Arg Asp Trp Glu Lys
 115 120 125

Thr Phe Glu Leu Ala His Phe Val Gly Val Thr Arg Pro Gly Tyr Glu
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Leu Asp Gly Asn Ile Ile Pro Glu Met His Gln Asp Arg Val Ser Leu
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Val Asp Ile Pro Ala Met Ala Ile Ser Ser Thr Asp Cys Arg Glu Arg
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Ser Ser Glu Glu Arg Pro Val Trp Tyr Leu Val Pro Asp Gly Val Val
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 Glu Ser Ile Arg Ile Ala Thr Ile Ala Ala Lys Ala Ala Asp Glu Lys
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 Lys Ala Asp Asp Ile Ala Val Ile Asp Val Ser Asp Met Ile Ala Ile
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 Ala Ile Val Glu Glu Ile Glu Asp Glu Met Thr Lys Ala Gly Phe Glu
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 Pro Lys Arg Arg Glu Gly Asn Arg Glu Asn Arg Trp Val Leu Leu Asp
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 Tyr Gly Leu Val Val Ile His Val Gln Arg Gln Ala Glu Arg Glu Phe
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 Tyr Gly Leu Asp Arg Leu Tyr Arg Asp Cys Pro Leu Ile Glu Ile Glu
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 Gly Leu Glu Thr Phe Lys Arg Glu Ser Ser Trp Ser Asp Glu Ala Asp
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 Ile Arg Asn Ile Asp Ser Ile Asp Glu Leu Pro Pro Leu Pro Ala Glu

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 Lys Ala Gly Phe Glu Pro Lys Arg Arg Glu Gly Asn Arg Glu Asn Arg
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 Ala Glu Arg Glu Phe Tyr Gly Leu Asp Arg Leu Tyr Arg Asp Cys Pro
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 Val Leu Gly Ala Val
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Gln	Phe	Gly	Gly	Met	Ala	Met	Ala	Ile	Ile	Val	Tyr	Val	Ala	Ile	Ser	
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 Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn Gly Leu Phe Ala Tyr
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 Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu Gly Trp Thr Leu Ser
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 Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu Val Leu Leu His Leu
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 Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser Leu Leu Ala Pro Leu
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 Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu Leu Gly Ala Ala Asn
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 Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly Ala Tyr Leu Leu Arg
 375 380 385
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 Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe Leu Leu Gly Thr Leu
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 Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val Leu Gly Val Phe Phe
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 Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser Glu Phe Ala Ala Thr
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 Pro Val Pro Pro Met Ser Ala Gly Ile Val Arg Gly Pro Arg Leu
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 Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe Arg Leu Leu Ala Asp
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 His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln Ala Arg Glu Ile Ala
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 Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp Thr Ser Gly Asn Ala
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 Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala Val Leu Ala Leu Pro
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 Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp Ala Lys Ser Leu Ala
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 Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu Ala Pro Ser Asp Val
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 745 750 755

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 Glu Glu Pro Thr His Leu Val Val Lys Lys Glu Lys Thr Pro Lys Pro
 760 765 770

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 Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr Thr Val Lys Gly Met
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2659

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Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr Asp Gly Asn Thr Ser
855 860 865

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935 940 945

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2995

Gly Gln Val Glu Ser Val Val Ile Leu Val Asp Glu Val Arg Ser Ser
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<400> 594

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Gly	Leu	Phe	Ala	Tyr	Gly	Gln	Phe	Asp	Ala	Asn	Ala	Ala	Asn	Ile	Leu
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Gly	Trp	Thr	Leu	Ser	Phe	Ser	Ala	Phe	Thr	Leu	Ile	Pro	Tyr	Ala	Leu
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 Ala Lys Thr Ser Leu Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala
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 485 490 495
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 Ala Arg Glu Ile Ala Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp
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 Gly Ile Ala Tyr Glu Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu
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 Gly Ser Leu Ala Val Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn
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 Gly Cys Leu Ile Val Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala
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 Val Ala Glu Ser Gly Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala
 645 650 655
 Glu Leu Thr Glu Thr Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala
 660 665 670

Gly Leu Asp Asn Lys Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala
 675 680 685
 Val Leu Ala Leu Pro Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp
 690 695 700
 Ala Lys Ser Leu Ala Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu
 705 710 715 720
 Ala Pro Ser Asp Val Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala
 725 730 735
 Thr Glu Asp Asn Pro Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr
 740 745 750
 Cys Gly Leu Phe Thr Glu Glu Pro Thr His Leu Val Val Lys Lys Glu
 755 760 765
 Lys Thr Pro Lys Pro Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr
 770 775 780
 Thr Val Lys Gly Met Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val
 785 790 795 800
 Ser Leu Val Ala Ala Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser
 805 810 815
 Ser Thr Asn Glu Gln Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser
 820 825 830
 Ala Thr Pro Glu Pro Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln
 835 840 845
 Ala Arg Thr Trp Asp Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr
 850 855 860
 Asp Gly Asn Thr Ser Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu
 865 870 875 880
 Leu Val Asp Leu Ser Thr Pro Ala Arg Leu Asp Arg Val Ile Leu Thr
 885 890 895
 Thr Gly Thr Gly Ser Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr
 900 905 910
 Ala Phe Asn Asp Ala Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile
 915 920 925
 Gly Thr Val Asp Tyr Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp
 930 935 940
 Ser Ser Lys Leu Pro Gly Gln Val Glu Ser Val Val Ile Leu Val Asp
 945 950 955 960
 Glu Val Arg Ser Ser Gln Thr Ser Asp Thr Asn Pro Gln Met Gln Ile
 965 970 975
 Ala Glu Val Gln Leu Val Gly Trp
 980

<210> 595
 <211> 915
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(892)
 <223> RXA01807

<400> 595
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gcagtggctg gaactcggcg aggaaatcga gggctagttc atg ccg tcg gca ggc 115
 Met Pro Ser Ala Gly
 1 5

gag gag att tta gag cag cgc gca cag ctg gag ttt gat cag cgc cgc 163
 Glu Glu Ile Leu Glu Gln Arg Ala Gln Leu Glu Phe Asp Gln Arg Arg
 10 15 20

gcc gat gtg gtg atg atc ggc agc cag gtg gtt tat ggt tcc gtg ggc 211
 Ala Asp Val Val Met Ile Gly Ser Gln Val Val Tyr Gly Ser Val Gly
 25 30 35

ctc agt gct gcc att ccg gtg atg cac aac gaa ggc ctc cgc gtg gtc 259
 Leu Ser Ala Ala Ile Pro Val Met His Asn Glu Gly Leu Arg Val Val
 40 45 50

gct gtc ccc acc gtg gtg tta agt tcc atg ccg cgt tat gca agt tct 307
 Ala Val Pro Thr Val Val Leu Ser Ser Met Pro Arg Tyr Ala Ser Ser
 55 60 65

cac cgc cag ccg atg tcg gac caa tgg ctc gcc gac gcg ctg caa gac 355
 His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala Asp Ala Leu Gln Asp
 70 75 80 85

ctg gtg gat ctg ggg att atc gat gag gtt tcc acc att tcc acc ggc 403
 Leu Val Asp Leu Gly Ile Ile Asp Glu Val Ser Thr Ile Ser Thr Gly
 90 95 100

tat ttt acc tcc gct tct cag gtg cgt gtg gtc gct gcg tgg ctg cag 451
 Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val Ala Ala Trp Leu Gln
 105 110 115

aaa atc cgc gaa acc cat ccg cat gtg cgc atc gtg gtg gat ccc atc 499
 Lys Ile Arg Glu Thr His Pro His Val Arg Ile Val Val Asp Pro Ile
 120 125 130

atg ggg gac agt gac gtg gga att tat gtc gcc gac gag atc gca acc 547
 Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala Asp Glu Ile Ala Thr
 135 140 145

gcc atc tgc cag gac tta tgc cct ctg gct acc gga atc att ccc aat 595
 Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr Gly Ile Ile Pro Asn
 150 155 160 165

gct ttc gag ctc tcc cac atg gtt ggc tcc ggc gat ccg cgc tcg ctg 643
 Ala Phe Glu Leu Ser His Met Val Gly Ser Gly Asp Pro Arg Ser Leu
 170 175 180

ctc ggc ccg ttt ggc gag tgg atc atc atc acc agc gcc act gaa act 691
 Leu Gly Pro Phe Gly Glu Trp Ile Ile Ile Thr Ser Ala Thr Glu Thr
 185 190 195

 gtg ggc acc acc gtc acc cgc atc gtc acc cgt gac agc gtc cag gaa 739
 Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg Asp Ser Val Gln Glu
 200 205 210

 atc gcc tcc gcc acc gtc gat acc acg gcc aaa ggg gca ggc gac gtc 787
 Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys Gly Ala Gly Asp Val
 215 220 225

 tac gcc gca gca tta atc gcc gcc ctg cat aaa gat ttt tcg ctt atc 835
 Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys Asp Phe Ser Leu Ile
 230 235 240 245

 gac gcc gcc agc cac gca tcc aac acc gtc tgc gcc ggc ctg cag acc 883
 Asp Ala Ala Ser His Ala Ser Asn Thr Val Cys Ala Gly Leu Gln Thr
 250 255 260

 aaa gcg ctt taggtttcgt ccgtctctga cag 915
 Lys Ala Leu

<210> 596

<211> 264

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 596

Met Pro Ser Ala Gly Glu Glu Ile Leu Glu Gln Arg Ala Gln Leu Glu
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 Phe Asp Gln Arg Arg Ala Asp Val Val Met Ile Gly Ser Gln Val Val
 20 25 30

 Tyr Gly Ser Val Gly Leu Ser Ala Ala Ile Pro Val Met His Asn Glu
 35 40 45

 Gly Leu Arg Val Val Ala Val Pro Thr Val Val Leu Ser Ser Met Pro
 50 55 60

 Arg Tyr Ala Ser Ser His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala
 65 70 75 80

 Asp Ala Leu Gln Asp Leu Val Asp Leu Gly Ile Ile Asp Glu Val Ser
 85 90 95

 Thr Ile Ser Thr Gly Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val
 100 105 110

 Ala Ala Trp Leu Gln Lys Ile Arg Glu Thr His Pro His Val Arg Ile
 115 120 125

 Val Val Asp Pro Ile Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala
 130 135 140

 Asp Glu Ile Ala Thr Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr
 145 150 155 160

Gly Ile Ile Pro Asn Ala Phe Glu Leu Ser His Met Val Gly Ser Gly
 165 170 175
 Asp Pro Arg Ser Leu Leu Gly Pro Phe Gly Glu Trp Ile Ile Ile Thr
 180 185 190
 Ser Ala Thr Glu Thr Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg
 195 200 205
 Asp Ser Val Gln Glu Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys
 210 215 220
 Gly Ala Gly Asp Val Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys
 225 230 235 240
 Asp Phe Ser Leu Ile Asp Ala Ala Ser His Ala Ser Asn Thr Val Cys
 245 250 255
 Ala Gly Leu Gln Thr Lys Ala Leu
 260

<210> 597
 <211> 1461
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1438)
 <223> RXN02754

<400> 597
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 agttcactgt agtccccgct gattccgtag aatcaacaga gtg aat acc aat ccg 115
 Val Asn Thr Asn Pro
 1 5
 tct gaa ttc tcc tca aac cgt tca aca gct ctc ctt act gat aaa tat 163
 Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu Leu Thr Asp Lys Tyr
 10 15 20
 gag ctg acc atg ctt caa gca gcg ctc gct gat ggt tct gca gaa cgc 211
 Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp Gly Ser Ala Glu Arg
 25 30 35
 ccc tca acg ttt gag gtc ttt agc cgc cgc ctc ccc aac gag cgc cga 259
 Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu Pro Asn Glu Arg Arg
 40 45 50
 tac ggt gtc gtc gca gga aca gca cga gtg ctg aag gcg att cgt gac 307
 Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu Lys Ala Ile Arg Asp
 55 60 65
 ttt gta ttc aca gag gaa caa ctc gcc gat ctt gac ttt tta gac gac 355
 Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu Asp Phe Leu Asp Asp
 70 75 80 85
 cgt acc ctg gaa tac ctc cgc aac tac cga ttc acc ggc caa gtt gat 403
 Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe Thr Gly Gln Val Asp

90										95					100					
ggc tac cgc gaa ggc gaa atc tac ttc ccg cag tcc cct ctt ctg act	451																			
Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln Ser Pro Leu Leu Thr																				
105 110 115																				
gtg cgt ggc acg ttt gca gaa tgc gtc atc cta gaa act gtc att ttg	499																			
Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu Glu Thr Val Ile Leu																				
120 125 130																				
tcc atc atg aat gca gat tct gcc gtc gct tcc gcc gct gcg cgc atg	547																			
Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser Ala Ala Ala Arg Met																				
135 140 145																				
gtc acc gca gct gat ggt cgc ccc atc atc gaa atg gga tcc agg cgc	595																			
Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu Met Gly Ser Arg Arg																				
150 155 160 165																				
acc cac gaa tac tcg gca gtc acc gca tcc cgc gca gca tac ctc gct	643																			
Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg Ala Ala Tyr Leu Ala																				
170 175 180																				
gga ttc tcc acc acc tcc aac ctc gag gcg gcc tac cgc tac gga att	691																			
Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala Tyr Arg Tyr Gly Ile																				
185 190 195																				
cca gca tcc gga acc tcc gcc cac gca tgg act ttg ctg cac atc aac	739																			
Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr Leu Leu His Ile Asn																				
200 205 210																				
gat gac ggc acc ccc aac gaa gca gca gct ttc aaa gca cag gtt gaa	787																			
Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe Lys Ala Gln Val Glu																				
215 220 225																				
tcc ctc ggc gtg gac acc acc ttg ctg gta gat act tat gac atc acc	835																			
Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp Thr Tyr Asp Ile Thr																				
230 235 240 245																				
caa ggt gtg gcc acc gcc att gaa gtt gca ggt cca gac ctt ggt ggc	883																			
Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly Pro Asp Leu Gly Gly																				
250 255 260																				
gta cgt atc gac tcc ggc gac cta ggt gtg ctt gcc cga aag gtc cgc	931																			
Val Arg Ile Asp Ser Gly Asp Leu Gly Val Leu Ala Arg Lys Val Arg																				
265 270 275																				
aag cag ctc gac gat ctc aac gcc cac aac acc aag att gtg gtc tcc	979																			
Lys Gln Leu Asp Asp Leu Asn Ala His Asn Thr Lys Ile Val Val Ser																				
280 285 290																				
tcc gac ctg gat gaa ttc gcc atc gcg ggt ctt cgc ggc gaa cca gtt																				
1027																				
Ser Asp Leu Asp Glu Phe Ala Ile Ala Gly Leu Arg Gly Glu Pro Val																				
295 300 305																				
gac gtc ttt ggc gtt ggc acc tcc gtt gtc aca ggt tct ggc gca cca																				
1075																				
Asp Val Phe Gly Val Gly Thr Ser Val Val Thr Gly Ser Gly Ala Pro																				
310 315 320 325																				

acc gct ggc ctc gtg tac aag atc ggg gaa gtt gcc ggt cac cct gtg
1123
Thr Ala Gly Leu Val Tyr Lys Ile Gly Glu Val Ala Gly His Pro Val
330 335 340

gcc aag cgt tcc cga aac aag gaa agc tac ggt ggt ggc aag aag gct
1171
Ala Lys Arg Ser Arg Asn Lys Glu Ser Tyr Gly Gly Gly Lys Lys Ala
345 350 355

gtg cgc acc cac cgc aag tcc ggt acc gca atc gaa gaa atc gtc tac
1219
Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile Glu Glu Ile Val Tyr
360 365 370

cca ttc aat gcc gaa gca cca gat act gga aag ctc gac act ttg agc
1267
Pro Phe Asn Ala Glu Ala Pro Asp Thr Gly Lys Leu Asp Thr Leu Ser
375 380 385

ctg acc atc cca ttg atg cgc gac ggt gaa atc gtt cca ggt ttg cct
1315
Leu Thr Ile Pro Leu Met Arg Asp Gly Glu Ile Val Pro Gly Leu Pro
390 395 400 405

act ttg gaa gat tcc cga gcg tat ttg gcc aag caa ttg gtc tct tta
1363
Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys Gln Leu Val Ser Leu
410 415 420

cca tgg gaa ggc ctt gca ctg tct cgc gat gag cct gtt ttg cac act
1411
Pro Trp Glu Gly Leu Ala Leu Ser Arg Asp Glu Pro Val Leu His Thr
425 430 435

cgt ttc gtg ggt ttc ccg ccg gcc gct tagacaattc ggtctcacca
1458
Arg Phe Val Gly Phe Pro Pro Ala Ala
440 445

aac
1461

<210> 598

<211> 446

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 598

Val Asn Thr Asn Pro Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu
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Leu Thr Asp Lys Tyr Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp
20 25 30

Gly Ser Ala Glu Arg Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu
35 40 45

Pro Asn Glu Arg Arg Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu
50 55 60

Lys Ala Ile Arg Asp Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu
 65 70 75 80
 Asp Phe Leu Asp Asp Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe
 85 90 95
 Thr Gly Gln Val Asp Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln
 100 105 110
 Ser Pro Leu Leu Thr Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu
 115 120 125
 Glu Thr Val Ile Leu Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser
 130 135 140
 Ala Ala Ala Arg Met Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu
 145 150 155 160
 Met Gly Ser Arg Arg Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg
 165 170 175
 Ala Ala Tyr Leu Ala Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala
 180 185 190
 Tyr Arg Tyr Gly Ile Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr
 195 200 205
 Leu Leu His Ile Asn Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe
 210 215 220
 Lys Ala Gln Val Glu Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp
 225 230 235 240
 Thr Tyr Asp Ile Thr Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly
 245 250 255
 Pro Asp Leu Gly Gly Val Arg Ile Asp Ser Gly Asp Leu Gly Val Leu
 260 265 270
 Ala Arg Lys Val Arg Lys Gln Leu Asp Asp Leu Asn Ala His Asn Thr
 275 280 285
 Lys Ile Val Val Ser Ser Asp Leu Asp Glu Phe Ala Ile Ala Gly Leu
 290 295 300
 Arg Gly Glu Pro Val Asp Val Phe Gly Val Gly Thr Ser Val Val Thr
 305 310 315 320
 Gly Ser Gly Ala Pro Thr Ala Gly Leu Val Tyr Lys Ile Gly Glu Val
 325 330 335
 Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys Glu Ser Tyr Gly
 340 345 350
 Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile
 355 360 365
 Glu Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro Asp Thr Gly Lys
 370 375 380

Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg Asp Gly Glu Ile
385 390 395 400

Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys
405 410 415

Gln Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu Ser Arg Asp Glu
420 425 430

Pro Val Leu His Thr Arg Phe Val Gly Phe Pro Pro Ala Ala
435 440 445

<210> 599

<211> 871

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(871)

<223> FRXA02405

<400> 599

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agttcactgt agctcccgct gattccgtag aatcaacaga gtg aat acc aat ccg 115
Val Asn Thr Asn Pro
1 5

tct gaa ttc tcc tca aac cgt tca aca gct ctc ctt act gat aaa tat 163
Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu Leu Thr Asp Lys Tyr
10 15 20

gag ctg acc atg ctt caa gca gcg ctc gct gat ggt tct gca gaa cgc 211
Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp Gly Ser Ala Glu Arg
25 30 35

ccc tca acg ttt gag gtc ttt agc cgc cgc ctc ccc aac gag cgc cga 259
Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu Pro Asn Glu Arg Arg
40 45 50

tac ggt gtc gtc gca gga aca gca cga gtg ctg aag gcg att cgt gac 307
Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu Lys Ala Ile Arg Asp
55 60 65

ttt gta ttc aca gag gaa caa ctc gcc gat ctt gac ttt tta gac gac 355
Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu Asp Phe Leu Asp Asp
70 75 80 85

cgt acc ctg gaa tac ctc cgc aac tac cga ttc acc ggc caa gtt gat 403
Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe Thr Gly Gln Val Asp
90 95 100

ggc tac cgc gaa ggc gaa atc tac ttc ccg cag tcc cct ctt ctg act 451
Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln Ser Pro Leu Leu Thr
105 110 115

gtg cgt ggc acg ttt gca gaa tgc gtc atc cta gaa act gtc att ttg 499
Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu Glu Thr Val Ile Leu
120 125 130

tcc atc atg aat gca gat tct gcc gtc gct tcc gcc gct gcg cgc atg	547
Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser Ala Ala Ala Arg Met	
135 140 145	
gtc acc gca gct gat ggt cgc ccc atc atc gaa atg gga tcc agg cgc	595
Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu Met Gly Ser Arg Arg	
150 155 160 165	
acc cac gaa tac tcg gca gtc acc gca tcc cgc gca gca tac ctc gct	643
Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg Ala Ala Tyr Leu Ala	
170 175 180	
gga ttc tcc acc acc tcc aac ctc gag gcg gcc tac cgc tac gga att	691
Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala Tyr Arg Tyr Gly Ile	
185 190 195	
cca gca tcc gga acc tcc gcc cac gca tgg act ttg ctg cac atc aac	739
Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr Leu Leu His Ile Asn	
200 205 210	
gat gac ggc acc ccc aac gaa gca gca gct ttc aaa gca cag gtt gaa	787
Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe Lys Ala Gln Val Glu	
215 220 225	
tcc ctc ggc gtg gac acc acc ttg ctg gta gat act tat gac atc acc	835
Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp Thr Tyr Asp Ile Thr	
230 235 240 245	
caa ggt gtg gcc acc gcc att gaa gtt gca ggt cca	871
Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly Pro	
250 255	

<210> 600

<211> 257

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 600

Val Asn Thr Asn Pro Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu
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Leu Thr Asp Lys Tyr Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp
20 25 30

Gly Ser Ala Glu Arg Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu
35 40 45

Pro Asn Glu Arg Arg Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu
50 55 60

Lys Ala Ile Arg Asp Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu
65 70 75 80

Asp Phe Leu Asp Asp Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe
85 90 95

Thr Gly Gln Val Asp Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln
100 105 110

Ser Pro Leu Leu Thr Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu
 115 120 125

Glu Thr Val Ile Leu Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser
 130 135 140

Ala Ala Ala Arg Met Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu
 145 150 155 160

Met Gly Ser Arg Arg Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg
 165 170 175

Ala Ala Tyr Leu Ala Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala
 180 185 190

Tyr Arg Tyr Gly Ile Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr
 195 200 205

Leu Leu His Ile Asn Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe
 210 215 220

Lys Ala Gln Val Glu Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp
 225 230 235 240

Thr Tyr Asp Ile Thr Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly
 245 250 255

Pro

<210> 601
 <211> 509
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(486)
 <223> FRXA02754

<400> 601
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 Pro Thr Asn Thr Lys Ile Val Val Ser Ser Asp Leu Asp Glu Phe Ala
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atc gcg ggt ctt cgc ggc gaa cca gtt gac gtc ttt ggc gtt ggc acc 96
 Ile Ala Gly Leu Arg Gly Glu Pro Val Asp Val Phe Gly Val Gly Thr
 20 25 30

tcc gtt gtc aca ggt tct ggc gca cca acc gct ggc ctc gtg tac aag 144
 Ser Val Val Thr Gly Ser Gly Ala Pro Thr Ala Gly Leu Val Tyr Lys
 35 40 45

atc ggg gaa gtt gcc ggt cac cct gtg gcc aag cgt tcc cga aac aag 192
 Ile Gly Glu Val Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys
 50 55 60

gaa agc tac ggt ggt ggc aag aag gct gtg cgc acc cac cgc aag tcc 240
 Glu Ser Tyr Gly Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser
 65 70 75 80

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ggt acc gca atc gaa gaa atc gtc tac cca ttc aat gcc gaa gca cca 288
Gly Thr Ala Ile Glu Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro
      85                      90                      95

gat act gga aag ctc gac act ttg agc ctg acc atc cca ttg atg cgc 336
Asp Thr Gly Lys Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg
      100                      105                      110

gac ggt gaa atc gtt cca ggt ttg cct act ttg gaa gat tcc cga gcg 384
Asp Gly Glu Ile Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala
      115                      120                      125

tat ttg gcc aag caa ttg gtc tct tta cca tgg gaa ggc ctt gca ctg 432
Tyr Leu Ala Lys Gln Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu
      130                      135                      140

tct cgc gat gag cct gtt ttg cac act cgt ttc gtg ggt ttc ccg ccg 480
Ser Arg Asp Glu Pro Val Leu His Thr Arg Phe Val Gly Phe Pro Pro
      145                      150                      155                      160

gcc gct tagacaattc ggtctcacca aac 509
Ala Ala

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<210> 602

<211> 162

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 602

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Pro Thr Asn Thr Lys Ile Val Val Ser Ser Asp Leu Asp Glu Phe Ala
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Ile Ala Gly Leu Arg Gly Glu Pro Val Asp Val Phe Gly Val Gly Thr
      20                      25                      30

Ser Val Val Thr Gly Ser Gly Ala Pro Thr Ala Gly Leu Val Tyr Lys
      35                      40                      45

Ile Gly Glu Val Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys
      50                      55                      60

Glu Ser Tyr Gly Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser
      65                      70                      75                      80

Gly Thr Ala Ile Glu Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro
      85                      90                      95

Asp Thr Gly Lys Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg
      100                      105                      110

Asp Gly Glu Ile Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala
      115                      120                      125

Tyr Leu Ala Lys Gln Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu
      130                      135                      140

Ser Arg Asp Glu Pro Val Leu His Thr Arg Phe Val Gly Phe Pro Pro
      145                      150                      155                      160

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Ala Ala

<210> 603
 <211> 960
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(937)
 <223> RXA02112

<400> 603
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agctcctggt actcctagct cctcgaagga tgcgtaattt atg act acc cat att 115
 Met Thr Thr His Ile
 1 5

gac cgc atc gtt ggc gca gcg tta tcc gag gat gcg cca tgg ggc gac 163
 Asp Arg Ile Val Gly Ala Ala Leu Ser Glu Asp Ala Pro Trp Gly Asp
 10 15 20

att acc tcc gac act ttt atc cca gga tcg gcg cag ctg agc gcc aag 211
 Ile Thr Ser Asp Thr Phe Ile Pro Gly Ser Ala Gln Leu Ser Ala Lys
 25 30 35

gtt gtt gcc cgg gag cca ggt gtg ttc agc ggg cag gcg ctt tta gac 259
 Val Val Ala Arg Glu Pro Gly Val Phe Ser Gly Gln Ala Leu Leu Asp
 40 45 50

gcc tcc ttc cgg ctc gtc gat cct agg ata aac gca tcc ctt aag gtg 307
 Ala Ser Phe Arg Leu Val Asp Pro Arg Ile Asn Ala Ser Leu Lys Val
 55 60 65

gct gat ggt gac agc ttt gaa acc ggg gac atc cta gga aca att acc 355
 Ala Asp Gly Asp Ser Phe Glu Thr Gly Asp Ile Leu Gly Thr Ile Thr
 70 75 80 85

ggc agt gct aga agc atc ctc cgt tca gag cgc att gct ctc aac ttc 403
 Gly Ser Ala Arg Ser Ile Leu Arg Ser Glu Arg Ile Ala Leu Asn Phe
 90 95 100

att cag agg acg tcc ggc atc gct aca ttg aca tcg tgc tat gtt gca 451
 Ile Gln Arg Thr Ser Gly Ile Ala Thr Leu Thr Ser Cys Tyr Val Ala
 105 110 115

gag gtt aaa ggc acc aaa gcc cgc att gtt gat acc cgg aaa acc aca 499
 Glu Val Lys Gly Thr Lys Ala Arg Ile Val Asp Thr Arg Lys Thr Thr
 120 125 130

ccc ggc ctg cgc atc att gaa cgc caa gct gtc cgt gac ggt ggc gga 547
 Pro Gly Leu Arg Ile Ile Glu Arg Gln Ala Val Arg Asp Gly Gly Gly
 135 140 145

ttt aat cac cga gcc acc ttg tcc gat gct gtc atg gtg aaa gat aac 595
 Phe Asn His Arg Ala Thr Leu Ser Asp Ala Val Met Val Lys Asp Asn
 150 155 160 165

cat ctc gca gcc atc gca tcc cag ggg ctc agc atc act gaa gcg ctg 643
 His Leu Ala Ala Ile Ala Ser Gln Gly Leu Ser Ile Thr Glu Ala Leu
 170 175 180
 tcg aat atg aaa gct aaa ctc ccc cac acc acc cat gtg gaa gtc gaa 691
 Ser Asn Met Lys Ala Lys Leu Pro His Thr Thr His Val Glu Val Glu
 185 190 195
 gtt gat cat ata gag cag atc gaa cca gtt ctt gct gct ggt gtg gac 739
 Val Asp His Ile Glu Gln Ile Glu Pro Val Leu Ala Ala Gly Val Asp
 200 205 210
 acc atc atg ttg gat aat ttc acc att gat cag ctc atc gaa ggc gtt 787
 Thr Ile Met Leu Asp Asn Phe Thr Ile Asp Gln Leu Ile Glu Gly Val
 215 220 225
 gat ctc att ggt gga cgt gca ctg gtg gaa gca tct ggc gga gtc aac 835
 Asp Leu Ile Gly Gly Arg Ala Leu Val Glu Ala Ser Gly Gly Val Asn
 230 235 240 245
 ctc aac acc gcg gga aag att gca tca acc ggt gtc gac gtc att tcc 883
 Leu Asn Thr Ala Gly Lys Ile Ala Ser Thr Gly Val Asp Val Ile Ser
 250 255 260
 gtt gga gcg ctt acc cat tct gtg cat gca ctt gac cta gga ctc gat 931
 Val Gly Ala Leu Thr His Ser Val His Ala Leu Asp Leu Gly Leu Asp
 265 270 275
 att ttc taatgctcta ccttgataat gca 960
 Ile Phe

<210> 604

<211> 279

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 604

Met Thr Thr His Ile Asp Arg Ile Val Gly Ala Ala Leu Ser Glu Asp
 1 5 10 15
 Ala Pro Trp Gly Asp Ile Thr Ser Asp Thr Phe Ile Pro Gly Ser Ala
 20 25 30
 Gln Leu Ser Ala Lys Val Val Ala Arg Glu Pro Gly Val Phe Ser Gly
 35 40 45
 Gln Ala Leu Leu Asp Ala Ser Phe Arg Leu Val Asp Pro Arg Ile Asn
 50 55 60
 Ala Ser Leu Lys Val Ala Asp Gly Asp Ser Phe Glu Thr Gly Asp Ile
 65 70 75 80
 Leu Gly Thr Ile Thr Gly Ser Ala Arg Ser Ile Leu Arg Ser Glu Arg
 85 90 95
 Ile Ala Leu Asn Phe Ile Gln Arg Thr Ser Gly Ile Ala Thr Leu Thr
 100 105 110

Ser Cys Tyr Val Ala Glu Val Lys Gly Thr Lys Ala Arg Ile Val Asp
 115 120 125
 Thr Arg Lys Thr Thr Pro Gly Leu Arg Ile Ile Glu Arg Gln Ala Val
 130 135 140
 Arg Asp Gly Gly Gly Phe Asn His Arg Ala Thr Leu Ser Asp Ala Val
 145 150 155 160
 Met Val Lys Asp Asn His Leu Ala Ala Ile Ala Ser Gln Gly Leu Ser
 165 170 175
 Ile Thr Glu Ala Leu Ser Asn Met Lys Ala Lys Leu Pro His Thr Thr
 180 185 190
 His Val Glu Val Glu Val Asp His Ile Glu Gln Ile Glu Pro Val Leu
 195 200 205
 Ala Ala Gly Val Asp Thr Ile Met Leu Asp Asn Phe Thr Ile Asp Gln
 210 215 220
 Leu Ile Glu Gly Val Asp Leu Ile Gly Gly Arg Ala Leu Val Glu Ala
 225 230 235 240
 Ser Gly Gly Val Asn Leu Asn Thr Ala Gly Lys Ile Ala Ser Thr Gly
 245 250 255
 Val Asp Val Ile Ser Val Gly Ala Leu Thr His Ser Val His Ala Leu
 260 265 270
 Asp Leu Gly Leu Asp Ile Phe
 275

<210> 605
 <211> 1407
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1384)
 <223> RXA02111

<400> 605
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 gctcattcca gccaccggt tagaagaaaa gaccccaatc atg acc acc tca atc 115
 Met Thr Thr Ser Ile
 1 5
 acc cca tct gtc aac ctt gca ttg aaa aat gcc aat agc tgc aac agt 163
 Thr Pro Ser Val Asn Leu Ala Leu Lys Asn Ala Asn Ser Cys Asn Ser
 10 15 20
 gaa ctc aaa gac gga ccc tgg ttc ctc gac cag ccc gga atg ccg gat 211
 Glu Leu Lys Asp Gly Pro Trp Phe Leu Asp Gln Pro Gly Met Pro Asp
 25 30 35
 gtc tac ggc ccc ggc gcg tca caa aac gat ccg atc cct gcg cat gct 259
 Val Tyr Gly Pro Gly Ala Ser Gln Asn Asp Pro Ile Pro Ala His Ala

40	45	50	
ccg cgc cag cag gtt ctc ccc gag gag tac cag cgc gca agt gat gac Pro Arg Gln Gln Val Leu Pro Glu Glu Tyr Gln Arg Ala Ser Asp Asp 55 60 65			307
gaa ctg cat cgt agg atc cgg gaa gcg aaa gac acc ctg ggt gac aaa Glu Leu His Arg Arg Ile Arg Glu Ala Lys Asp Thr Leu Gly Asp Lys 70 75 80 85			355
gtg gtt atc cta gga cac ttc tac cag cgc gat gaa gtt atc caa cac Val Val Ile Leu Gly His Phe Tyr Gln Arg Asp Glu Val Ile Gln His 90 95 100			403
gca gat ttt gtt ggt gac tct ttc caa ctt gcc cgc gct gcc aaa acc Ala Asp Phe Val Gly Asp Ser Phe Gln Leu Ala Arg Ala Ala Lys Thr 105 110 115			451
cga ccc gag gcg gaa gcg att gtg ttc tgc ggt gtg cac ttc atg gct Arg Pro Glu Ala Glu Ala Ile Val Phe Cys Gly Val His Phe Met Ala 120 125 130			499
gaa acc gct gat ctg tta tcc acg gat gaa caa tca gtg atc ctc ccc Glu Thr Ala Asp Leu Leu Ser Thr Asp Glu Gln Ser Val Ile Leu Pro 135 140 145			547
aac ctt gcc gca ggt tgc tcc atg gca gac atg gct gac ctt gat tcc Asn Leu Ala Ala Gly Cys Ser Met Ala Asp Met Ala Asp Leu Asp Ser 150 155 160 165			595
gtc gaa gac tgc tgg gag caa ctc acc tca att tat ggc gat gac acc Val Glu Asp Cys Trp Glu Gln Leu Thr Ser Ile Tyr Gly Asp Asp Thr 170 175 180			643
ctg atc cct gtg acc tac atg aat tcc tct gca gcg ctc aaa ggt ttc Leu Ile Pro Val Thr Tyr Met Asn Ser Ser Ala Ala Leu Lys Gly Phe 185 190 195			691
gtg ggt gag cac ggc gga att gta tgc acc tcc tca aat gca cgt tcc Val Gly Glu His Gly Gly Ile Val Cys Thr Ser Ser Asn Ala Arg Ser 200 205 210			739
gta ttg gag tgg gcg ttt gaa cgc ggc caa cga gtc ctg ttc ttc ccc Val Leu Glu Trp Ala Phe Glu Arg Gly Gln Arg Val Leu Phe Phe Pro 215 220 225			787
gat cag cac ttg ggt cga aac acc gcg aaa gcc atg ggc att ggg atc Asp Gln His Leu Gly Arg Asn Thr Ala Lys Ala Met Gly Ile Gly Ile 230 235 240 245			835
gat caa atg ccc ctg tgg aat ccc aac aaa cca ctg ggt ggc aac acc Asp Gln Met Pro Leu Trp Asn Pro Asn Lys Pro Leu Gly Gly Asn Thr 250 255 260			883
gtt tcc gag cta gaa aac gca aag gta ctg ctc tgg cat ggt ttc tgc Val Ser Glu Leu Glu Asn Ala Lys Val Leu Leu Trp His Gly Phe Cys 265 270 275			931
tct gta cac aag cgc ttt act gtc gag cag atc aac aaa gcc cgc gcc Ser Val His Lys Arg Phe Thr Val Glu Gln Ile Asn Lys Ala Arg Ala 280 285 290			979

gag tac ccc gac gtt cac gtc atc gtg cac cct gaa tcc ccc atg cca
1027

Glu Tyr Pro Asp Val His Val Ile Val His Pro Glu Ser Pro Met Pro
295 300 305

gtt gtt gac gcc gcc gac tca tcc gga tcc act gac ttc att gtg aaa
1075

Val Val Asp Ala Ala Asp Ser Ser Gly Ser Thr Asp Phe Ile Val Lys
310 315 320 325

gcc att caa gca gca ccg gca gga tct acc ttt gcg atc ggc acc gaa
1123

Ala Ile Gln Ala Ala Pro Ala Gly Ser Thr Phe Ala Ile Gly Thr Glu
330 335 340

atc aac ttg gtt cag cgc ctg gca gcc cag tac ccg cag cac acc atc
1171

Ile Asn Leu Val Gln Arg Leu Ala Ala Gln Tyr Pro Gln His Thr Ile
345 350 355

ttc tgc ctc gac cct gtc atc tgc cca tgc tcc acc atg tat cgc att
1219

Phe Cys Leu Asp Pro Val Ile Cys Pro Cys Ser Thr Met Tyr Arg Ile
360 365 370

cac cct ggt tac ctg gcc tgg gca ctt gag gag ttg gtg gct gga aac
1267

His Pro Gly Tyr Leu Ala Trp Ala Leu Glu Glu Leu Val Ala Gly Asn
375 380 385

gtg att aac cag att tct gtc tct gaa tcc gtg gcg gca ccg gcg cga
1315

Val Ile Asn Gln Ile Ser Val Ser Glu Ser Val Ala Ala Pro Ala Arg
390 395 400 405

gtc gct ttg gaa agg atg cta tct gtt gtt cca gca gct cct gtt act
1363

Val Ala Leu Glu Arg Met Leu Ser Val Val Pro Ala Ala Pro Val Thr
410 415 420

cct agc tcc tcg aag gat gcg taatttatga ctacccatat tga
1407

Pro Ser Ser Ser Lys Asp Ala
425

<210> 606

<211> 428

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 606

Met Thr Thr Ser Ile Thr Pro Ser Val Asn Leu Ala Leu Lys Asn Ala
1 5 10 15

Asn Ser Cys Asn Ser Glu Leu Lys Asp Gly Pro Trp Phe Leu Asp Gln
20 25 30

Pro Gly Met Pro Asp Val Tyr Gly Pro Gly Ala Ser Gln Asn Asp Pro
35 40 45

Ile Pro Ala His Ala Pro Arg Gln Gln Val Leu Pro Glu Glu Tyr Gln
 50 55 60
 Arg Ala Ser Asp Asp Glu Leu His Arg Arg Ile Arg Glu Ala Lys Asp
 65 70 75 80
 Thr Leu Gly Asp Lys Val Val Ile Leu Gly His Phe Tyr Gln Arg Asp
 85 90 95
 Glu Val Ile Gln His Ala Asp Phe Val Gly Asp Ser Phe Gln Leu Ala
 100 105 110
 Arg Ala Ala Lys Thr Arg Pro Glu Ala Glu Ala Ile Val Phe Cys Gly
 115 120 125
 Val His Phe Met Ala Glu Thr Ala Asp Leu Leu Ser Thr Asp Glu Gln
 130 135 140
 Ser Val Ile Leu Pro Asn Leu Ala Ala Gly Cys Ser Met Ala Asp Met
 145 150 155 160
 Ala Asp Leu Asp Ser Val Glu Asp Cys Trp Glu Gln Leu Thr Ser Ile
 165 170 175
 Tyr Gly Asp Asp Thr Leu Ile Pro Val Thr Tyr Met Asn Ser Ser Ala
 180 185 190
 Ala Leu Lys Gly Phe Val Gly Glu His Gly Gly Ile Val Cys Thr Ser
 195 200 205
 Ser Asn Ala Arg Ser Val Leu Glu Trp Ala Phe Glu Arg Gly Gln Arg
 210 215 220
 Val Leu Phe Phe Pro Asp Gln His Leu Gly Arg Asn Thr Ala Lys Ala
 225 230 235 240
 Met Gly Ile Gly Ile Asp Gln Met Pro Leu Trp Asn Pro Asn Lys Pro
 245 250 255
 Leu Gly Gly Asn Thr Val Ser Glu Leu Glu Asn Ala Lys Val Leu Leu
 260 265 270
 Trp His Gly Phe Cys Ser Val His Lys Arg Phe Thr Val Glu Gln Ile
 275 280 285
 Asn Lys Ala Arg Ala Glu Tyr Pro Asp Val His Val Ile Val His Pro
 290 295 300
 Glu Ser Pro Met Pro Val Val Asp Ala Ala Asp Ser Ser Gly Ser Thr
 305 310 315 320
 Asp Phe Ile Val Lys Ala Ile Gln Ala Ala Pro Ala Gly Ser Thr Phe
 325 330 335
 Ala Ile Gly Thr Glu Ile Asn Leu Val Gln Arg Leu Ala Ala Gln Tyr
 340 345 350
 Pro Gln His Thr Ile Phe Cys Leu Asp Pro Val Ile Cys Pro Cys Ser
 355 360 365

Thr Met Tyr Arg Ile His Pro Gly Tyr Leu Ala Trp Ala Leu Glu Glu
370 375 380

Leu Val Ala Gly Asn Val Ile Asn Gln Ile Ser Val Ser Glu Ser Val
385 390 395 400

Ala Ala Pro Ala Arg Val Ala Leu Glu Arg Met Leu Ser Val Val Pro
405 410 415

Ala Ala Pro Val Thr Pro Ser Ser Ser Lys Asp Ala
420 425

<210> 607

<211> 954

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(931)

<223> RXA01073

<400> 607

taaccgactc cagcactaaa ctccaaaccc ttggcccgca ccgccaaagt ttagcgcgcc 60

ccaagacacc accgcgccat gtttgcctag gattaggtac atg aca aac act caa 115
Met Thr Asn Thr Gln
1 5

acc gag atc att aat gaa cta aag gtg agc cca gca atc gac gtg gcc 163
Thr Glu Ile Ile Asn Glu Leu Lys Val Ser Pro Ala Ile Asp Val Ala
10 15 20

aag gaa gtt gaa ttc cgt gtg cag ttc ctc gtc gat tac ctg cgg gct 211
Lys Glu Val Glu Phe Arg Val Gln Phe Leu Val Asp Tyr Leu Arg Ala
25 30 35

tcc cat aca aaa ggc ttt gtt ctt ggt att tca ggt ggc cag gat tcc 259
Ser His Thr Lys Gly Phe Val Leu Gly Ile Ser Gly Gly Gln Asp Ser
40 45 50

act ctt gcg gga cga ctc acg cag ctg gca gta gag cgc att cgt gcg 307
Thr Leu Ala Gly Arg Leu Thr Gln Leu Ala Val Glu Arg Ile Arg Ala
55 60 65

gaa gaa aac agc acg gat tat gtc ttc tac gca gtt cgc ctc ccc tac 355
Glu Glu Asn Ser Thr Asp Tyr Val Phe Tyr Ala Val Arg Leu Pro Tyr
70 75 80 85

gcg atc cag gca gat gag gac gat gcg caa gtt gca ttg gaa ttc atc 403
Ala Ile Gln Ala Asp Glu Asp Asp Ala Gln Val Ala Leu Glu Phe Ile
90 95 100

gca cct gac aag agc gtg acc gtc aac gtt aaa gac gca acg gac gcc 451
Ala Pro Asp Lys Ser Val Thr Val Asn Val Lys Asp Ala Thr Asp Ala
105 110 115

acc gaa gca act gtt gca gct gct ttg gaa ctt cct gag ctg acc gac 499
Thr Glu Ala Thr Val Ala Ala Ala Leu Glu Leu Pro Glu Leu Thr Asp
120 125 130

ttc aat cgg ggc aat att aaa gct cgc caa cgc atg gtt gcc cag tac 547
 Phe Asn Arg Gly Asn Ile Lys Ala Arg Gln Arg Met Val Ala Gln Tyr
 135 140 145

 gca atc gca ggc cag ttg ggc ttg ctg gtt att ggc act gat cac gcg 595
 Ala Ile Ala Gly Gln Leu Gly Leu Leu Val Ile Gly Thr Asp His Ala
 150 155 160 165

 gct gaa aac gtc acg ggg ttc ttc acc aaa ttc ggt gat ggc gca gct 643
 Ala Glu Asn Val Thr Gly Phe Phe Thr Lys Phe Gly Asp Gly Ala Ala
 170 175 180

 gac ctg ctt cct ttg gca ggt ttg agc aag cgt caa gga gct gcc att 691
 Asp Leu Leu Pro Leu Ala Gly Leu Ser Lys Arg Gln Gly Ala Ala Ile
 185 190 195

 ctg gag cac ctg ggt gca cct tca agc acg tgg acc aag gtt cct acc 739
 Leu Glu His Leu Gly Ala Pro Ser Ser Thr Trp Thr Lys Val Pro Thr
 200 205 210

 gct gat ttg gaa gag gat cgc cca gcg ttg cca gat gag gaa gca ctt 787
 Ala Asp Leu Glu Glu Asp Arg Pro Ala Leu Pro Asp Glu Glu Ala Leu
 215 220 225

 ggt gtg tcg tat gcg gac atc gat aat tac ctg gaa aac aag ccc gat 835
 Gly Val Ser Tyr Ala Asp Ile Asp Asn Tyr Leu Glu Asn Lys Pro Asp
 230 235 240 245

 gtc agt gaa aaa gcc cag cag cgc att gag cac ctg tgg aag gtg ggc 883
 Val Ser Glu Lys Ala Gln Gln Arg Ile Glu His Leu Trp Lys Val Gly
 250 255 260

 cag cac aag cgc cac ctc cct gct acc ccg cag gaa aat tgg tgg cgt 931
 Gln His Lys Arg His Leu Pro Ala Thr Pro Gln Glu Asn Trp Trp Arg
 265 270 275

 taatccaaca gtttgagtgt cgc 954

<210> 608

<211> 277

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 608

Met Thr Asn Thr Gln Thr Glu Ile Ile Asn Glu Leu Lys Val Ser Pro
 1 5 10 15

 Ala Ile Asp Val Ala Lys Glu Val Glu Phe Arg Val Gln Phe Leu Val
 20 25 30

 Asp Tyr Leu Arg Ala Ser His Thr Lys Gly Phe Val Leu Gly Ile Ser
 35 40 45

 Gly Gly Gln Asp Ser Thr Leu Ala Gly Arg Leu Thr Gln Leu Ala Val
 50 55 60

 Glu Arg Ile Arg Ala Glu Glu Asn Ser Thr Asp Tyr Val Phe Tyr Ala
 65 70 75 80

Val	Arg	Leu	Pro	Tyr	Ala	Ile	Gln	Ala	Asp	Glu	Asp	Asp	Ala	Gln	Val		
				85					90					95			
Ala	Leu	Glu	Phe	Ile	Ala	Pro	Asp	Lys	Ser	Val	Thr	Val	Asn	Val	Lys		
			100					105					110				
Asp	Ala	Thr	Asp	Ala	Thr	Glu	Ala	Thr	Val	Ala	Ala	Ala	Leu	Glu	Leu		
		115					120					125					
Pro	Glu	Leu	Thr	Asp	Phe	Asn	Arg	Gly	Asn	Ile	Lys	Ala	Arg	Gln	Arg		
	130					135					140						
Met	Val	Ala	Gln	Tyr	Ala	Ile	Ala	Gly	Gln	Leu	Gly	Leu	Leu	Val	Ile		
145					150					155					160		
Gly	Thr	Asp	His	Ala	Ala	Glu	Asn	Val	Thr	Gly	Phe	Phe	Thr	Lys	Phe		
			165						170					175			
Gly	Asp	Gly	Ala	Ala	Asp	Leu	Leu	Pro	Leu	Ala	Gly	Leu	Ser	Lys	Arg		
			180					185					190				
Gln	Gly	Ala	Ala	Ile	Leu	Glu	His	Leu	Gly	Ala	Pro	Ser	Ser	Thr	Trp		
	195						200					205					
Thr	Lys	Val	Pro	Thr	Ala	Asp	Leu	Glu	Glu	Asp	Arg	Pro	Ala	Leu	Pro		
	210					215					220						
Asp	Glu	Glu	Ala	Leu	Gly	Val	Ser	Tyr	Ala	Asp	Ile	Asp	Asn	Tyr	Leu		
225					230					235					240		
Glu	Asn	Lys	Pro	Asp	Val	Ser	Glu	Lys	Ala	Gln	Gln	Arg	Ile	Glu	His		
				245					250					255			
Leu	Trp	Lys	Val	Gly	Gln	His	Lys	Arg	His	Leu	Pro	Ala	Thr	Pro	Gln		
			260					265					270				
Glu	Asn	Trp	Trp	Arg													
		275															

<210> 609
 <211> 1461
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1438)
 <223> RXN02754

<400> 609
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 agttcactgt agctcccgtc gattccgtag aatcaacaga gtg aat acc aat ccg 115
 Val Asn Thr Asn Pro
 1 5

tct gaa ttc tcc tca aac cgt tca aca gct ctc ctt act gat aaa tat 163
 Ser Glu Phe Ser Ser Asn Arg Ser Thr Ala Leu Leu Thr Asp Lys Tyr
 10 15 20

gag	ctg	acc	atg	ctt	caa	gca	gcg	ctc	gct	gat	ggg	tct	gca	gaa	cgc	211
Glu	Leu	Thr	Met	Leu	Gln	Ala	Ala	Leu	Ala	Asp	Gly	Ser	Ala	Glu	Arg	
			25					30					35			
ccc	tca	acg	ttt	gag	gtc	ttt	agc	cgc	cgc	ctc	ccc	aac	gag	cgc	cga	259
Pro	Ser	Thr	Phe	Glu	Val	Phe	Ser	Arg	Arg	Leu	Pro	Asn	Glu	Arg	Arg	
		40					45					50				
tac	ggg	gtc	gtc	gca	gga	aca	gca	cga	gtg	ctg	aag	gcg	att	cgt	gac	307
Tyr	Gly	Val	Val	Ala	Gly	Thr	Ala	Arg	Val	Leu	Lys	Ala	Ile	Arg	Asp	
	55					60					65					
ttt	gta	ttc	aca	gag	gaa	caa	ctc	gcc	gat	ctt	gac	ttt	tta	gac	gac	355
Phe	Val	Phe	Thr	Glu	Glu	Gln	Leu	Ala	Asp	Leu	Asp	Phe	Leu	Asp	Asp	
	70					75				80					85	
cgt	acc	ctg	gaa	tac	ctc	cgc	aac	tac	cga	ttc	acc	ggc	caa	gtt	gat	403
Arg	Thr	Leu	Glu	Tyr	Leu	Arg	Asn	Tyr	Arg	Phe	Thr	Gly	Gln	Val	Asp	
			90					95						100		
ggc	tac	cgc	gaa	ggc	gaa	atc	tac	ttc	ccg	cag	tcc	cct	ctt	ctg	act	451
Gly	Tyr	Arg	Glu	Gly	Glu	Ile	Tyr	Phe	Pro	Gln	Ser	Pro	Leu	Leu	Thr	
			105					110					115			
gtg	cgt	ggc	acg	ttt	gca	gaa	tgc	gtc	atc	cta	gaa	act	gtc	att	ttg	499
Val	Arg	Gly	Thr	Phe	Ala	Glu	Cys	Val	Ile	Leu	Glu	Thr	Val	Ile	Leu	
		120					125					130				
tcc	atc	atg	aat	gca	gat	tct	gcc	gtc	gct	tcc	gcc	gct	gcg	cgc	atg	547
Ser	Ile	Met	Asn	Ala	Asp	Ser	Ala	Val	Ala	Ser	Ala	Ala	Ala	Arg	Met	
	135					140				145						
gtc	acc	gca	gct	gat	ggg	cgc	ccc	atc	atc	gaa	atg	gga	tcc	agg	cgc	595
Val	Thr	Ala	Ala	Asp	Gly	Arg	Pro	Ile	Ile	Glu	Met	Gly	Ser	Arg	Arg	
	150				155					160					165	
acc	cac	gaa	tac	tcg	gca	gtc	acc	gca	tcc	cgc	gca	gca	tac	ctc	gct	643
Thr	His	Glu	Tyr	Ser	Ala	Val	Thr	Ala	Ser	Arg	Ala	Ala	Tyr	Leu	Ala	
				170				175						180		
gga	ttc	tcc	acc	acc	tcc	aac	ctc	gag	gcg	gcc	tac	cgc	tac	gga	att	691
Gly	Phe	Ser	Thr	Thr	Ser	Asn	Leu	Glu	Ala	Ala	Tyr	Arg	Tyr	Gly	Ile	
			185				190						195			
cca	gca	tcc	gga	acc	tcc	gcc	cac	gca	tgg	act	ttg	ctg	cac	atc	aac	739
Pro	Ala	Ser	Gly	Thr	Ser	Ala	His	Ala	Trp	Thr	Leu	Leu	His	Ile	Asn	
		200				205						210				
gat	gac	ggc	acc	ccc	aac	gaa	gca	gca	gct	ttc	aaa	gca	cag	gtt	gaa	787
Asp	Asp	Gly	Thr	Pro	Asn	Glu	Ala	Ala	Ala	Phe	Lys	Ala	Gln	Val	Glu	
	215					220					225					
tcc	ctc	ggc	gtg	gac	acc	acc	ttg	ctg	gta	gat	act	tat	gac	atc	acc	835
Ser	Leu	Gly	Val	Asp	Thr	Thr	Leu	Leu	Val	Asp	Thr	Tyr	Asp	Ile	Thr	
	230				235					240					245	
caa	ggg	gtg	gcc	acc	gcc	att	gaa	gtt	gca	ggg	cca	gac	ctt	ggg	ggc	883
Gln	Gly	Val	Ala	Thr	Ala	Ile	Glu	Val	Ala	Gly	Pro	Asp	Leu	Gly	Gly	
			250					255						260		
gta	cgt	atc	gac	tcc	ggc	gac	cta	ggg	gtg	ctt	gcc	cga	aag	gtc	cgc	931

Val Arg Ile Asp Ser Gly Asp Leu Gly Val Leu Ala Arg Lys Val Arg
 265 270 275

aag cag ctc gac gat ctc aac gcc cac aac acc aag att gtg gtc tcc 979
 Lys Gln Leu Asp Asp Leu Asn Ala His Asn Thr Lys Ile Val Val Ser
 280 285 290

tcc gac ctg gat gaa ttc gcc atc gcg ggt ctt cgc ggc gaa cca gtt
 1027
 Ser Asp Leu Asp Glu Phe Ala Ile Ala Gly Leu Arg Gly Glu Pro Val
 295 300 305

gac gtc ttt ggc gtt ggc acc tcc gtt gtc aca ggt tct ggc gca cca
 1075
 Asp Val Phe Gly Val Gly Thr Ser Val Val Thr Gly Ser Gly Ala Pro
 310 315 320 325

acc gct ggc ctc gtg tac aag atc ggg gaa gtt gcc ggt cac cct gtg
 1123
 Thr Ala Gly Leu Val Tyr Lys Ile Gly Glu Val Ala Gly His Pro Val
 330 335 340

gcc aag cgt tcc cga aac aag gaa agc tac ggt ggt ggc aag aag gct
 1171
 Ala Lys Arg Ser Arg Asn Lys Glu Ser Tyr Gly Gly Gly Lys Lys Ala
 345 350 355

gtg cgc acc cac cgc aag tcc ggt acc gca atc gaa gaa atc gtc tac
 1219
 Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile Glu Glu Ile Val Tyr
 360 365 370

cca ttc aat gcc gaa gca cca gat act gga aag ctc gac act ttg agc
 1267
 Pro Phe Asn Ala Glu Ala Pro Asp Thr Gly Lys Leu Asp Thr Leu Ser
 375 380 385

ctg acc atc cca ttg atg cgc gac ggt gaa atc gtt cca ggt ttg cct
 1315
 Leu Thr Ile Pro Leu Met Arg Asp Gly Glu Ile Val Pro Gly Leu Pro
 390 395 400 405

act ttg gaa gat tcc cga gcg tat ttg gcc aag caa ttg gtc tct tta
 1363
 Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys Gln Leu Val Ser Leu
 410 415 420

cca tgg gaa ggc ctt gca ctg tct cgc gat gag cct gtt ttg cac act
 1411
 Pro Trp Glu Gly Leu Ala Leu Ser Arg Asp Glu Pro Val Leu His Thr
 425 430 435

cgt ttc gtg ggt ttc ccg ccg gcc gct tagacaattc ggtctcacca
 1458
 Arg Phe Val Gly Phe Pro Pro Ala Ala
 440 445

aac
 1461

<210> 610
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 610

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Leu Thr Asp Lys Tyr Glu Leu Thr Met Leu Gln Ala Ala Leu Ala Asp
          20              25              30

Gly Ser Ala Glu Arg Pro Ser Thr Phe Glu Val Phe Ser Arg Arg Leu
          35              40              45

Pro Asn Glu Arg Arg Tyr Gly Val Val Ala Gly Thr Ala Arg Val Leu
          50              55              60

Lys Ala Ile Arg Asp Phe Val Phe Thr Glu Glu Gln Leu Ala Asp Leu
          65              70              75

Asp Phe Leu Asp Asp Arg Thr Leu Glu Tyr Leu Arg Asn Tyr Arg Phe
          85              90              95

Thr Gly Gln Val Asp Gly Tyr Arg Glu Gly Glu Ile Tyr Phe Pro Gln
          100              105              110

Ser Pro Leu Leu Thr Val Arg Gly Thr Phe Ala Glu Cys Val Ile Leu
          115              120              125

Glu Thr Val Ile Leu Ser Ile Met Asn Ala Asp Ser Ala Val Ala Ser
          130              135              140

Ala Ala Ala Arg Met Val Thr Ala Ala Asp Gly Arg Pro Ile Ile Glu
          145              150              155              160

Met Gly Ser Arg Arg Thr His Glu Tyr Ser Ala Val Thr Ala Ser Arg
          165              170              175

Ala Ala Tyr Leu Ala Gly Phe Ser Thr Thr Ser Asn Leu Glu Ala Ala
          180              185              190

Tyr Arg Tyr Gly Ile Pro Ala Ser Gly Thr Ser Ala His Ala Trp Thr
          195              200              205

Leu Leu His Ile Asn Asp Asp Gly Thr Pro Asn Glu Ala Ala Ala Phe
          210              215              220

Lys Ala Gln Val Glu Ser Leu Gly Val Asp Thr Thr Leu Leu Val Asp
          225              230              235              240

Thr Tyr Asp Ile Thr Gln Gly Val Ala Thr Ala Ile Glu Val Ala Gly
          245              250              255

Pro Asp Leu Gly Gly Val Arg Ile Asp Ser Gly Asp Leu Gly Val Leu
          260              265              270

Ala Arg Lys Val Arg Lys Gln Leu Asp Asp Leu Asn Ala His Asn Thr
          275              280              285

Lys Ile Val Val Ser Ser Asp Leu Asp Glu Phe Ala Ile Ala Gly Leu
  
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290	295	300
Arg Gly Glu Pro Val Asp Val Phe Gly Val Gly Thr Ser Val Val Thr 305 310 315 320		
Gly Ser Gly Ala Pro Thr Ala Gly Leu Val Tyr Lys Ile Gly Glu Val 325 330 335		
Ala Gly His Pro Val Ala Lys Arg Ser Arg Asn Lys Glu Ser Tyr Gly 340 345 350		
Gly Gly Lys Lys Ala Val Arg Thr His Arg Lys Ser Gly Thr Ala Ile 355 360 365		
Glu Glu Ile Val Tyr Pro Phe Asn Ala Glu Ala Pro Asp Thr Gly Lys 370 375 380		
Leu Asp Thr Leu Ser Leu Thr Ile Pro Leu Met Arg Asp Gly Glu Ile 385 390 395 400		
Val Pro Gly Leu Pro Thr Leu Glu Asp Ser Arg Ala Tyr Leu Ala Lys 405 410 415		
Gln Leu Val Ser Leu Pro Trp Glu Gly Leu Ala Leu Ser Arg Asp Glu 420 425 430		
Pro Val Leu His Thr Arg Phe Val Gly Phe Pro Pro Ala Ala 435 440 445		

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<211> 531

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(508)

<223> RXA02299

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Met Leu Arg Thr Ile	
1 5	

ctc gga agt aag att cac cga gcc act gtc act caa gct gat cta gat	163
Leu Gly Ser Lys Ile His Arg Ala Thr Val Thr Gln Ala Asp Leu Asp	
10 15 20	

tat gtt ggc tct gta acc atc gac gcc gac ctg gtt cac gcc gcc gga	211
Tyr Val Gly Ser Val Thr Ile Asp Ala Asp Leu Val His Ala Ala Gly	
25 30 35	

ttg atc gaa ggc gaa aaa gtt gcc atc gta gac atc acc aac ggc gct	259
Leu Ile Glu Gly Glu Lys Val Ala Ile Val Asp Ile Thr Asn Gly Ala	
40 45 50	

cgt ctg gaa act tat gtc att gtg ggc gac gcc gga acg ggc aat att	307
Arg Leu Glu Thr Tyr Val Ile Val Gly Asp Ala Gly Thr Gly Asn Ile	

55	60	65	
tgc atc aat ggt gcc gct gca cac ctt att aat cct ggc gat ctt gtg			355
Cys Ile Asn Gly Ala Ala Ala His Leu Ile Asn Pro Gly Asp Leu Val			
70	75	80	85
atc atc atg agc tac ctt cag gca act gat gcg gaa gcc aag gcg tat			403
Ile Ile Met Ser Tyr Leu Gln Ala Thr Asp Ala Glu Ala Lys Ala Tyr			
	90	95	100
gag cca aag att gtg cac gtg gac gcc gac aac cgc atc gtt gcg ctc			451
Glu Pro Lys Ile Val His Val Asp Ala Asp Asn Arg Ile Val Ala Leu			
	105	110	115
ggc aac gat ctt gcg gaa gca cta cct gga tcc ggg ctt ttg acg tcg			499
Gly Asn Asp Leu Ala Glu Ala Leu Pro Gly Ser Gly Leu Leu Thr Ser			
	120	125	130
aga agc att tagcggtttta gctcgccaat att			531
Arg Ser Ile			
135			

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<211> 136

<212> PRT

<213> Corynebacterium glutamicum

<400> 612

Met Leu Arg Thr Ile Leu Gly Ser Lys Ile His Arg Ala Thr Val Thr			
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Gln Ala Asp Leu Asp Tyr Val Gly Ser Val Thr Ile Asp Ala Asp Leu			
	20	25	30
Val His Ala Ala Gly Leu Ile Glu Gly Glu Lys Val Ala Ile Val Asp			
	35	40	45
Ile Thr Asn Gly Ala Arg Leu Glu Thr Tyr Val Ile Val Gly Asp Ala			
	50	55	60
Gly Thr Gly Asn Ile Cys Ile Asn Gly Ala Ala Ala His Leu Ile Asn			
	65	70	75
Pro Gly Asp Leu Val Ile Ile Met Ser Tyr Leu Gln Ala Thr Asp Ala			
	85	90	95
Glu Ala Lys Ala Tyr Glu Pro Lys Ile Val His Val Asp Ala Asp Asn			
	100	105	110
Arg Ile Val Ala Leu Gly Asn Asp Leu Ala Glu Ala Leu Pro Gly Ser			
	115	120	125
Gly Leu Leu Thr Ser Arg Ser Ile			
130	135		

<210> 613

<211> 960

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(937)

<223> RXA01928

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tccacgcggg taccttccca ggcgaagcgg agtcctttta atg cag gta gca acc 115
                                         Met Gln Val Ala Thr
                                         1                               5

aca aag cag gcg ctt atc gac gcc ctc ctc cac cac aaa tcc gtc ggg 163
Thr Lys Gln Ala Leu Ile Asp Ala Leu Leu His His Lys Ser Val Gly
                        10                        15                        20

ctc gtc ccc acc atg ggt gcg cta cac agc gga cac gcc tcg ttg gtt 211
Leu Val Pro Thr Met Gly Ala Leu His Ser Gly His Ala Ser Leu Val
                        25                        30                        35

aaa gca gca cgc gct gaa aac gac act gtt gta gcc agt att ttt gtc 259
Lys Ala Ala Arg Ala Glu Asn Asp Thr Val Val Ala Ser Ile Phe Val
                        40                        45                        50

aat ccc ctg cag ttt gaa gca ctc ggt gat tgc gat gat tac cgc aac 307
Asn Pro Leu Gln Phe Glu Ala Leu Gly Asp Cys Asp Asp Tyr Arg Asn
                        55                        60                        65

tat ccc cgc caa ctc gac gcc gat tta gca ctg ctt gaa gag gca ggt 355
Tyr Pro Arg Gln Leu Asp Ala Asp Leu Ala Leu Leu Glu Glu Ala Gly
                        70                        75                        80                        85

gtg gat att gtg ttc gca ccc gat gtg gag gaa atg tac ccc ggt ggc 403
Val Asp Ile Val Phe Ala Pro Asp Val Glu Glu Met Tyr Pro Gly Gly
                        90                        95                        100

ttg cca cta gtg tgg gcg cgc acc ggt tcc atc gga aca aaa ttg gag 451
Leu Pro Leu Val Trp Ala Arg Thr Gly Ser Ile Gly Thr Lys Leu Glu
                        105                        110                        115

ggt gcc agc agg cct ggc cat ttc gat ggt gtg gct acc gtg gtg gcg 499
Gly Ala Ser Arg Pro Gly His Phe Asp Gly Val Ala Thr Val Val Ala
                        120                        125                        130

aag ctg ttc aat ttg gtg cgc cct gat cgt gca tat ttt gga caa aaa 547
Lys Leu Phe Asn Leu Val Arg Pro Asp Arg Ala Tyr Phe Gly Gln Lys
                        135                        140                        145

gat gct cag cag gtt gcg gtg att cgg cga ttg gtt gcc gat cta gac 595
Asp Ala Gln Gln Val Ala Val Ile Arg Arg Leu Val Ala Asp Leu Asp
                        150                        155                        160                        165

att ccc gtg gag att cgt ccc gtt ccg att att cgt ggc gcc gat ggc 643
Ile Pro Val Glu Ile Arg Pro Val Pro Ile Ile Arg Gly Ala Asp Gly
                        170                        175                        180

tta gcc gaa tcc agc cgc aat caa cgt ctt tct gcg gat cag cga gcg 691
Leu Ala Glu Ser Ser Arg Asn Gln Arg Leu Ser Ala Asp Gln Arg Ala
                        185                        190                        195

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caa gct ctg gtg ctg ccg cag gtg ttg agt ggg ttg cag cgt cga aaa 739
 Gln Ala Leu Val Leu Pro Gln Val Leu Ser Gly Leu Gln Arg Arg Lys
 200 205 210

 gca gct ggt gaa gcg cta gat atc caa ggt gcg cgc gac acc ttg gcc 787
 Ala Ala Gly Glu Ala Leu Asp Ile Gln Gly Ala Arg Asp Thr Leu Ala
 215 220 225

 agc gcc gac ggc gtg cgc ttg gat cac ctg gaa att gtc gat cca gcc 835
 Ser Ala Asp Gly Val Arg Leu Asp His Leu Glu Ile Val Asp Pro Ala
 230 235 240 245

 acc ctc gaa cca tta gaa atc gac ggc ctg ctc acc caa cca gcg ttg 883
 Thr Leu Glu Pro Leu Glu Ile Asp Gly Leu Leu Thr Gln Pro Ala Leu
 250 255 260

 gtg gtc ggc gcg att ttc gtg ggg ccg gtg cgg ttg atc gac aat atc 931
 Val Val Gly Ala Ile Phe Val Gly Pro Val Arg Leu Ile Asp Asn Ile
 265 270 275

 gag ctc tagtaccaac cctgcgttgc agc 960
 Glu Leu

<210> 614

<211> 279

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 614

Met Gln Val Ala Thr Thr Lys Gln Ala Leu Ile Asp Ala Leu Leu His
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 His Lys Ser Val Gly Leu Val Pro Thr Met Gly Ala Leu His Ser Gly
 20 25 30

 His Ala Ser Leu Val Lys Ala Ala Arg Ala Glu Asn Asp Thr Val Val
 35 40 45

 Ala Ser Ile Phe Val Asn Pro Leu Gln Phe Glu Ala Leu Gly Asp Cys
 50 55 60

 Asp Asp Tyr Arg Asn Tyr Pro Arg Gln Leu Asp Ala Asp Leu Ala Leu
 65 70 75 80

 Leu Glu Glu Ala Gly Val Asp Ile Val Phe Ala Pro Asp Val Glu Glu
 85 90 95

 Met Tyr Pro Gly Gly Leu Pro Leu Val Trp Ala Arg Thr Gly Ser Ile
 100 105 110

 Gly Thr Lys Leu Glu Gly Ala Ser Arg Pro Gly His Phe Asp Gly Val
 115 120 125

 Ala Thr Val Val Ala Lys Leu Phe Asn Leu Val Arg Pro Asp Arg Ala
 130 135 140

 Tyr Phe Gly Gln Lys Asp Ala Gln Gln Val Ala Val Ile Arg Arg Leu
 145 150 155 160

Val Ala Asp Leu Asp Ile Pro Val Glu Ile Arg Pro Val Pro Ile Ile
 165 170 175

Arg Gly Ala Asp Gly Leu Ala Glu Ser Ser Arg Asn Gln Arg Leu Ser
 180 185 190

Ala Asp Gln Arg Ala Gln Ala Leu Val Leu Pro Gln Val Leu Ser Gly
 195 200 205

Leu Gln Arg Arg Lys Ala Ala Gly Glu Ala Leu Asp Ile Gln Gly Ala
 210 215 220

Arg Asp Thr Leu Ala Ser Ala Asp Gly Val Arg Leu Asp His Leu Glu
 225 230 235 240

Ile Val Asp Pro Ala Thr Leu Glu Pro Leu Glu Ile Asp Gly Leu Leu
 245 250 255

Thr Gln Pro Ala Leu Val Val Gly Ala Ile Phe Val Gly Pro Val Arg
 260 265 270

Leu Ile Asp Asn Ile Glu Leu
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<210> 615
 <211> 936
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(913)
 <223> RXN01929

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ggaatttatt tattctgagc tggatcatcac atctataactc atg ccc atg tca ggc 115
 Met Pro Met Ser Gly
 1 5

att gat gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta 163
 Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val
 10 15 20

aac ggc cag aaa gtt tcg gtt ctc acc agc tat gat gcg ctt tcg gcg 211
 Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala
 25 30 35

cgc att ttt gat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc 259
 Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser
 40 45 50

gct gcc aac gtt gtg ctg ggt cgc gat acc acc ttg tcg atc acc ttg 307
 Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu
 55 60 65

gat gag atg att gtg ctg gcc aag gcg gtg acg atc gct acg aag cgt 355
 Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala Thr Lys Arg
 70 75 80 85

gcg ctt gtg gtg gtt gat ctg ccg ttt ggt acc tat gag gtg agc cca 403
 Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu Val Ser Pro
 90 95 100

aat cag gcg gtg gag tcc gcg atc cgg gtc atg cgt gaa acg ggt gcg 451
 Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu Thr Gly Ala
 105 110 115

gct gcg gtg aag atc gag ggt ggc gtg gag atc gcg cag acg att cga 499
 Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln Thr Ile Arg
 120 125 130

cgc att gtt gat gct gga att ccg gtt gtc ggc cac atc ggg tac acc 547
 Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile Gly Tyr Thr
 135 140 145

ccg cag tcc gag cat tcc ttg ggc ggc cac gtg gtt cag ggt cgt ggc 595
 Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln Gly Arg Gly
 150 155 160 165

gcg agt tct gga aag ctc atc gcc gat gcc cgc gcg ttg gag cag gcg 643
 Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu Glu Gln Ala
 170 175 180

ggt gcg ttt gcg gtt gtg ttg gag atg gtt cca gca gag gca gcg cgc 691
 Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu Ala Ala Arg
 185 190 195

gag gtt acc gag gat ctt tcc atc acc act atc gga atc ggt gcc ggc 739
 Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile Gly Ala Gly
 200 205 210

aat ggc aca gat ggg cag gtt ttg gtg tgg cag gat gcc ttc ggc ctc 787
 Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala Phe Gly Leu
 215 220 225

aac cgc ggc aag aag cca cgc ttc gtc cgc gag tac gcc acc ttg ggc 835
 Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala Thr Leu Gly
 230 235 240 245

gat tcc ttg cac gac gcc gcg cag gcc tac atc gcc gat atc cac gcg 883
 Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp Ile His Ala
 250 255 260

ggt acc ttc cca ggc gaa gcg gag tcc ttt taatgcaggt agcaaccaca 933
 Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe
 265 270

aag 936

<210> 616

<211> 271

<212> PRT

<213> Corynebacterium glutamicum

<400> 616

Met Pro Met Ser Gly Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe
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tattttattct	gagctgggtca	tcacatctat	actcatgccc	atg	tca	ggc	att	gat	115
				Met	Ser	Gly	Ile	Asp	
				1				5	
gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta aac ggc	163								
Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val Asn Gly									
	10 15 20								
cag aaa gtt tcg gtt ctc acc agc tat gat gcg ctt tcg gcg cgc att	211								
Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala Arg Ile									
	25 30 35								
ttt gat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc gct gcc	259								
Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser Ala Ala									
	40 45 50								
aac gtt gtg ctg ggt cgc gat acc acc ttg tcg atc acc ttg gat gag	307								
Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu Asp Glu									
	55 60 65								
atg att gtg ctg gcc aag gcg gtg acg atc gct acg aag cgt gcg ctt	355								
Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala Thr Lys Arg Ala Leu									
	70 75 80 85								
gtg gtg gtt gat ctg ccg ttt ggt acc tat gag gtg agc cca aat cag	403								
Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu Val Ser Pro Asn Gln									
	90 95 100								
gcg gtg gag tcc gcg atc cgg gtc atg cgt gaa acg ggt gcg gct gcg	451								
Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu Thr Gly Ala Ala Ala									
	105 110 115								
gtg aag atc gag ggt ggc gtg gag atc gcg cag acg att cga cgc att	499								
Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln Thr Ile Arg Arg Ile									
	120 125 130								
gtt gat gct gga att ccg gtt gtc ggc cac atc ggg tac acc ccg cag	547								
Val Asp Ala Gly Ile Pro Val Val Gly His Ile Gly Tyr Thr Pro Gln									
	135 140 145								
tcc gag cat tcc ttg ggc ggc cac gtg gtt cag ggt cgt ggc gcg agt	595								
Ser Glu His Ser Leu Gly Gly His Val Val Gln Gly Arg Gly Ala Ser									
	150 155 160 165								
tct gga aag ctc atc gcc gat gcc cgc gcg ttg gag cag gcg ggt gcg	643								
Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu Glu Gln Ala Gly Ala									
	170 175 180								
ttt gcg gtt gtg ttg gag atg gtt cca gca gag gca gcg cgc gag gtt	691								
Phe Ala Val Val Leu Glu Met Val Pro Ala Glu Ala Ala Arg Glu Val									
	185 190 195								
acc gag gat ctt tcc atc acc act atc gga atc ggt gcc ggc aat ggc	739								
Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile Gly Ala Gly Asn Gly									
	200 205 210								
aca gat ggg cag gtt ttg gtg tgg cag gat gcc ttc ggc ctc aac cgc	787								
Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala Phe Gly Leu Asn Arg									
	215 220 225								

ggc aag aag cca cgc ttc gtc cgc gag tac gcc acc ttg ggc gat tcc 835
 Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala Thr Leu Gly Asp Ser
 230 235 240 245

ttg cac gac gcc gcg cag gcc tac atc gcc gat atc cac gcg ggt acc 883
 Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp Ile His Ala Gly Thr
 250 255 260

ttc cca ggc gaa gcg gag tcc ttt taatgcaggt agcaaccaca aag 930
 Phe Pro Gly Glu Ala Glu Ser Phe
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<210> 618

<211> 269

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 618

Met Ser Gly Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu
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Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala
 20 25 30

Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val
 35 40 45

Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser
 50 55 60

Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala
 65 70 75 80

Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu
 85 90 95

Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu
 100 105 110

Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln
 115 120 125

Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile
 130 135 140

Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln
 145 150 155 160

Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu
 165 170 175

Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu
 180 185 190

Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile
 195 200 205

Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala
 210 215 220

Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala
 225 230 235 240

Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp
 245 250 255

Ile His Ala Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe
 260 265

<210> 619

<211> 921

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(898)

<223> RXA01521

<400> 619

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cgcaagatat tgagctgtgg gcaattcaga aggaggaccg ttg agt ttc acg cat 115
 Leu Ser Phe Thr His
 1 5

ggt cag ggc aga gtt ttt gat acc gtc gag cag atc cgc atg ttc ggc 163
 Gly Gln Gly Arg Val Phe Asp Thr Val Glu Gln Ile Arg Met Phe Gly
 10 15 20

agc gcc ctg cgc aaa acc ggc aaa cca gtg gtg ctc gta ccc ttg gga 211
 Ser Ala Leu Arg Lys Thr Gly Lys Pro Val Val Leu Val Pro Leu Gly
 25 30 35

aat ggc ctc cac gca ggc cat att gcg ctc atc cgc gca gca aaa cgc 259
 Asn Gly Leu His Ala Gly His Ile Ala Leu Ile Arg Ala Ala Lys Arg
 40 45 50

atc ccc ggt gcg gtg gtc gtc gtc gcc tat gcc ggc ccg gaa tcg gat 307
 Ile Pro Gly Ala Val Val Val Val Ala Tyr Ala Gly Pro Glu Ser Asp
 55 60 65

cac gca cgt tta agg gaa gag ctt atc gac gcg atc ttc ccg ttc aat 355
 His Ala Arg Leu Arg Glu Glu Leu Ile Asp Ala Ile Phe Pro Phe Asn
 70 75 80 85

ccc gaa acg cta tgg cct cac ggc atc cgg gtg gaa gtt aca ggt ggc 403
 Pro Glu Thr Leu Trp Pro His Gly Ile Arg Val Glu Val Thr Gly Gly
 90 95 100

cca aca ctt acc cca caa ggt gcg gaa gta acc aag gtg ctg ggg ctg 451
 Pro Thr Leu Thr Pro Gln Gly Ala Glu Val Thr Lys Val Leu Gly Leu
 105 110 115

ttg gga atc acc gga gca act gat gtg gtg ctc ggt gaa aag gac tat 499
 Leu Gly Ile Thr Gly Ala Thr Asp Val Val Leu Gly Glu Lys Asp Tyr
 120 125 130

gag ctg gtg gtt cta gtc cag cgc gcc ctt aat gat ctg cat att cca 547
 Glu Leu Val Val Leu Val Gln Arg Ala Leu Asn Asp Leu His Ile Pro

135	140	145	
gta aaa ctg cat tct gtt cca acc gtg cgc atg cca gat gga cta gcc			595
Val Lys Leu His Ser Val Pro Thr Val Arg Met Pro Asp Gly Leu Ala			
150	155	160	165
att tcc ctg cgt aat att tca gtg ccc gaa gac tcc cgc gaa acg gca			643
Ile Ser Leu Arg Asn Ile Ser Val Pro Glu Asp Ser Arg Glu Thr Ala			
	170	175	180
ttg agc ctg gca gca gcc ctc acc gcc ggt gcg cat tcg gca gaa cac			691
Leu Ser Leu Ala Ala Ala Leu Thr Ala Gly Ala His Ser Ala Glu His			
	185	190	195
ggc gag gca gtg gtt aaa gaa aca gtc acg caa gtg ctc aaa gcc gca			739
Gly Glu Ala Val Val Lys Glu Thr Val Thr Gln Val Leu Lys Ala Ala			
	200	205	210
ggc gtg acc ccc gat tat gta gaa atc cgt ggc ctg gat ctt gga cca			787
Gly Val Thr Pro Asp Tyr Val Glu Ile Arg Gly Leu Asp Leu Gly Pro			
	215	220	225
gcc ccc gaa atc gga gac gcc cga ctc ttc gca gcc atc acg ctt ggc			835
Ala Pro Glu Ile Gly Asp Ala Arg Leu Phe Ala Ala Ile Thr Leu Gly			
	230	235	240
gat gtc caa ctc cac gac aac gtc ggc cta ccc ctt gga atc ggc ttc			883
Asp Val Gln Leu His Asp Asn Val Gly Leu Pro Leu Gly Ile Gly Phe			
	250	255	260
aaa aac atc gaa ggc tgatcccggt ttaccagtt cgc			921
Lys Asn Ile Glu Gly			
	265		

<210> 620

<211> 266

<212> PRT

<213> Corynebacterium glutamicum

<400> 620

Leu Ser Phe Thr His Gly Gln Gly Arg Val Phe Asp Thr Val Glu Gln
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Ile Arg Met Phe Gly Ser Ala Leu Arg Lys Thr Gly Lys Pro Val Val
20 25 30

Leu Val Pro Leu Gly Asn Gly Leu His Ala Gly His Ile Ala Leu Ile
35 40 45

Arg Ala Ala Lys Arg Ile Pro Gly Ala Val Val Val Ala Tyr Ala
50 55 60

Gly Pro Glu Ser Asp His Ala Arg Leu Arg Glu Glu Leu Ile Asp Ala
65 70 75 80

Ile Phe Pro Phe Asn Pro Glu Thr Leu Trp Pro His Gly Ile Arg Val
85 90 95

Glu Val Thr Gly Gly Pro Thr Leu Thr Pro Gln Gly Ala Glu Val Thr
100 105 110

Lys Val Leu Gly Leu Leu Gly Ile Thr Gly Ala Thr Asp Val Val Leu
 115 120 125
 Gly Glu Lys Asp Tyr Glu Leu Val Val Leu Val Gln Arg Ala Leu Asn
 130 135 140
 Asp Leu His Ile Pro Val Lys Leu His Ser Val Pro Thr Val Arg Met
 145 150 155 160
 Pro Asp Gly Leu Ala Ile Ser Leu Arg Asn Ile Ser Val Pro Glu Asp
 165 170 175
 Ser Arg Glu Thr Ala Leu Ser Leu Ala Ala Ala Leu Thr Ala Gly Ala
 180 185 190
 His Ser Ala Glu His Gly Glu Ala Val Val Lys Glu Thr Val Thr Gln
 195 200 205
 Val Leu Lys Ala Ala Gly Val Thr Pro Asp Tyr Val Glu Ile Arg Gly
 210 215 220
 Leu Asp Leu Gly Pro Ala Pro Glu Ile Gly Asp Ala Arg Leu Phe Ala
 225 230 235 240
 Ala Ile Thr Leu Gly Asp Val Gln Leu His Asp Asn Val Gly Leu Pro
 245 250 255
 Leu Gly Ile Gly Phe Lys Asn Ile Glu Gly
 260 265

<210> 621

<211> 1137

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1114)

<223> RXS01145

<400> 621

taatgtagtt gtctgcccac gcgaggttaa ctcccacgat ttacagtggg gggcagacat 60

 cttttcacca aaatttttac gaaaggcgag attttctccc atg gct att gaa ctg 115
 Met Ala Ile Glu Leu
 1 5

 ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163
 Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val
 10 15 20

 gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211
 Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu
 25 30 35

 cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259
 Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys
 40 45 50

tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct	307
Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala	
55 60 65	
gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc	355
Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr	
70 75 80 85	
tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca	403
Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala	
90 95 100	
ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg	451
Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu	
105 110 115	
atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc	499
Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly	
120 125 130	
cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct	547
Pro Gly His Leu Val Arg Arg Gln Phe Val Asp Gly Lys Gly Val Pro	
135 140 145	
tgc ctc atc gca gtc gac cag gac cca acc gga acc gca cag gct ctg	595
Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly Thr Ala Gln Ala Leu	
150 155 160 165	
acc ctg tcc tac gca gca gca atc ggt ggc gca cgc gca ggc gtt atc	643
Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala Arg Ala Gly Val Ile	
170 175 180	
cca acc acc ttc gaa gct gag acc gtc acc gac ctc ttc ggc gag cag	691
Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp Leu Phe Gly Glu Gln	
185 190 195	
gct gtt ctc tgc ggt ggc acc gag gaa ctg gtc aag gtt ggc ttc gag	739
Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val Lys Val Gly Phe Glu	
200 205 210	
gtt ctc acc gaa gct ggc tac gag cca gag atg gca tac ttc gag gtt	787
Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met Ala Tyr Phe Glu Val	
215 220 225	
ctt cac gag ctc aag ctc atc gtt gac ctc atg ttc gaa ggt ggc atc	835
Leu His Glu Leu Lys Leu Ile Val Asp Leu Met Phe Glu Gly Gly Ile	
230 235 240 245	
agc aac atg aac tac tct gtt tct gac acc gct gag ttc ggt ggc tac	883
Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala Glu Phe Gly Gly Tyr	
250 255 260	
ctc tcc ggc cca cgc gtc atc gat gca gac acc aag tcc cgc atg aag	931
Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr Lys Ser Arg Met Lys	
265 270 275	
gac atc ctg acc gat atc cag gac ggc acc ttc acc aag cgc ctc atc	979
Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe Thr Lys Arg Leu Ile	
280 285 290	

gca aac gtt gag aac ggc aac acc gag ctt gag ggc ctt cgt gct tcc
 1027
 Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu Gly Leu Arg Ala Ser
 295 300 305

tac aac aac cac cca atc gag gag acc ggc gct aag ctc cgc gac ctc
 1075
 Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala Lys Leu Arg Asp Leu
 310 315 320 325

atg agc tgg gtc aag gtt gac gct cgc gca gaa acc gct taagtttcac
 1124
 Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu Thr Ala
 330 335

ccctttgacg gct
 1137

<210> 622
 <211> 338
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 622
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 1 5 10 15
 Gln Gly Arg Lys Val Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala
 20 25 30
 His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu
 35 40 45
 Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu
 50 55 60
 Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu
 65 70 75 80
 Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu
 85 90 95
 Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn
 100 105 110
 Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met
 115 120 125
 Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp
 130 135 140
 Gly Lys Gly Val Pro Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly
 145 150 155 160
 Thr Ala Gln Ala Leu Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala
 165 170 175
 Arg Ala Gly Val Ile Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp
 180 185 190

Leu Phe Gly Glu Gln Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val
 195 200 205
 Lys Val Gly Phe Glu Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met
 210 215 220
 Ala Tyr Phe Glu Val Leu His Glu Leu Lys Leu Ile Val Asp Leu Met
 225 230 235 240
 Phe Glu Gly Gly Ile Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala
 245 250 255
 Glu Phe Gly Gly Tyr Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr
 260 265 270
 Lys Ser Arg Met Lys Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe
 275 280 285
 Thr Lys Arg Leu Ile Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu
 290 295 300
 Gly Leu Arg Ala Ser Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala
 305 310 315 320
 Lys Leu Arg Asp Leu Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu
 325 330 335
 Thr Ala

<210> 623
 <211> 556
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(556)
 <223> FRXA01145

<400> 623
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 cttttcacca aaatttttac gaaaggcgag attttctccc atg gct att gaa ctg 115
 Met Ala Ile Glu Leu
 1 5
 ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163
 Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val
 10 15 20
 gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211
 Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu
 25 30 35
 cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259
 Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys
 40 45 50
 tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct 307

Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala
 55 60 65
 gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc 355
 Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr
 70 75 80 85
 tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca 403
 Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala
 90 95 100
 ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg 451
 Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu
 105 110 115
 atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc 499
 Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly
 120 125 130
 cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct 547
 Pro Gly His Leu Val Arg Arg Gln Phe Val Asp Gly Lys Gly Val Pro
 135 140 145
 tgc ctc atc 556
 Cys Leu Ile
 150

<210> 624

<211> 152

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 624

Met Ala Ile Glu Leu Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile
 1 5 10 15
 Gln Gly Arg Lys Val Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala
 20 25 30
 His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu
 35 40 45
 Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu
 50 55 60
 Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu
 65 70 75 80
 Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu
 85 90 95
 Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn
 100 105 110
 Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met
 115 120 125
 Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp
 130 135 140

Gly Lys Gly Val Pro Cys Leu Ile
145 150

<210> 625
<211> 1389
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (101)..(1366)
<223> RXA02239

<400> 625
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gtgtgggaac ccagccagcc tcttactttg aaggattgtt gtg ccc atg act cat 115
Val Pro Met Thr His
1 5
gtt tca agc ccc tcc gca ccc cgc aac gtg gtt gtt ggt gtt gcc ggc 163
Val Ser Ser Pro Ser Ala Pro Arg Asn Val Val Val Gly Val Ala Gly
10 15 20
gga atc gca gcg tac aag gcg tgt cac atc gtg cgc gcg ttt aaa gaa 211
Gly Ile Ala Ala Tyr Lys Ala Cys His Ile Val Arg Ala Phe Lys Glu
25 30 35
gcg ggc gat aat gtg cgg gtg gtt cct acg gaa tcc gcg ttg aag ttt 259
Ala Gly Asp Asn Val Arg Val Val Pro Thr Glu Ser Ala Leu Lys Phe
40 45 50
gtg ggg aag gcg acg ttt gaa gcg ttg tct ggc aat ccg gtg tct aca 307
Val Gly Lys Ala Thr Phe Glu Ala Leu Ser Gly Asn Pro Val Ser Thr
55 60 65
acg gtg ttt gat gcg gtg gat tcg gtg cag cat gtg aaa gtt ggc cag 355
Thr Val Phe Asp Ala Val Asp Ser Val Gln His Val Lys Val Gly Gln
70 75 80 85
gaa gct gat ttg atc gtg att gcg ccg gcg aca gcc gat ttg atg gcg 403
Glu Ala Asp Leu Ile Val Ile Ala Pro Ala Thr Ala Asp Leu Met Ala
90 95 100
cgt gtg gtg gca ggt ctc ggt gac gat ctg ttg gcg gcg acg ctg ctg 451
Arg Val Val Ala Gly Leu Gly Asp Asp Leu Leu Ala Ala Thr Leu Leu
105 110 115
gtg gca acg tgc ccc gtg gtt att gcg ccg gcc atg cat acg gag atg 499
Val Ala Thr Cys Pro Val Val Ile Ala Pro Ala Met His Thr Glu Met
120 125 130
tgg ttt aat ccg gct acc gta gcc aat gtg gca acg ctg agg cag cgg 547
Trp Phe Asn Pro Ala Thr Val Ala Asn Val Ala Thr Leu Arg Gln Arg
135 140 145
ggg att acc gtg att gag cct gcg cat ggt cga ctc acc ggt aaa gat 595
Gly Ile Thr Val Ile Glu Pro Ala His Gly Arg Leu Thr Gly Lys Asp
150 155 160 165

aca ggc cct ggc cgg ctg ccg gat cca gag cag att gtt gat tta gcc 643
 Thr Gly Pro Gly Arg Leu Pro Asp Pro Glu Gln Ile Val Asp Leu Ala
 170 175 180

aat gcg gtg cac gcc ggg gcg agg ttg cct cag gat ttg gcg ggc aag 691
 Asn Ala Val His Ala Gly Ala Arg Leu Pro Gln Asp Leu Ala Gly Lys
 185 190 195

aaa gtg ctg atc act gct ggt ggc acg cat gag cat att gat cct gtg 739
 Lys Val Leu Ile Thr Ala Gly Gly Thr His Glu His Ile Asp Pro Val
 200 205 210

cgc ttt att ggc aat agt tcc tcg ggc cgt caa ggt ttt gcg ttg ggt 787
 Arg Phe Ile Gly Asn Ser Ser Ser Gly Arg Gln Gly Phe Ala Leu Gly
 215 220 225

gaa atc gca gca cag cga ggt gct cat gtc agc atc gtg gcg gga aat 835
 Glu Ile Ala Ala Gln Arg Gly Ala His Val Ser Ile Val Ala Gly Asn
 230 235 240 245

gct gcg gag ctg ccc act ccg gca ggc gca gag atc gtg ccg gtg gtg 883
 Ala Ala Glu Leu Pro Thr Pro Ala Gly Ala Glu Ile Val Pro Val Val
 250 255 260

tcc aca caa gac atg ttt gat gca gtc cag gaa cga gct ggc caa tct 931
 Ser Thr Gln Asp Met Phe Asp Ala Val Gln Glu Arg Ala Gly Gln Ser
 265 270 275

gat ttc atc gtc atg gcg gca gcg gta gct gat ttc acg ccc gca tcg 979
 Asp Phe Ile Val Met Ala Ala Ala Val Ala Asp Phe Thr Pro Ala Ser
 280 285 290

cag gcg aca tcg aag ttg aag aag ggc tca gat tct gat gaa gac gca
 1027
 Gln Ala Thr Ser Lys Leu Lys Lys Gly Ser Asp Ser Asp Glu Asp Ala
 295 300 305

ttg agc acc atc tcg ttg gtg gaa aac ccg gat att ttg gct acc acg
 1075
 Leu Ser Thr Ile Ser Leu Val Glu Asn Pro Asp Ile Leu Ala Thr Thr
 310 315 320 325

gtg aag cgt cgt gaa gca gga gag ctg gac agt aat cct gtc atc gtg
 1123
 Val Lys Arg Arg Glu Ala Gly Glu Leu Asp Ser Asn Pro Val Ile Val
 330 335 340

ggt ttt gct gcg gaa act gga gac gag cac acc acc gcc ttg gag tat
 1171
 Gly Phe Ala Ala Glu Thr Gly Asp Glu His Thr Thr Ala Leu Glu Tyr
 345 350 355

gcg cgc aag aaa ctg cag aag aag ggc tgc gac ctc ctc atg tgt aat
 1219
 Ala Arg Lys Lys Leu Gln Lys Lys Gly Cys Asp Leu Leu Met Cys Asn
 360 365 370

gag gtg ggc atg ggc aaa gtg ttt ggg caa aag cac aat gag ggc tgg
 1267
 Glu Val Gly Met Gly Lys Val Phe Gly Gln Lys His Asn Glu Gly Trp
 375 380 385

att ttg gat gct cac ggt ggg gta gtc gat gtg gag cac ggc agc aaa
 1315
 Ile Leu Asp Ala His Gly Gly Val Val Asp Val Glu His Gly Ser Lys
 390 395 400 405

atc gag gtt gct gcg caa att tgg gac gcg gca ctg gcg tat cgc gaa
 1363
 Ile Glu Val Ala Ala Gln Ile Trp Asp Ala Ala Leu Ala Tyr Arg Glu
 410 415 420

gtc tagaaaaatc cagctagacc act
 1389
 Val

<210> 626
 <211> 422
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 626
 Val Pro Met Thr His Val Ser Ser Pro Ser Ala Pro Arg Asn Val Val
 1 5 10 15
 Val Gly Val Ala Gly Gly Ile Ala Ala Tyr Lys Ala Cys His Ile Val
 20 25 30
 Arg Ala Phe Lys Glu Ala Gly Asp Asn Val Arg Val Val Pro Thr Glu
 35 40 45
 Ser Ala Leu Lys Phe Val Gly Lys Ala Thr Phe Glu Ala Leu Ser Gly
 50 55 60
 Asn Pro Val Ser Thr Thr Val Phe Asp Ala Val Asp Ser Val Gln His
 65 70 75 80
 Val Lys Val Gly Gln Glu Ala Asp Leu Ile Val Ile Ala Pro Ala Thr
 85 90 95
 Ala Asp Leu Met Ala Arg Val Val Ala Gly Leu Gly Asp Asp Leu Leu
 100 105 110
 Ala Ala Thr Leu Leu Val Ala Thr Cys Pro Val Val Ile Ala Pro Ala
 115 120 125
 Met His Thr Glu Met Trp Phe Asn Pro Ala Thr Val Ala Asn Val Ala
 130 135 140
 Thr Leu Arg Gln Arg Gly Ile Thr Val Ile Glu Pro Ala His Gly Arg
 145 150 155 160
 Leu Thr Gly Lys Asp Thr Gly Pro Gly Arg Leu Pro Asp Pro Glu Gln
 165 170 175
 Ile Val Asp Leu Ala Asn Ala Val His Ala Gly Ala Arg Leu Pro Gln
 180 185 190
 Asp Leu Ala Gly Lys Lys Val Leu Ile Thr Ala Gly Gly Thr His Glu
 195 200 205

His Ile Asp Pro Val Arg Phe Ile Gly Asn Ser Ser Ser Gly Arg Gln
 210 215 220
 Gly Phe Ala Leu Gly Glu Ile Ala Ala Gln Arg Gly Ala His Val Ser
 225 230 235 240
 Ile Val Ala Gly Asn Ala Ala Glu Leu Pro Thr Pro Ala Gly Ala Glu
 245 250 255
 Ile Val Pro Val Val Ser Thr Gln Asp Met Phe Asp Ala Val Gln Glu
 260 265 270
 Arg Ala Gly Gln Ser Asp Phe Ile Val Met Ala Ala Ala Val Ala Asp
 275 280 285
 Phe Thr Pro Ala Ser Gln Ala Thr Ser Lys Leu Lys Lys Gly Ser Asp
 290 295 300
 Ser Asp Glu Asp Ala Leu Ser Thr Ile Ser Leu Val Glu Asn Pro Asp
 305 310 315 320
 Ile Leu Ala Thr Thr Val Lys Arg Arg Glu Ala Gly Glu Leu Asp Ser
 325 330 335
 Asn Pro Val Ile Val Gly Phe Ala Ala Glu Thr Gly Asp Glu His Thr
 340 345 350
 Thr Ala Leu Glu Tyr Ala Arg Lys Lys Leu Gln Lys Lys Gly Cys Asp
 355 360 365
 Leu Leu Met Cys Asn Glu Val Gly Met Gly Lys Val Phe Gly Gln Lys
 370 375 380
 His Asn Glu Gly Trp Ile Leu Asp Ala His Gly Gly Val Val Asp Val
 385 390 395 400
 Glu His Gly Ser Lys Ile Glu Val Ala Ala Gln Ile Trp Asp Ala Ala
 405 410 415
 Leu Ala Tyr Arg Glu Val
 420

<210> 627

<211> 1092

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) .. (1069)

<223> RXA00581

<400> 627

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 cgatcacact agtggagtag ctaaggtgca caatggattc atg gca gag caa aac 115
 Met Ala Glu Gln Asn

1

5

gct gca agc aca act ggt gtg aaa cct tcc cca cgc aca cca gat ttc	163
Ala Ala Ser Thr Thr Gly Val Lys Pro Ser Pro Arg Thr Pro Asp Phe	
10 15 20	
agc ccc tac ctt gat ttc gac cgc gca caa tgg cgc gag ctg aga aac	211
Ser Pro Tyr Leu Asp Phe Asp Arg Ala Gln Trp Arg Glu Leu Arg Asn	
25 30 35	
tca atg cct cag gtg ctg acc caa aaa gaa gtc att gaa ctt cga ggc	259
Ser Met Pro Gln Val Leu Thr Gln Lys Glu Val Ile Glu Leu Arg Gly	
40 45 50	
atc gga gaa aac att gac ctc gct gaa gtg gca gaa gtc tac ctt ccg	307
Ile Gly Glu Asn Ile Asp Leu Ala Glu Val Ala Glu Val Tyr Leu Pro	
55 60 65	
ctg tcc cgt ctg att cac ctc cag gta gcg gcc cga cag caa ctt act	355
Leu Ser Arg Leu Ile His Leu Gln Val Ala Ala Arg Gln Gln Leu Thr	
70 75 80 85	
gca gcc acc gaa acc ttc ctc gga act tcc ccc tct atc tct gtg ccg	403
Ala Ala Thr Glu Thr Phe Leu Gly Thr Ser Pro Ser Ile Ser Val Pro	
90 95 100	
ttt gtc att ggt gtc gcg gga tcc gtc gcc gtc ggt aaa tca acc acc	451
Phe Val Ile Gly Val Ala Gly Ser Val Ala Val Gly Lys Ser Thr Thr	
105 110 115	
gcc cga ctc ctc caa gtt ctg ctt cag cgc tgg aat tcc cac ccc cgc	499
Ala Arg Leu Leu Gln Val Leu Leu Gln Arg Trp Asn Ser His Pro Arg	
120 125 130	
gtg gac ctc gtc acc acc gac gga ttc ctc tat ccc ggc gcg gaa cta	547
Val Asp Leu Val Thr Thr Asp Gly Phe Leu Tyr Pro Gly Ala Glu Leu	
135 140 145	
atc cgc cgc gga tta atg tcc cga aaa gga ttc ccc gaa agc tac gac	595
Ile Arg Arg Gly Leu Met Ser Arg Lys Gly Phe Pro Glu Ser Tyr Asp	
150 155 160 165	
caa cgt gca ctc ctc cgc ttt gtc acc gac gta aaa tcc gga aaa ctc	643
Gln Arg Ala Leu Leu Arg Phe Val Thr Asp Val Lys Ser Gly Lys Leu	
170 175 180	
gaa gtc aac gca cct gtc tac tcc cac acc gcg tac gac cga gtt cca	691
Glu Val Asn Ala Pro Val Tyr Ser His Thr Ala Tyr Asp Arg Val Pro	
185 190 195	
ggc gaa ttc acc aca gtc cgc caa ccc gac att ttg atc gtc gaa ggc	739
Gly Glu Phe Thr Thr Val Arg Gln Pro Asp Ile Leu Ile Val Glu Gly	
200 205 210	
tta aac gtc ctc caa act ggc cca aca ttg atg gtc agt gac ctt ttc	787
Leu Asn Val Leu Gln Thr Gly Pro Thr Leu Met Val Ser Asp Leu Phe	
215 220 225	
gac ttc agc gtc tac gta gat gcc cgc acc gaa gat atc gaa aaa tgg	835
Asp Phe Ser Val Tyr Val Asp Ala Arg Thr Glu Asp Ile Glu Lys Trp	
230 235 240 245	
tac atc gac cgc ttc ctc aaa ctc cgc gac act gca ttc cgt cgc ccc	883

Tyr Ile Asp Arg Phe Leu Lys Leu Arg Asp Thr Ala Phe Arg Arg Pro
 250 255 260
 ggt gcc cac ttc tcc cat tac gcc gac atg gct gat cca gag tcc atc 931
 Gly Ala His Phe Ser His Tyr Ala Asp Met Ala Asp Pro Glu Ser Ile
 265 270 275
 gcc gtc gct cga gaa ctg tgg caa tcg atc aac ctg ccc aac ttg gtg 979
 Ala Val Ala Arg Glu Leu Trp Gln Ser Ile Asn Leu Pro Asn Leu Val
 280 285 290
 gag aat att ctt ccc acc cga gtt cgc gcg tcg ttg gta ctg aaa aaa
 1027
 Glu Asn Ile Leu Pro Thr Arg Val Arg Ala Ser Leu Val Leu Lys Lys
 295 300 305
 ggt agc gat cac ttg gtg gaa cgg gtg agg atg cgc aag atc
 1069
 Gly Ser Asp His Leu Val Glu Arg Val Arg Met Arg Lys Ile
 310 315 320
 taggggttct tgctggtttt gag
 1092

<210> 628

<211> 323

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 628

Met Ala Glu Gln Asn Ala Ala Ser Thr Thr Gly Val Lys Pro Ser Pro
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 20 25 30
 Arg Glu Leu Arg Asn Ser Met Pro Gln Val Leu Thr Gln Lys Glu Val
 35 40 45
 Ile Glu Leu Arg Gly Ile Gly Glu Asn Ile Asp Leu Ala Glu Val Ala
 50 55 60
 Glu Val Tyr Leu Pro Leu Ser Arg Leu Ile His Leu Gln Val Ala Ala
 65 70 75 80
 Arg Gln Gln Leu Thr Ala Ala Thr Glu Thr Phe Leu Gly Thr Ser Pro
 85 90 95
 Ser Ile Ser Val Pro Phe Val Ile Gly Val Ala Gly Ser Val Ala Val
 100 105 110
 Gly Lys Ser Thr Thr Ala Arg Leu Leu Gln Val Leu Leu Gln Arg Trp
 115 120 125
 Asn Ser His Pro Arg Val Asp Leu Val Thr Thr Asp Gly Phe Leu Tyr
 130 135 140
 Pro Gly Ala Glu Leu Ile Arg Arg Gly Leu Met Ser Arg Lys Gly Phe
 145 150 155 160

Pro Glu Ser Tyr Asp Gln Arg Ala Leu Leu Arg Phe Val Thr Asp Val
 165 170 175
 Lys Ser Gly Lys Leu Glu Val Asn Ala Pro Val Tyr Ser His Thr Ala
 180 185 190
 Tyr Asp Arg Val Pro Gly Glu Phe Thr Thr Val Arg Gln Pro Asp Ile
 195 200 205
 Leu Ile Val Glu Gly Leu Asn Val Leu Gln Thr Gly Pro Thr Leu Met
 210 215 220
 Val Ser Asp Leu Phe Asp Phe Ser Val Tyr Val Asp Ala Arg Thr Glu
 225 230 235 240
 Asp Ile Glu Lys Trp Tyr Ile Asp Arg Phe Leu Lys Leu Arg Asp Thr
 245 250 255
 Ala Phe Arg Arg Pro Gly Ala His Phe Ser His Tyr Ala Asp Met Ala
 260 265 270
 Asp Pro Glu Ser Ile Ala Val Ala Arg Glu Leu Trp Gln Ser Ile Asn
 275 280 285
 Leu Pro Asn Leu Val Glu Asn Ile Leu Pro Thr Arg Val Arg Ala Ser
 290 295 300
 Leu Val Leu Lys Lys Gly Ser Asp His Leu Val Glu Arg Val Arg Met
 305 310 315 320
 Arg Lys Ile

<210> 629
 <211> 1023
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1000)
 <223> RXS00838

<400> 629
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 tgcttacaaa tcttatctgt gctcaggcaa gatagcaggt atg aaa att gcg atc 115
 Met Lys Ile Ala Ile
 1 5
 gtt ggc gct ggt gca gtt ggt gga tat ttc gga gcg ttg tta caa gaa 163
 Val Gly Ala Gly Ala Val Gly Gly Tyr Phe Gly Ala Leu Leu Gln Glu
 10 15 20
 tct ggt gca gat atc acg atg gtt gca cgt gga cga aca tta gaa gcc 211
 Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly Arg Thr Leu Glu Ala
 25 30 35
 ttg aag tct aaa gga ctc cac atc aac gat gca aga ggc gaa cgc tac 259
 Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala Arg Gly Glu Arg Tyr

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aat tcg att gaa tct gct gat cta gca gcg aag agt atc ggt gct gat Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys Ser Ile Gly Ala Asp 105 110 115			451
cgt gtg tgg cct ggt gtg gtt cgt ggg ttc ttt gtt cat gag ggg cca Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe Val His Glu Gly Pro 120 125 130			499
gcc tca gtg tca tac aag gga ggc cca ctg tcc tac acg ttt ggt gat Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser Tyr Thr Phe Gly Asp 135 140 145			547
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att gac gga gtt ctg cat ccc gat att ttg gtg gat gtg tgg gag aaa Ile Asp Gly Val Leu His Pro Asp Ile Leu Val Asp Val Trp Glu Lys 170 175 180			643
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gag ctt gag gct cag aca ggt gca att gtg cgg gca gcg cac aaa gtg Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg Ala Ala His Lys Val 265 270 275			931
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 <213> Corynebacterium glutamicum

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 35 40 45
 Arg Gly Glu Arg Tyr Val Pro Ile Pro Ala Val Ala Ser Val Gln Glu
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 Leu Lys Asp Ala Asp Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg
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 Ser Leu Asp Leu Ala Glu Leu Leu Gly Gly Ile Pro Ala Asn Ser Val
 85 90 95
 Val Ala Ile Thr Gln Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys
 100 105 110
 Ser Ile Gly Ala Asp Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe
 115 120 125
 Val His Glu Gly Pro Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser
 130 135 140
 Tyr Thr Phe Gly Asp Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr
 145 150 155 160
 Leu Glu Gln Ala Gly Ile Asp Gly Val Leu His Pro Asp Ile Leu Val
 165 170 175
 Asp Val Trp Glu Lys Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly
 180 185 190
 Ala Phe Val Glu Lys Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala
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 Ser Leu Glu Ala Leu Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala
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 Gly Val Ala Leu Pro Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala
 225 230 235 240
 Asp Arg Met Pro Glu Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala
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Ala	Gly	Val	Ala	Ser	Glu	Leu	Glu	Ala	Gln	Thr	Gly	Ala	Ile	Val	Arg
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Val Thr Asn Val Ser															
1 5															
aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att															163
Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile															
10 15 20															
acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac															211
Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr															
25 30 35															
gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc															259
Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe															
40 45 50															
tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt															307
Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val															
55 60 65															
act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc															355
Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile															
70 75 80 85															
aat gca ggt ctg ttg gac cac gag gaa ggt taaaagacct tataacttca															405
Asn Ala Gly Leu Leu Asp His Glu Glu Gly															
90 95															
cac															408

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Val Thr Ser Lys Tyr Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg	35	40	45
Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe	50	55	60
Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile	65	70	75
Ala Leu Arg Glu Ile Asn Ala Gly Leu Leu Asp His Glu Glu Gly	85	90	95

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 <212> DNA
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 Val Ser Lys Leu Lys 5

ggc tca aga tcg ctt ctc gac gtc ggc tcc ggc gat cac tcc ttc gcc 163
 Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly Asp His Ser Phe Ala 20

gac ctg gcc ggc cgc cag gtc gcg cat gtc gat gtc gtg gat cct ctt 211
 Asp Leu Ala Gly Arg Gln Val Ala His Val Asp Val Val Asp Pro Leu 35

att aat aca acc ttt gaa gaa ttc cag ccg acc caa agc tac gat gcc 259
 Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr Gln Ser Tyr Asp Ala 50

atc acg ttc atc gcg tcc ctc cat cac atg aac gcg gaa gaa gga ctt 307
 Ile Thr Phe Ile Ala Ser Leu His His Met Asn Ala Glu Glu Gly Leu 65

aac aaa gca gtc cga atc ctc aat cct ggc ggc aag ctc ctc atc gta 355
 Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly Lys Leu Leu Ile Val 85

ggc ctc gcc aaa aac aaa acc gcc tcc gac tgg atc atc tcc gga cta 403
 Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp Ile Ile Ser Gly Leu 100

caa gct ttt ctc tcc cga cca atc agc ctc atc aat agg gaa caa caa 451
 Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile Asn Arg Glu Gln Gln

105										110					115					
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Ile	Tyr	Pro	Phe	Pro	Thr	Lys	Glu	Pro	Ser	Glu	Ser	Leu	His	Glu	Ile					
		120					125					130								
cga	caa	ctc	acc	aag	cag	ctc	ctc	cct	cac	cgc	cgt	att	cgc	cgt	gga	547				
Arg	Gln	Leu	Thr	Lys	Gln	Leu	Leu	Pro	His	Arg	Arg	Ile	Arg	Arg	Gly					
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atc	cac	ttc	cga	tac	ctc	ctc	gag	tgg	aca	aag	cct	taa	acag	ccc		593				
Ile	His	Phe	Arg	Tyr	Leu	Leu	Glu	Trp	Thr	Lys	Pro									
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Val	Val	Asp	Pro	Leu	Ile	Asn	Thr	Thr	Phe	Glu	Glu	Phe	Gln	Pro	Thr
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Gln	Ser	Tyr	Asp	Ala	Ile	Thr	Phe	Ile	Ala	Ser	Leu	His	His	Met	Asn
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Ala	Glu	Glu	Gly	Leu	Asn	Lys	Ala	Val	Arg	Ile	Leu	Asn	Pro	Gly	Gly
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Lys	Leu	Leu	Ile	Val	Gly	Leu	Ala	Lys	Asn	Lys	Thr	Ala	Ser	Asp	Trp
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Ile	Ile	Ser	Gly	Leu	Gln	Ala	Phe	Leu	Ser	Arg	Pro	Ile	Ser	Leu	Ile
			100					105					110		

Asn	Arg	Glu	Gln	Gln	Ile	Tyr	Pro	Phe	Pro	Thr	Lys	Glu	Pro	Ser	Glu
		115					120					125			

Ser	Leu	His	Glu	Ile	Arg	Gln	Leu	Thr	Lys	Gln	Leu	Leu	Pro	His	Arg
	130					135					140				

Arg	Ile	Arg	Arg	Gly	Ile	His	Phe	Arg	Tyr	Leu	Leu	Glu	Trp	Thr	Lys
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Pro

<210> 635

<211> 606

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(583)

<223> FRXA02903

<400> 635

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                                         Val Ser Lys Leu Lys
                                         1 5
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Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly Asp His Ser Phe Ala
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gac ctg gcc ggc cgc cag gtc gcg cat gtc gat gtc gtg gat cct ctt 211
Asp Leu Ala Gly Arg Gln Val Ala His Val Asp Val Val Asp Pro Leu
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Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr Gln Ser Tyr Asp Ala
                        40 45 50
atc acg ttc atc gcg tcc ctc cat cac atg aac gcg gaa gaa gga ctt 307
Ile Thr Phe Ile Ala Ser Leu His His Met Asn Ala Glu Glu Gly Leu
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Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly Lys Leu Leu Ile Val
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Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile Asn Arg Glu Gln Gln
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Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu Ser Leu His Glu Ile
                        120 125 130
cga caa ctc acc aag cag ctc ctc cct cac cgc cgt att cgc cgt gga 547
Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg Arg Ile Arg Arg Gly
                        135 140 145
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<211> 161

<212> PRT

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<400> 636

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 35 40 45
 Gln Ser Tyr Asp Ala Ile Thr Phe Ile Ala Ser Leu His His Met Asn
 50 55 60
 Ala Glu Glu Gly Leu Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly
 65 70 75 80
 Lys Leu Leu Ile Val Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp
 85 90 95
 Ile Ile Ser Gly Leu Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile
 100 105 110
 Asn Arg Glu Gln Gln Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu
 115 120 125
 Ser Leu His Glu Ile Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg
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 145 150 155 160
 Pro

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<211> 783

<212> DNA

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<223> RXA00166

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 Val Glu Leu Ala Arg 5
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 Gly Phe Gly Arg Val Leu Asp Val Gly Ala Gly Thr Gly Lys Leu Thr 20
 10 15
 agt gag cta aca gct gat cag gtc cta gcc ctt gat cca agc atg gac 211
 Ser Glu Leu Thr Ala Asp Gln Val Leu Ala Leu Asp Pro Ser Met Asp 35
 25 30
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Met Leu Arg Val Phe Arg Ser Ala Leu Pro Ala Val Pro Cys Trp Gln
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gcg aca gca gaa cac aca gga ata cgt gac aac gcg gtt gat ctg att 307
Ala Thr Ala Glu His Thr Gly Ile Arg Asp Asn Ala Val Asp Leu Ile
55 60 65

acg tgc gca caa acg tgg cat tgg gtt gac gtg acg gct gcc tca gcg 355
Thr Cys Ala Gln Thr Trp His Trp Val Asp Val Thr Ala Ala Ser Ala
70 75 80 85

gaa ttt gat cgg gtg att gca cct gag ggt gca gtc ctg ctc gtg tgg 403
Glu Phe Asp Arg Val Ile Ala Pro Glu Gly Ala Val Leu Leu Val Trp
90 95 100

aat aac ctg gac acc tcc atc gcg tgg gta cac cga ctc agt cgc att 451
Asn Asn Leu Asp Thr Ser Ile Ala Trp Val His Arg Leu Ser Arg Ile
105 110 115

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Met His Ala Gly Asp Val Leu Lys Pro Gly Phe Thr Pro Glu Thr Ala
120 125 130

gct ccc tgg ata att gat cga gaa att cgc acc acg tgg aat cag cac 547
Ala Pro Trp Ile Ile Asp Arg Glu Ile Arg Thr Thr Trp Asn Gln His
135 140 145

ctc acc cct gaa gaa atc atc cag ctc gct cac acg agg tcc tac tgg 595
Leu Thr Pro Glu Glu Ile Ile Gln Leu Ala His Thr Arg Ser Tyr Trp
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tta aac gcg tca gag aaa atc aaa gag cgt gtt gat cag aac ctt cag 643
Leu Asn Ala Ser Glu Lys Ile Lys Glu Arg Val Asp Gln Asn Leu Gln
170 175 180

tgg tat ctc tac gag cat ttg ggt ttc agt ccc gac aat cca gtg gaa 691
Trp Tyr Leu Tyr Glu His Leu Gly Phe Ser Pro Asp Asn Pro Val Glu
185 190 195

ctt ccc tat cgc tgt gat gca ttt tta ctt tca cgt tcc ggt acc ctg 739
Leu Pro Tyr Arg Cys Asp Ala Phe Leu Leu Ser Arg Ser Gly Thr Leu
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Ala Gly Arg Ser Ser Asn Leu
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<210> 638

<211> 220

<212> PRT

<213> Corynebacterium glutamicum

<400> 638

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20 25 30

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Ala	Val	Asp	Leu	Ile	Thr	Cys	Ala	Gln	Thr	Trp	His	Trp	Val	Asp	Val				
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Val	Leu	Leu	Val	Trp	Asn	Asn	Leu	Asp	Thr	Ser	Ile	Ala	Trp	Val	His				
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Arg	Leu	Ser	Arg	Ile	Met	His	Ala	Gly	Asp	Val	Leu	Lys	Pro	Gly	Phe				
		115					120					125							
Thr	Pro	Glu	Thr	Ala	Ala	Pro	Trp	Ile	Ile	Asp	Arg	Glu	Ile	Arg	Thr				
	130					135					140								
Thr	Trp	Asn	Gln	His	Leu	Thr	Pro	Glu	Glu	Ile	Ile	Gln	Leu	Ala	His				
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Asp	Gln	Asn	Leu	Gln	Trp	Tyr	Leu	Tyr	Glu	His	Leu	Gly	Phe	Ser	Pro				
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Leu Arg Glu Leu Asp His Arg Asn Ile Trp His Pro Tyr Ala Ala Pro																			
				10					15					20			</		

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Ala Ile His Gly His Gly His Pro Arg Leu Lys Ala Ala Ala Gln Lys	
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caa atc gac acc atg agt cac gtc atg ttt ggc gga cta acc cac gag	355
Gln Ile Asp Thr Met Ser His Val Met Phe Gly Gly Leu Thr His Glu	
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Pro Ala Ile Lys Leu Thr His Lys Leu Leu Asn Leu Thr Gly Asn Ser	
90 95 100	
ttt gac cac gtc ttt tat tcc gat tcg ggc tcg gtc tca gtg gag gtc	451
Phe Asp His Val Phe Tyr Ser Asp Ser Gly Ser Val Ser Val Glu Val	
105 110 115	
gcc atc aaa atg gca ctg cag gcc tcc aaa gga caa ggc cac ccg gaa	499
Ala Ile Lys Met Ala Leu Gln Ala Ser Lys Gly Gln Gly His Pro Glu	
120 125 130	
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Arg Thr Lys Leu Leu Thr Trp Arg Ser Gly Tyr His Gly Asp Thr Phe	
135 140 145	
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Thr Ala Met Ser Val Cys Asp Pro Glu Asn Gly Met His Ser Leu Trp	
150 155 160 165	
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Lys Gly Thr Leu Pro Glu Gln Ile Phe Ala Pro Ala Pro Pro Val Arg	
170 175 180	
ggg tca tcg ccg cag gcg att tcc gag tac ctg cgc agc atg gaa ttg	691
Gly Ser Ser Pro Gln Ala Ile Ser Glu Tyr Leu Arg Ser Met Glu Leu	
185 190 195	
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Leu Ile Asp Glu Ala Val Ser Ala Ile Ile Ile Glu Pro Ile Val Gln	
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Gly Ala Gly Gly Met Arg Phe His Asp Val Ala Leu Ile Glu Gly Val	
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Gly Leu Gln Pro Asp Ile Met Cys Val Gly Lys Ala Leu Thr Gly Gly	
265 270 275	
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Phe Met Ser Phe Ala Ala Thr Leu Cys Thr Asp Lys Val Ala Gln Leu
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 Ile Ser Thr Pro Asn Gly Gly Gly Ala Leu Met His Gly Pro Thr Phe
 295 300 305
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 1075
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 310 315 320 325
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 ctt atc gca ggc ctt tcc cca ctt caa cac ctt cca ggg gtt gcc gat
 1171
 Leu Ile Ala Gly Leu Ser Pro Leu Gln His Leu Pro Gly Val Ala Asp
 345 350 355
 gtc cgg gtt ctc ggc gcg att ggt gtc atc gaa atg gaa caa aat gtc
 1219
 Val Arg Val Leu Gly Ala Ile Gly Val Ile Glu Met Glu Gln Asn Val
 360 365 370
 aat gtc gaa gaa gct act cag gct gca tta gat cac ggt gtg tgg atc
 1267
 Asn Val Glu Glu Ala Thr Gln Ala Ala Leu Asp His Gly Val Trp Ile
 375 380 385
 cgc ccc ttt gga cgc ttg ctc tat gtc atg cct cca tat atc acc acg
 1315
 Arg Pro Phe Gly Arg Leu Leu Tyr Val Met Pro Pro Tyr Ile Thr Thr
 390 395 400 405
 tca gag cag tgc gca cag atc tgc act gcg ctt cat gct gca gtt aaa
 1363
 Ser Glu Gln Cys Ala Gln Ile Cys Thr Ala Leu His Ala Ala Val Lys
 410 415 420
 ggg aaa taaaccatgc catttttatt tgt
 1392
 Gly Lys

<210> 640

<211> 423

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 640

Met Glu Asn Pro Ser Leu Arg Glu Leu Asp His Arg Asn Ile Trp His
 1 5 10 15

Pro Tyr Ala Ala Pro Gly Val Arg Asn Arg Leu Val Thr Lys Thr Asp
 20 25 30

Gly Val Phe Leu Thr Leu Glu Asp Gly Ser Thr Val Ile Asp Ala Met
 35 40 45
 Ser Ser Trp Trp Ser Ala Ile His Gly His Gly His Pro Arg Leu Lys
 50 55 60
 Ala Ala Ala Gln Lys Gln Ile Asp Thr Met Ser His Val Met Phe Gly
 65 70 75 80
 Gly Leu Thr His Glu Pro Ala Ile Lys Leu Thr His Lys Leu Leu Asn
 85 90 95
 Leu Thr Gly Asn Ser Phe Asp His Val Phe Tyr Ser Asp Ser Gly Ser
 100 105 110
 Val Ser Val Glu Val Ala Ile Lys Met Ala Leu Gln Ala Ser Lys Gly
 115 120 125
 Gln Gly His Pro Glu Arg Thr Lys Leu Leu Thr Trp Arg Ser Gly Tyr
 130 135 140
 His Gly Asp Thr Phe Thr Ala Met Ser Val Cys Asp Pro Glu Asn Gly
 145 150 155 160
 Met His Ser Leu Trp Lys Gly Thr Leu Pro Glu Gln Ile Phe Ala Pro
 165 170 175
 Ala Pro Pro Val Arg Gly Ser Ser Pro Gln Ala Ile Ser Glu Tyr Leu
 180 185 190
 Arg Ser Met Glu Leu Leu Ile Asp Glu Ala Val Ser Ala Ile Ile Ile
 195 200 205
 Glu Pro Ile Val Gln Gly Ala Gly Gly Met Arg Phe His Asp Val Ala
 210 215 220
 Leu Ile Glu Gly Val Ala Thr Leu Cys Lys Lys His Asp Arg Phe Leu
 225 230 235 240
 Ile Val Asp Glu Ile Ala Thr Gly Phe Gly Arg Thr Gly Glu Leu Phe
 245 250 255
 Ala Thr Leu Ser Asn Gly Leu Gln Pro Asp Ile Met Cys Val Gly Lys
 260 265 270
 Ala Leu Thr Gly Gly Phe Met Ser Phe Ala Ala Thr Leu Cys Thr Asp
 275 280 285
 Lys Val Ala Gln Leu Ile Ser Thr Pro Asn Gly Gly Gly Ala Leu Met
 290 295 300
 His Gly Pro Thr Phe Met Ala Asn Pro Leu Ala Cys Ala Val Ser His
 305 310 315 320
 Ala Ser Leu Glu Ile Ile Glu Thr Gly Met Trp Gln Lys Gln Val Lys
 325 330 335
 Arg Ile Glu Ala Glu Leu Ile Ala Gly Leu Ser Pro Leu Gln His Leu
 340 345 350
 Pro Gly Val Ala Asp Val Arg Val Leu Gly Ala Ile Gly Val Ile Glu

355		360		365
Met Glu Gln Asn Val Asn Val Glu Glu Ala Thr Gln Ala Ala Leu Asp				
370		375		380
His Gly Val Trp Ile Arg Pro Phe Gly Arg Leu Leu Tyr Val Met Pro				
385		390		400
Pro Tyr Ile Thr Thr Ser Glu Gln Cys Ala Gln Ile Cys Thr Ala Leu				
	405		410	415
His Ala Ala Val Lys Gly Lys				
420				

<210> 641
 <211> 795
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(772)
 <223> RXA00632

<400> 641
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 ctgcactgcg cttcatgctg cagttaaagg gaaataaacc atg cca ttt tta ttt 115
 Met Pro Phe Leu Phe
 1 5
 gtc agc ggt acc gga act ggg gtt ggg aaa acc ttc tcc aca gcc gtt 163
 Val Ser Gly Thr Gly Thr Gly Val Gly Lys Thr Phe Ser Thr Ala Val
 10 15 20
 ttg gtt cga tac tta gcc gat caa gga cac gat gtt ctg ccc gta aag 211
 Leu Val Arg Tyr Leu Ala Asp Gln Gly His Asp Val Leu Pro Val Lys
 25 30 35
 cta gtc caa acc ggt gaa ctt cca ggc gag gga gac atc ttt aac att 259
 Leu Val Gln Thr Gly Glu Leu Pro Gly Glu Gly Asp Ile Phe Asn Ile
 40 45 50
 gaa cgc ttg act gga att gct gga gag gaa ttt gct cgt ttc aaa gac 307
 Glu Arg Leu Thr Gly Ile Ala Gly Glu Glu Phe Ala Arg Phe Lys Asp
 55 60 65
 cct ctt gcg cca aat ctg gca gcc cga cga gag ggg gtc gag cca ata 355
 Pro Leu Ala Pro Asn Leu Ala Ala Arg Arg Glu Gly Val Glu Pro Ile
 70 75 80 85
 cag ttt gat cag att atc tcg tgg ctt cgt ggt ttt gac gac cca gat 403
 Gln Phe Asp Gln Ile Ile Ser Trp Leu Arg Gly Phe Asp Asp Pro Asp
 90 95 100
 cgc atc att gtg gtg gag ggc gct ggt ggc ctg ctg gtc aga tta ggg 451
 Arg Ile Ile Val Val Glu Gly Ala Gly Gly Leu Leu Val Arg Leu Gly
 105 110 115
 gaa gat ttc acc ctg gca gat gtt gcc tcc gct ttg aat gca ccc tta 499

Glu Asp Phe Thr Leu Ala Asp Val Ala Ser Ala Leu Asn Ala Pro Leu
 120 125 130
 gtg att gtg aca agc acc gga ttg gga agc ctc aac gct gct gaa tta 547
 Val Ile Val Thr Ser Thr Gly Leu Gly Ser Leu Asn Ala Ala Glu Leu
 135 140 145
 agc gtt gag gca gca aac cgc cga gga ctc aca gtg ttg gga gtc ctc 595
 Ser Val Glu Ala Ala Asn Arg Arg Gly Leu Thr Val Leu Gly Val Leu
 150 155 160 165
 ggc ggt tcg atc cct caa aat cct gat cta gct acg atg ctt aat ctc 643
 Gly Gly Ser Ile Pro Gln Asn Pro Asp Leu Ala Thr Met Leu Asn Leu
 170 175 180
 gaa gaa ttt gag aga gtc acc ggc gtg ccc ttt tgg gga gct ttg ccg 691
 Glu Glu Phe Glu Arg Val Thr Gly Val Pro Phe Trp Gly Ala Leu Pro
 185 190 195
 gaa ggg ttg tca cgg gtg gag ggg ttc gtc gaa aag caa tct ttt ccg 739
 Glu Gly Leu Ser Arg Val Glu Gly Phe Val Glu Lys Gln Ser Phe Pro
 200 205 210
 gcc ctt gat gcc ttt aag aaa ccg ccg gca agg tgatcgtgaa caccgtgcct 792
 Ala Leu Asp Ala Phe Lys Lys Pro Pro Ala Arg
 215 220
 tcg 795

<210> 642

<211> 224

<212> PRT

<213> Corynebacterium glutamicum

<400> 642

Met Pro Phe Leu Phe Val Ser Gly Thr Gly Thr Gly Val Gly Lys Thr
 1 5 10 15
 Phe Ser Thr Ala Val Leu Val Arg Tyr Leu Ala Asp Gln Gly His Asp
 20 25 30
 Val Leu Pro Val Lys Leu Val Gln Thr Gly Glu Leu Pro Gly Glu Gly
 35 40 45
 Asp Ile Phe Asn Ile Glu Arg Leu Thr Gly Ile Ala Gly Glu Glu Phe
 50 55 60
 Ala Arg Phe Lys Asp Pro Leu Ala Pro Asn Leu Ala Ala Arg Arg Glu
 65 70 75 80
 Gly Val Glu Pro Ile Gln Phe Asp Gln Ile Ile Ser Trp Leu Arg Gly
 85 90 95
 Phe Asp Asp Pro Asp Arg Ile Ile Val Val Glu Gly Ala Gly Gly Leu
 100 105 110
 Leu Val Arg Leu Gly Glu Asp Phe Thr Leu Ala Asp Val Ala Ser Ala
 115 120 125
 Leu Asn Ala Pro Leu Val Ile Val Thr Ser Thr Gly Leu Gly Ser Leu

130	135	140
Asn Ala Ala Glu Leu Ser Val Glu Ala Ala Asn Arg Arg Gly Leu Thr		
145	150	155
Val Leu Gly Val Leu Gly Gly Ser Ile Pro Gln Asn Pro Asp Leu Ala		
	165	170
Thr Met Leu Asn Leu Glu Glu Phe Glu Arg Val Thr Gly Val Pro Phe		
	180	185
Trp Gly Ala Leu Pro Glu Gly Leu Ser Arg Val Glu Gly Phe Val Glu		
	195	200
Lys Gln Ser Phe Pro Ala Leu Asp Ala Phe Lys Lys Pro Pro Ala Arg		
	210	220

<210> 643
 <211> 1125
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1102)
 <223> RXA00295

<400> 643
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 ttaagcgcgc agttattgac aaccagcctc taggagatcc atg acc atc ccc ggc 115
 Met Thr Ile Pro Gly
 1 5
 acc atc ctt gac acc gcc cgc acc caa gtt ctg gaa cag gga att ggc 163
 Thr Ile Leu Asp Thr Ala Arg Thr Gln Val Leu Glu Gln Gly Ile Gly
 10 15 20
 ctt aat cag cag cag ttg atg gag gtt ctc acc ttg cct gaa gag caa 211
 Leu Asn Gln Gln Gln Leu Met Glu Val Leu Thr Leu Pro Glu Glu Gln
 25 30 35
 atc cca gac ttg atg gaa tta gcc cac cag gtt cgg ttg aag tgg tgt 259
 Ile Pro Asp Leu Met Glu Leu Ala His Gln Val Arg Leu Lys Trp Cys
 40 45 50
 ggg gaa gaa atc gag gtc gag ggc att att tcc ctc aaa act ggc ggt 307
 Gly Glu Glu Ile Glu Val Glu Gly Ile Ile Ser Leu Lys Thr Gly Gly
 55 60 65
 tgc cct gaa gat tgt cat ttc tgc tca cag tct ggg ttg ttt gaa tcg 355
 Cys Pro Glu Asp Cys His Phe Cys Ser Gln Ser Gly Leu Phe Glu Ser
 70 75 80 85
 ccg gtg cgt tcg gtg tgg ctg gat att ccg aat ctg gtt gaa gcc gct 403
 Pro Val Arg Ser Val Trp Leu Asp Ile Pro Asn Leu Val Glu Ala Ala
 90 95 100

aaa cag acc gca aaa act ggc gct acc gaa ttc tgt atc gtc gcc gca 451
 Lys Gln Thr Ala Lys Thr Gly Ala Thr Glu Phe Cys Ile Val Ala Ala
 105 110 115

gtc aag ggg cct gat gag agg ctc atg acc cag ctg gag gaa gca gtc 499
 Val Lys Gly Pro Asp Glu Arg Leu Met Thr Gln Leu Glu Glu Ala Val
 120 125 130

ctc gcg att cac tct gaa gtt gaa att gaa gtc gca gca tcg atc gga 547
 Leu Ala Ile His Ser Glu Val Glu Ile Glu Val Ala Ala Ser Ile Gly
 135 140 145

acg tta aat aag gaa cag gtg gat cgc ctc gct gct gcc ggc gtg cac 595
 Thr Leu Asn Lys Glu Gln Val Asp Arg Leu Ala Ala Gly Val His
 150 155 160 165

cgc tac aac cat aat ttg gaa act gcg cgt tcc tat ttc cct gaa gtt 643
 Arg Tyr Asn His Asn Leu Glu Thr Ala Arg Ser Tyr Phe Pro Glu Val
 170 175 180

gtc acc act cat aca tgg gaa gag cgc cgc gaa act ttg cgc ctg gtg 691
 Val Thr Thr His Thr Trp Glu Glu Arg Arg Glu Thr Leu Arg Leu Val
 185 190 195

gca gaa gct gga atg gaa gtc tgt tcc ggc gga atc tta gga atg ggc 739
 Ala Glu Ala Gly Met Glu Val Cys Ser Gly Gly Ile Leu Gly Met Gly
 200 205 210

gaa act tta gag cag cgc gcc gag ttt gcc gtg cag ctg gcg gag ctt 787
 Glu Thr Leu Glu Gln Arg Ala Glu Phe Ala Val Gln Leu Ala Glu Leu
 215 220 225

gat ccg cac gaa gtc ccc atg aac ttc ctt gat cct cgc ccg ggc acc 835
 Asp Pro His Glu Val Pro Met Asn Phe Leu Asp Pro Arg Pro Gly Thr
 230 235 240 245

cca ttt gcc gat agg gaa ttg atg gac agc cgt gac gct ctg cgc tct 883
 Pro Phe Ala Asp Arg Glu Leu Met Asp Ser Arg Asp Ala Leu Arg Ser
 250 255 260

att ggt gcg ttc cgc ctt gcg atg cct cac acc atg ctt cgt ttt gct 931
 Ile Gly Ala Phe Arg Leu Ala Met Pro His Thr Met Leu Arg Phe Ala
 265 270 275

ggc ggt cgc gag ctg act ttg ggc gac aag ggt tcc gag caa gcc ctc 979
 Gly Gly Arg Glu Leu Thr Leu Gly Asp Lys Gly Ser Glu Gln Ala Leu
 280 285 290

ctg gga ggc atc aat gcg atg atc gtc gga aac tac ctg act acg ctc
 1027
 Leu Gly Gly Ile Asn Ala Met Ile Val Gly Asn Tyr Leu Thr Thr Leu
 295 300 305

ggc cgc cca atg gaa gat gac ctc gac atg atg gat cgt ctc cag ctg
 1075
 Gly Arg Pro Met Glu Asp Asp Leu Asp Met Met Asp Arg Leu Gln Leu
 310 315 320 325

ccc atc aaa gtc ctt aat aag gtc atc taagaagcac gcgcatgaac
 1122

Pro Ile Lys Val Leu Asn Lys Val Ile
330

gac
1125

<210> 644
<211> 334
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 644
Met Thr Ile Pro Gly Thr Ile Leu Asp Thr Ala Arg Thr Gln Val Leu
1 5 10 15
Glu Gln Gly Ile Gly Leu Asn Gln Gln Gln Leu Met Glu Val Leu Thr
20 25 30
Leu Pro Glu Glu Gln Ile Pro Asp Leu Met Glu Leu Ala His Gln Val
35 40 45
Arg Leu Lys Trp Cys Gly Glu Glu Ile Glu Val Glu Gly Ile Ile Ser
50 55 60
Leu Lys Thr Gly Gly Cys Pro Glu Asp Cys His Phe Cys Ser Gln Ser
65 70 75 80
Gly Leu Phe Glu Ser Pro Val Arg Ser Val Trp Leu Asp Ile Pro Asn
85 90 95
Leu Val Glu Ala Ala Lys Gln Thr Ala Lys Thr Gly Ala Thr Glu Phe
100 105 110
Cys Ile Val Ala Ala Val Lys Gly Pro Asp Glu Arg Leu Met Thr Gln
115 120 125
Leu Glu Glu Ala Val Leu Ala Ile His Ser Glu Val Glu Ile Glu Val
130 135 140
Ala Ala Ser Ile Gly Thr Leu Asn Lys Glu Gln Val Asp Arg Leu Ala
145 150 155 160
Ala Ala Gly Val His Arg Tyr Asn His Asn Leu Glu Thr Ala Arg Ser
165 170 175
Tyr Phe Pro Glu Val Val Thr Thr His Thr Trp Glu Glu Arg Arg Glu
180 185 190
Thr Leu Arg Leu Val Ala Glu Ala Gly Met Glu Val Cys Ser Gly Gly
195 200 205
Ile Leu Gly Met Gly Glu Thr Leu Glu Gln Arg Ala Glu Phe Ala Val
210 215 220
Gln Leu Ala Glu Leu Asp Pro His Glu Val Pro Met Asn Phe Leu Asp
225 230 235 240
Pro Arg Pro Gly Thr Pro Phe Ala Asp Arg Glu Leu Met Asp Ser Arg
245 250 255

[illegible]

gac aag cct gcc gcg gtt gcc act atg atg tgg gcg aac aat gag acc 499
 Asp Lys Pro Ala Ala Val Ala Thr Met Met Trp Ala Asn Asn Glu Thr
 120 125 130

ggc gcg att cag ccg gtt tct gag ttc atc gcc gcc gcg cag gcg tcc 547
 Gly Ala Ile Gln Pro Val Ser Glu Phe Ile Ala Ala Ala Gln Ala Ser
 135 140 145

ggc acg cca aca cac atc gat gcg gtt cag gtc gtt ggc cat ctg ccg 595
 Gly Thr Pro Thr His Ile Asp Ala Val Gln Val Val Gly His Leu Pro
 150 155 160 165

gtc aat ttt gat gag ctc ggc gcc acc act ttg gct gcc tcc gcg cac 643
 Val Asn Phe Asp Glu Leu Gly Ala Thr Thr Leu Ala Ala Ser Ala His
 170 175 180

aaa ttc ggt gga cca cgt ggc gtc ggc ctg ctg ttg gtg agg cgc tca 691
 Lys Phe Gly Gly Pro Arg Gly Val Gly Leu Leu Leu Val Arg Arg Ser
 185 190 195

cca gca cct tca gcc gta ttg cac gga ggt ggt cag gag cgc ggc atc 739
 Pro Ala Pro Ser Ala Val Leu His Gly Gly Gly Gln Glu Arg Gly Ile
 200 205 210

cgt cca ggc acc ctt gat gtc gcc ggc gca gct gcc acc gca gcc gca 787
 Arg Pro Gly Thr Leu Asp Val Ala Gly Ala Ala Thr Ala Ala Ala
 215 220 225

tta cgc gaa gca gtg gcc gag ctt gac ggc gaa gcc acc cgc ctg cgc 835
 Leu Arg Glu Ala Val Ala Glu Leu Asp Gly Glu Ala Thr Arg Leu Arg
 230 235 240 245

gga ctt aaa aag atg ctt ctc gac gcc atc ctc cac acc atc ccc aac 883
 Gly Leu Lys Lys Met Leu Leu Asp Ala Ile Leu His Thr Ile Pro Asn
 250 255 260

gta ctg gtc cac acc acc gaa cca tcc ctg cca gga cac ctg cat ctc 931
 Val Leu Val His Thr Thr Glu Pro Ser Leu Pro Gly His Leu His Leu
 265 270 275

tcc ttc cca gga gca gaa ggc gat agt ttg atc atg ctg ctc gac tcc 979
 Ser Phe Pro Gly Ala Glu Gly Asp Ser Leu Ile Met Leu Leu Asp Ser
 280 285 290

ttg cgg atc gaa gcc tcc aca ggt tgc gcc tgc tcc aac ggt gta aac
 1027
 Leu Arg Ile Glu Ala Ser Thr Gly Ser Ala Cys Ser Asn Gly Val Asn
 295 300 305

cgt gcc agc cac gtc ctt ttg gcc atg gga att tcc gaa acc gac gcc
 1075
 Arg Ala Ser His Val Leu Leu Ala Met Gly Ile Ser Glu Thr Asp Ala
 310 315 320 325

cgt ggt gcc atc cga ttc acc ctc gga aga acc acc act gaa gaa tcc
 1123
 Arg Gly Ala Ile Arg Phe Thr Leu Gly Arg Thr Thr Thr Glu Glu Ser
 330 335 340

atc aag gca gtg atc gcc gtg atc gaa gac gta gtg acc agg gct cgt
 1171

Ile Lys Ala Val Ile Ala Val Ile Glu Asp Val Val Thr Arg Ala Arg
 345 350 355

act gcg gga atg gct ttt tagcgaccgt aaatcgcata gtg
 1212
 Thr Ala Gly Met Ala Phe
 360

<210> 646

<211> 363

<212> PRT

<213> Corynebacterium glutamicum

<400> 646

Met Arg Glu Val Ala Ala Ala Ala Trp Met Glu Asn Ala Gln Ala Leu
 1 5 10 15

Asn Pro Ala Ser Gln Tyr Gly Ser Gly Arg Lys Ala Arg Ser Val Ala
 20 25 30

Asp Ser Ala Arg Glu Glu Ile Ala Ser Leu Leu Gly Cys Glu Pro Ile
 35 40 45

Glu Val Val Phe Thr Ala Ser Gly Thr Glu Ala Asp Asn Leu Ala Val
 50 55 60

Gln Gly Leu Phe His Ala Ser Pro Leu Asn Arg Ile Ile Ser Thr Pro
 65 70 75 80

Ile Glu His Pro Gly Ile Leu Glu Thr Val Lys Ala Leu Glu Leu Gly
 85 90 95

Gly Ala Glu Ala Glu Leu Met Pro Ile Gly Pro Asp Gly Arg Val Ser
 100 105 110

Ser Phe Glu Ala Leu Asp Lys Pro Ala Ala Val Ala Thr Met Met Trp
 115 120 125

Ala Asn Asn Glu Thr Gly Ala Ile Gln Pro Val Ser Glu Phe Ile Ala
 130 135 140

Ala Ala Gln Ala Ser Gly Thr Pro Thr His Ile Asp Ala Val Gln Val
 145 150 155 160

Val Gly His Leu Pro Val Asn Phe Asp Glu Leu Gly Ala Thr Thr Leu
 165 170 175

Ala Ala Ser Ala His Lys Phe Gly Gly Pro Arg Gly Val Gly Leu Leu
 180 185 190

Leu Val Arg Arg Ser Pro Ala Pro Ser Ala Val Leu His Gly Gly Gly
 195 200 205

Gln Glu Arg Gly Ile Arg Pro Gly Thr Leu Asp Val Ala Gly Ala Ala
 210 215 220

Ala Thr Ala Ala Ala Leu Arg Glu Ala Val Ala Glu Leu Asp Gly Glu
 225 230 235 240

Ala Thr Arg Leu Arg Gly Leu Lys Lys Met Leu Leu Asp Ala Ile Leu

245	250	255
His Thr Ile Pro Asn Val Leu Val	His Thr Thr Glu Pro Ser Leu Pro	
260	265	270
Gly His Leu His Leu Ser Phe Pro Gly Ala Glu Gly Asp Ser Leu Ile		
275	280	285
Met Leu Leu Asp Ser Leu Arg Ile Glu Ala Ser Thr Gly Ser Ala Cys		
290	295	300
Ser Asn Gly Val Asn Arg Ala Ser His Val Leu Leu Ala Met Gly Ile		
305	310	315
Ser Glu Thr Asp Ala Arg Gly Ala Ile Arg Phe Thr Leu Gly Arg Thr		
325	330	335
Thr Thr Glu Glu Ser Ile Lys Ala Val Ile Ala Val Ile Glu Asp Val		
340	345	350
Val Thr Arg Ala Arg Thr Ala Gly Met Ala Phe		
355	360	

<210> 647

<211> 1197

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1174)

<223> RXN00262

<400> 647

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attctgtgca tgcacttgac ctaggactcg atattttcta	atg ctc tac ctt gat	115
	Met Leu Tyr Leu Asp	
	1 5	

aat gca gcc acc acc agt gtg cgc aat gaa gca ctt gag gcc atg tgg	163
Asn Ala Ala Thr Thr Ser Val Arg Asn Glu Ala Leu Glu Ala Met Trp	
10 15 20	

cct tat ctc acc gga gcg ttt ggc aat ccg tca agt ccc cat gag gtg	211
Pro Tyr Leu Thr Gly Ala Phe Gly Asn Pro Ser Ser Pro His Glu Val	
25 30 35	

gga aga ctc gcc tct gcg ggg ctg gag gat gct cga act cgg gtg gcc	259
Gly Arg Leu Ala Ser Ala Gly Leu Glu Asp Ala Arg Thr Arg Val Ala	
40 45 50	

cgc att atc gga gga cgc ccc aca cag gtg acg ttt acg tcg ggt gga	307
Arg Ile Ile Gly Gly Arg Pro Thr Gln Val Thr Phe Thr Ser Gly Gly	
55 60 65	

tca gaa gcc aac aac ctc gct atc aaa gga gcg tgc tta gct aat cct	355
Ser Glu Ala Asn Asn Leu Ala Ile Lys Gly Ala Cys Leu Ala Asn Pro	
70 75 80 85	

cgt ggc cgg cac ctc atc acc acc ccg atc gag cat gac agt gtc cta	403
Arg Gly Arg His Leu Ile Thr Thr Pro Ile Glu His Asp Ser Val Leu	
90 95 100	
gaa act gct gct tat ctt gaa agg ttt cat gat ttc gag atc acc tac	451
Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp Phe Glu Ile Thr Tyr	
105 110 115	
cta tcc ccc gat cac act ggg ctg atc tcc ccg gag ggt ctc cgc aaa	499
Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro Glu Gly Leu Arg Lys	
120 125 130	
gca gtc agg ccg gac acc aca ttg atc agc att ggt tat gcc aac aat	547
Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile Gly Tyr Ala Asn Asn	
135 140 145	
gag gtg gga acc att cag ccg ata gct gag ttg gcg gcg gta agc agt	595
Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu Ala Ala Val Ser Ser	
150 155 160 165	
acg cct ttt cac acc gat gca gtg caa gct gca cat tta acc ttt gac	643
Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala His Leu Thr Phe Asp	
170 175 180	
ttg gga gtt gac gcg tta agt ttg tcg ggt cat aaa ttc ggt gcg cct	691
Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His Lys Phe Gly Ala Pro	
185 190 195	
aaa ggg att gga gtg tta tgg tca aag ctt ccc ctg gag ccg gta atc	739
Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro Leu Glu Pro Val Ile	
200 205 210	
cat ggc ggc ggc cag gaa aaa ggg ccg cgt agt ggc acg gaa aac gtt	787
His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser Gly Thr Glu Asn Val	
215 220 225	
gcg ggg gct atc gcc ttt gcc act gcc ttg gaa ttg gcc agg gcg gaa	835
Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu Leu Ala Arg Ala Glu	
230 235 240 245	
tcc tat cca gat ctt ggc gaa ttc atc gag gaa gtt ctc act atc ccg	883
Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu Val Leu Thr Ile Pro	
250 255 260	
gga gca cac ctg act gga cat cct agg atg cgc att gat gga cac gca	931
Gly Ala His Leu Thr Gly His Pro Arg Met Arg Ile Asp Gly His Ala	
265 270 275	
tct ttt ctc ttc gac agc ata gga tct gaa act gtt ctt ctg gaa ttg	979
Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr Val Leu Leu Glu Leu	
280 285 290	
gaa cgc caa ggc att gtg tgc tcc cct ggt tct gcc tgt ggt tcc gga	
1027	
Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser Ala Cys Gly Ser Gly	
295 300 305	
gag gta tcc cat gtg ttg ctg gcg ttg ggg ctt gag gag gat caa gca	
1075	
Glu Val Ser His Val Leu Leu Ala Leu Gly Leu Glu Glu Asp Gln Ala	
310 315 320 325	

cga acg gct gtg cgc tgt act ttt agt aca aca cac agc cgt gaa gat
1123

Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr His Ser Arg Glu Asp
330 335 340

gcg ctc gtg gca gcc tct gct ctt aaa tcc gcg gtc gcc tta atc aga
1171

Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala Val Ala Leu Ile Arg
345 350 355

ggg tgacgctagt cagaggttta cgg

1197

Gly

<210> 648

<211> 358

<212> PRT

<213> Corynebacterium glutamicum

<400> 648

Met Leu Tyr Leu Asp Asn Ala Ala Thr Thr Ser Val Arg Asn Glu Ala
1 5 10 15

Leu Glu Ala Met Trp Pro Tyr Leu Thr Gly Ala Phe Gly Asn Pro Ser
20 25 30

Ser Pro His Glu Val Gly Arg Leu Ala Ser Ala Gly Leu Glu Asp Ala
35 40 45

Arg Thr Arg Val Ala Arg Ile Ile Gly Gly Arg Pro Thr Gln Val Thr
50 55 60

Phe Thr Ser Gly Gly Ser Glu Ala Asn Asn Leu Ala Ile Lys Gly Ala
65 70 75 80

Cys Leu Ala Asn Pro Arg Gly Arg His Leu Ile Thr Thr Pro Ile Glu
85 90 95

His Asp Ser Val Leu Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp
100 105 110

Phe Glu Ile Thr Tyr Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro
115 120 125

Glu Gly Leu Arg Lys Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile
130 135 140

Gly Tyr Ala Asn Asn Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu
145 150 155 160

Ala Ala Val Ser Ser Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala
165 170 175

His Leu Thr Phe Asp Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His
180 185 190

Lys Phe Gly Ala Pro Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro
195 200 205

Leu Glu Pro Val Ile His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser
 210 215 220
 Gly Thr Glu Asn Val Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu
 225 230 235 240
 Leu Ala Arg Ala Glu Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu
 245 250 255
 Val Leu Thr Ile Pro Gly Ala His Leu Thr Gly His Pro Arg Met Arg
 260 265 270
 Ile Asp Gly His Ala Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr
 275 280 285
 Val Leu Leu Glu Leu Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser
 290 295 300
 Ala Cys Gly Ser Gly Glu Val Ser His Val Leu Leu Ala Leu Gly Leu
 305 310 315 320
 Glu Glu Asp Gln Ala Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr
 325 330 335
 His Ser Arg Glu Asp Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala
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 Val Ala Leu Ile Arg Gly
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 <222> (79)..(897)
 <223> FRXA00262

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 Val Ala Gly His Leu Ile Thr Thr Pro Ile Glu
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 cat gac agt gtc cta gaa act gct gct tat ctt gaa agg ttt cat gat 159
 His Asp Ser Val Leu Glu Thr Ala Ala Tyr Leu Glu Arg Phe His Asp
 15 20 25
 ttc gag atc acc tac cta tcc ccc gat cac act ggg ctg atc tcc ccg 207
 Phe Glu Ile Thr Tyr Leu Ser Pro Asp His Thr Gly Leu Ile Ser Pro
 30 35 40
 gag ggt ctc cgc aaa gca gtc agg ccg gac acc aca ttg atc agc att 255
 Glu Gly Leu Arg Lys Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile
 45 50 55

ggt tat gcc aac aat gag gtg gga acc att cag ccg ata gct gag ttg 303
 Gly Tyr Ala Asn Asn Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu
 60 65 70 75
 gcg gcg gta agc agt acg cct ttt cac acc gat gca gtg caa gct gca 351
 Ala Ala Val Ser Ser Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala
 80 85 90
 cat tta acc ttt gac ttg gga gtt gac gcg tta agt ttg tcg ggt cat 399
 His Leu Thr Phe Asp Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His
 95 100 105
 aaa ttc ggt gcg cct aaa ggg att gga gtg tta tgg tca aag ctt ccc 447
 Lys Phe Gly Ala Pro Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro
 110 115 120
 ctg gag ccg gta atc cat ggc ggc ggc cag gaa aaa ggg cgg cgt agt 495
 Leu Glu Pro Val Ile His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser
 125 130 135
 ggc acg gaa aac gtt gcg ggg gct atc gcc ttt gcc act gcc ttg gaa 543
 Gly Thr Glu Asn Val Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu
 140 145 150 155
 ttg gcc agg gcg gaa tcc tat cca gat ctt ggc gaa ttc atc gag gaa 591
 Leu Ala Arg Ala Glu Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu
 160 165 170
 gtt ctc act atc ccg gga gca cac ctg act gga cat cct agg atg cgc 639
 Val Leu Thr Ile Pro Gly Ala His Leu Thr Gly His Pro Arg Met Arg
 175 180 185
 att gat gga cac gca tct ttt ctc ttc gac agc ata gga tct gaa act 687
 Ile Asp Gly His Ala Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr
 190 195 200
 gtt ctt ctg gaa ttg gaa cgc caa ggc att gtg tgc tcc cct ggt tct 735
 Val Leu Leu Glu Leu Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser
 205 210 215
 gcc tgt ggt tcc gga gag gta tcc cat gtg ttg ctg gcg ttg ggg ctt 783
 Ala Cys Gly Ser Gly Glu Val Ser His Val Leu Leu Ala Leu Gly Leu
 220 225 230 235
 gag gag gat caa gca cga acg gct gtg cgc tgt act ttt agt aca aca 831
 Glu Glu Asp Gln Ala Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr
 240 245 250
 cac agc cgt gaa gat gcg ctc gtg gca gcc tct gct ctt aaa tcc gcg 879
 His Ser Arg Glu Asp Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala
 255 260 265
 gtc gcc tta atc aga ggg tgacgctagt cagaggttta cgg 920
 Val Ala Leu Ile Arg Gly
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<210> 650

<211> 273

<212> PRT

<213> Corynebacterium glutamicum

<400> 650

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 35 40 45

Ala Val Arg Pro Asp Thr Thr Leu Ile Ser Ile Gly Tyr Ala Asn Asn
 50 55 60

Glu Val Gly Thr Ile Gln Pro Ile Ala Glu Leu Ala Ala Val Ser Ser
 65 70 75 80

Thr Pro Phe His Thr Asp Ala Val Gln Ala Ala His Leu Thr Phe Asp
 85 90 95

Leu Gly Val Asp Ala Leu Ser Leu Ser Gly His Lys Phe Gly Ala Pro
 100 105 110

Lys Gly Ile Gly Val Leu Trp Ser Lys Leu Pro Leu Glu Pro Val Ile
 115 120 125

His Gly Gly Gly Gln Glu Lys Gly Arg Arg Ser Gly Thr Glu Asn Val
 130 135 140

Ala Gly Ala Ile Ala Phe Ala Thr Ala Leu Glu Leu Ala Arg Ala Glu
 145 150 155 160

Ser Tyr Pro Asp Leu Gly Glu Phe Ile Glu Glu Val Leu Thr Ile Pro
 165 170 175

Gly Ala His Leu Thr Gly His Pro Arg Met Arg Ile Asp Gly His Ala
 180 185 190

Ser Phe Leu Phe Asp Ser Ile Gly Ser Glu Thr Val Leu Leu Glu Leu
 195 200 205

Glu Arg Gln Gly Ile Val Cys Ser Pro Gly Ser Ala Cys Gly Ser Gly
 210 215 220

Glu Val Ser His Val Leu Leu Ala Leu Gly Leu Glu Glu Asp Gln Ala
 225 230 235 240

Arg Thr Ala Val Arg Cys Thr Phe Ser Thr Thr His Ser Arg Glu Asp
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Ala Leu Val Ala Ala Ser Ala Leu Lys Ser Ala Val Ala Leu Ile Arg
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Gly

<210> 651

<211> 1296

<212> DNA

<213> *Corynebacterium glutamicum*

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<222> (101)..(1273)

<223> RXN00435

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                               Val Gly Phe Asp Val
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gcc agg gtt cgg ggg ctt tat acc tct ttg ggc gat ggc tgg acg tac 163
Ala Arg Val Arg Gly Leu Tyr Thr Ser Leu Gly Asp Gly Trp Thr Tyr
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ctt aat tca cat caa att ccg cag gtt ccg gag cgg gtg gcg tcg gga 211
Leu Asn Ser His Gln Ile Pro Gln Val Pro Glu Arg Val Ala Ser Gly
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gtt gcg gcg gct ttc cgc acg cat gcg cag att tct gag gtg acg tcg 259
Val Ala Ala Ala Phe Arg Thr His Ala Gln Ile Ser Glu Val Thr Ser
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cag ccg att gcg gtg gat cag ttg gag gct gct cgc gag gca gtt gcg 307
Gln Pro Ile Ala Val Asp Gln Leu Glu Ala Ala Arg Glu Ala Val Ala
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tcg ttg gcg ggt gtg gat ccg gac tgt gtt gtg ctg ggt ccc acg agg 355
Ser Leu Ala Gly Val Asp Pro Asp Cys Val Val Leu Gly Pro Thr Arg
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cag ttt ttg gct cat aca ttg gcg cgc ggt ttg ggt ggg ttt gta cgt 403
Gln Phe Leu Ala His Thr Leu Ala Arg Gly Leu Gly Gly Phe Val Arg
90                               95                               100

cga aaa gcg ggc gtg gtg ttg tcg cgc gcg gac gcg gac tgg ctg acc 451
Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp Ala Asp Trp Leu Thr
105                               110                               115

gcg ccg ttc cgc tcc ctc gac ggc gtt ttt agc tgg gcc gag ccc gat 499
Ala Pro Phe Arg Ser Leu Asp Gly Val Phe Ser Trp Ala Glu Pro Asp
120                               125                               130

ttg ggc acc ggc atg ctg ccg gat tgg cag tac gag aag ctt gtt gac 547
Leu Gly Thr Gly Met Leu Pro Asp Trp Gln Tyr Glu Lys Leu Val Asp
135                               140                               145

ggc tcg acg cgc ctt gtc gtg ctc agc gcc gcg cac ccg ctg ctc ggc 595
Gly Ser Thr Arg Leu Val Val Leu Ser Ala Ala His Pro Leu Leu Gly
150                               155                               160                               165

acg gtc gcc cca gtg ggc aag att gtg gat aaa gtg cgg gcg cgt tcg 643
Thr Val Ala Pro Val Gly Lys Ile Val Asp Lys Val Arg Ala Arg Ser
170                               175                               180

cgt gcc tgg gtg ctt gtc gac gcc acc acc tac gca gcc tac cgc ccc 691
Arg Ala Trp Val Leu Val Asp Ala Thr Thr Tyr Ala Ala Tyr Arg Pro
185                               190                               195

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ctg cgc cta gac gag tgg gaa gcc gat atc gtc atg ctt gat ctc ggc 739
 Leu Arg Leu Asp Glu Trp Glu Ala Asp Ile Val Met Leu Asp Leu Gly
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gag ttg ggc ggc ccg cag att tcg gcg ttg att ttc cgt gat acc tcg 787
 Glu Leu Gly Gly Pro Gln Ile Ser Ala Leu Ile Phe Arg Asp Thr Ser
 215 220 225

atg ttc ccg cgc ctg gat cgc acc gtt cca ctc gaa ctg ccc gca agc 835
 Met Phe Pro Arg Leu Asp Arg Thr Val Pro Leu Glu Leu Pro Ala Ser
 230 235 240 245

tcc ctg ccg cat ggg ctg ctc ggc ggc gtg ccc aac ctg gtg cgg cac 883
 Ser Leu Pro His Gly Leu Leu Gly Gly Val Pro Asn Leu Val Arg His
 250 255 260

ctg gga aac ctg gat gaa aac gcc ccg tcc gtc gtt gag gcg atg ggc 931
 Leu Gly Asn Leu Asp Glu Asn Ala Pro Ser Val Val Glu Ala Met Gly
 265 270 275

gag atg gcg aaa ttc cac aag gga ctt ttt gag cat ctt gtg gaa tcg 979
 Glu Met Ala Lys Phe His Lys Gly Leu Phe Glu His Leu Val Glu Ser
 280 285 290

ctc gaa gga ctt cac gcg gtg cat atc gtg gga att tcc ggc gat gcc
 1027
 Leu Glu Gly Leu His Ala Val His Ile Val Gly Ile Ser Gly Asp Ala
 295 300 305

gca ggt caa gac gcc ccg ttc ctg gat cga gtg ccc cgc ttg acc ttc
 1075
 Ala Gly Gln Asp Ala Pro Phe Leu Asp Arg Val Pro Arg Leu Thr Phe
 310 315 320 325

acc atg gaa ggc gtg ccc gca gat atg gtg tac cgc cga ttg gtg gac
 1123
 Thr Met Glu Gly Val Pro Ala Asp Met Val Tyr Arg Arg Leu Val Asp
 330 335 340

aat cgt ttg atc act acc gtc agc cct gct gac ccg ctg ctc gaa gca
 1171
 Asn Arg Leu Ile Thr Thr Val Ser Pro Ala Asp Pro Leu Leu Glu Ala
 345 350 355

atg ggt gtg act gaa gct ggc gga tcg atc act atc gga cta agc ccg
 1219
 Met Gly Val Thr Glu Ala Gly Gly Ser Ile Thr Ile Gly Leu Ser Pro
 360 365 370

ttt agc acc tac tat gaa gtg gat cag ctg acc agg gtg ctg gca tcg
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 Phe Ser Thr Tyr Tyr Glu Val Asp Gln Leu Thr Arg Val Leu Ala Ser
 375 380 385

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 Leu Ala
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<210> 652

<211> 391

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 652

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Arg Val Ala Ser Gly Val Ala Ala Ala Phe Arg Thr His Ala Gln Ile
      35              40              45

Ser Glu Val Thr Ser Gln Pro Ile Ala Val Asp Gln Leu Glu Ala Ala
  50              55              60

Arg Glu Ala Val Ala Ser Leu Ala Gly Val Asp Pro Asp Cys Val Val
  65              70              75              80

Leu Gly Pro Thr Arg Gln Phe Leu Ala His Thr Leu Ala Arg Gly Leu
      85              90              95

Gly Gly Phe Val Arg Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp
      100              105              110

Ala Asp Trp Leu Thr Ala Pro Phe Arg Ser Leu Asp Gly Val Phe Ser
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Trp Ala Glu Pro Asp Leu Gly Thr Gly Met Leu Pro Asp Trp Gln Tyr
      130              135              140

Glu Lys Leu Val Asp Gly Ser Thr Arg Leu Val Val Leu Ser Ala Ala
      145              150              155              160

His Pro Leu Leu Gly Thr Val Ala Pro Val Gly Lys Ile Val Asp Lys
      165              170              175

Val Arg Ala Arg Ser Arg Ala Trp Val Leu Val Asp Ala Thr Thr Tyr
      180              185              190

Ala Ala Tyr Arg Pro Leu Arg Leu Asp Glu Trp Glu Ala Asp Ile Val
      195              200              205

Met Leu Asp Leu Gly Glu Leu Gly Gly Pro Gln Ile Ser Ala Leu Ile
      210              215              220

Phe Arg Asp Thr Ser Met Phe Pro Arg Leu Asp Arg Thr Val Pro Leu
      225              230              235              240

Glu Leu Pro Ala Ser Ser Leu Pro His Gly Leu Leu Gly Gly Val Pro
      245              250              255

Asn Leu Val Arg His Leu Gly Asn Leu Asp Glu Asn Ala Pro Ser Val
      260              265              270

Val Glu Ala Met Gly Glu Met Ala Lys Phe His Lys Gly Leu Phe Glu
      275              280              285

His Leu Val Glu Ser Leu Glu Gly Leu His Ala Val His Ile Val Gly
      290              295              300

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Ile Ser Gly Asp Ala Ala Gly Gln Asp Ala Pro Phe Leu Asp Arg Val
 305 310 315 320

Pro Arg Leu Thr Phe Thr Met Glu Gly Val Pro Ala Asp Met Val Tyr
 325 330 335

Arg Arg Leu Val Asp Asn Arg Leu Ile Thr Thr Val Ser Pro Ala Asp
 340 345 350

Pro Leu Leu Glu Ala Met Gly Val Thr Glu Ala Gly Gly Ser Ile Thr
 355 360 365

Ile Gly Leu Ser Pro Phe Ser Thr Tyr Tyr Glu Val Asp Gln Leu Thr
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Arg Val Leu Ala Ser Leu Ala
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 <222> (1)..(615)
 <223> FRXA00435

<400> 653

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Trp Glu Ala Asp Ile Val Met Leu Asp Leu Gly Glu Leu Gly Gly Pro	
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cag att tcg gcg ttg att ttc cgt gat acc tcg atg ttc ccg cgc ctg	144
Gln Ile Ser Ala Leu Ile Phe Arg Asp Thr Ser Met Phe Pro Arg Leu	
35 40 45	
gat cgc acc gtt cca ctc gaa ctg ccc gca agc tcc ctg ccg cat ggg	192
Asp Arg Thr Val Pro Leu Glu Leu Pro Ala Ser Ser Leu Pro His Gly	
50 55 60	
ctg ctc ggc ggc gtg ccc aac ctg gtg cgg cac ctg gga aac ctg gat	240
Leu Leu Gly Gly Val Pro Asn Leu Val Arg His Leu Gly Asn Leu Asp	
65 70 75 80	
gaa aac gcc ccg tcc gtc gtt gag gcg atg ggg gag atg gcg aaa ttc	288
Glu Asn Ala Pro Ser Val Val Glu Ala Met Gly Glu Met Ala Lys Phe	
85 90 95	
cac aag gga ctt ttt gag cat ctt gtg gaa tcg ctc gaa gga ctt cac	336
His Lys Gly Leu Phe Glu His Leu Val Glu Ser Leu Glu Gly Leu His	
100 105 110	
gcg gtg cat atc gtg gga att tcc ggc gat gcc gca ggt caa gac gcc	384
Ala Val His Ile Val Gly Ile Ser Gly Asp Ala Ala Gly Gln Asp Ala	

115	120	125	
ccg ttc ctg gat cga gtg	ccc cgc ttg acc ttc acc	atg gaa ggc gtg	432
Pro Phe Leu Asp Arg Val	Pro Arg Leu Thr Phe Thr	Met Glu Gly Val	
130	135	140	
ccc gca gat atg gtg tac	cgc cga ttg gtg gac	aat cgt ttg atc act	480
Pro Ala Asp Met Val Tyr	Arg Arg Leu Val Asp Asn	Arg Leu Ile Thr	
145	150	155 160	
acc gtc agc cct gct gac	ccg ctg ctc gaa gca	atg ggt gtg act gaa	528
Thr Val Ser Pro Ala Asp	Pro Leu Leu Glu Ala	Met Gly Val Thr Glu	
165	170	175	
gct ggc gga tcg atc act	atc gga cta agc ccg	ttt agc acc tac tat	576
Ala Gly Gly Ser Ile Thr	Ile Gly Leu Ser Pro	Phe Ser Thr Tyr Tyr	
180	185	190	
gaa gtg gat cag ctg acc	agg gtg ctg gca tcg	ctt gcc taaaccgcaa	625
Glu Val Asp Gln Leu Thr	Arg Val Leu Ala Ser	Leu Ala	
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<211> 205

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 654

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Gln	Ile	Ser	Ala	Leu	Ile	Phe	Arg	Asp	Thr	Ser	Met	Phe	Pro	Arg	Leu
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Asp	Arg	Thr	Val	Pro	Leu	Glu	Leu	Pro	Ala	Ser	Ser	Leu	Pro	His	Gly
	50					55					60				

Leu	Leu	Gly	Gly	Val	Pro	Asn	Leu	Val	Arg	His	Leu	Gly	Asn	Leu	Asp
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Glu	Asn	Ala	Pro	Ser	Val	Val	Glu	Ala	Met	Gly	Glu	Met	Ala	Lys	Phe
				85					90					95	

His	Lys	Gly	Leu	Phe	Glu	His	Leu	Val	Glu	Ser	Leu	Glu	Gly	Leu	His
			100					105					110		

Ala	Val	His	Ile	Val	Gly	Ile	Ser	Gly	Asp	Ala	Ala	Gly	Gln	Asp	Ala
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Pro	Phe	Leu	Asp	Arg	Val	Pro	Arg	Leu	Thr	Phe	Thr	Met	Glu	Gly	Val
	130					135						140			

Pro	Ala	Asp	Met	Val	Tyr	Arg	Arg	Leu	Val	Asp	Asn	Arg	Leu	Ile	Thr
145					150					155				160	

Thr Val Ser Pro Ala Asp Pro Leu Leu Glu Ala Met Gly Val Thr Glu
165 170 175

Ala Gly Gly Ser Ile Thr Ile Gly Leu Ser Pro Phe Ser Thr Tyr Tyr
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Glu Val Asp Gln Leu Thr Arg Val Leu Ala Ser Leu Ala
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<210> 655

<211> 535

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

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<222> (101)..(535)

<223> FRXA02801

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Val Gly Phe Asp Val
1 5

gcc agg gtt cgg ggg ctt tat acc tct ttg ggc gat ggc tgg acg tac 163
Ala Arg Val Arg Gly Leu Tyr Thr Ser Leu Gly Asp Gly Trp Thr Tyr
10 15 20

ctt aat tca cat caa att ccg cag gtt ccg gag cgg gtg gcg tcg gga 211
Leu Asn Ser His Gln Ile Pro Gln Val Pro Glu Arg Val Ala Ser Gly
25 30 35

gtt gcg gcg gct ttc cgc acg cat gcg cag att tct gag gtg acg tcg 259
Val Ala Ala Ala Phe Arg Thr His Ala Gln Ile Ser Glu Val Thr Ser
40 45 50

cag ccg att gcg gtg gat cag ttg gag gct gct cgc gag gca gtt gcg 307
Gln Pro Ile Ala Val Asp Gln Leu Glu Ala Ala Arg Glu Ala Val Ala
55 60 65

tcg ttg gcg ggt gtg gat ccg gac tgt gtt gtg ctg ggt ccc acg agg 355
Ser Leu Ala Gly Val Asp Pro Asp Cys Val Val Leu Gly Pro Thr Arg
70 75 80 85

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Gln Phe Leu Ala His Thr Leu Ala Arg Gly Leu Gly Gly Phe Val Arg
90 95 100

cga aaa gcg ggc gtg gtg ttg tcg cgc gcg gac gcg gac tgg ctg acc 451
Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp Ala Asp Trp Leu Thr
105 110 115

gcg ccg ttc cgc tcc ctc gac ggc gtt ttt agc tgg gcc gag ccc gat 499
Ala Pro Phe Arg Ser Leu Asp Gly Val Phe Ser Trp Ala Glu Pro Asp
120 125 130

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Leu Gly Thr Gly Met Leu Pro Asp Trp Gln Tyr Gln

135

140

145

<210> 656
 <211> 145
 <212> PRT
 <213> Corynebacterium glutamicum

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 35 40 45
 Ser Glu Val Thr Ser Gln Pro Ile Ala Val Asp Gln Leu Glu Ala Ala
 50 55 60
 Arg Glu Ala Val Ala Ser Leu Ala Gly Val Asp Pro Asp Cys Val Val
 65 70 75 80
 Leu Gly Pro Thr Arg Gln Phe Leu Ala His Thr Leu Ala Arg Gly Leu
 85 90 95
 Gly Gly Phe Val Arg Arg Lys Ala Gly Val Val Leu Ser Arg Ala Asp
 100 105 110
 Ala Asp Trp Leu Thr Ala Pro Phe Arg Ser Leu Asp Gly Val Phe Ser
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 Trp Ala Glu Pro Asp Leu Gly Thr Gly Met Leu Pro Asp Trp Gln Tyr
 130 135 140

Gln
 145

<210> 657
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<220>
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 <222> (101)..(1363)
 <223> RXA02516

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 Met Ser Asp Phe Leu
 1 5
 aat gca gat gga tcc ctc aat gtg gat aag gtg cgg gaa gaa ttc cca 163
 Asn Ala Asp Gly Ser Leu Asn Val Asp Lys Val Arg Glu Glu Phe Pro
 10 15 20

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Ile	Leu	Lys	Arg	Thr	Val	Arg	Asp	Gly	Lys	Pro	Leu	Ala	Tyr	Leu	Asp	
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tca	ggg	gcg	aca	tcg	cag	cga	ccc	gag	cgg	gtg	tgg	cgt	gca	gag	gag	259
Ser	Gly	Ala	Thr	Ser	Gln	Arg	Pro	Glu	Arg	Val	Trp	Arg	Ala	Glu	Glu	
		40					45					50				
cac	ttt	gtg	ctg	cac	acc	aac	gcc	ccc	gtg	cac	cgc	ggg	gcc	tac	caa	307
His	Phe	Val	Leu	His	Thr	Asn	Ala	Pro	Val	His	Arg	Gly	Ala	Tyr	Gln	
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ctg	gct	gag	gaa	gca	acg	gat	gct	tat	gaa	ggg	gcc	cgc	gag	aag	atc	355
Leu	Ala	Glu	Glu	Ala	Thr	Asp	Ala	Tyr	Glu	Gly	Ala	Arg	Glu	Lys	Ile	
	70				75				80						85	
gct	gcc	ttt	gtt	ggg	gcc	gag	cag	cat	gaa	att	gcg	ttc	act	aag	aat	403
Ala	Ala	Phe	Val	Gly	Ala	Glu	Gln	His	Glu	Ile	Ala	Phe	Thr	Lys	Asn	
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Ala	Thr	Glu	Ala	Leu	Asn	Leu	Val	Ala	Tyr	Thr	Leu	Gly	Asp	Asp	Arg	
			105					110					115			
tcc	ggg	aag	tat	cgt	gtc	cag	gcc	ggg	gat	acc	gtg	gtc	atc	acg	gag	499
Ser	Gly	Lys	Tyr	Arg	Val	Gln	Ala	Gly	Asp	Thr	Val	Val	Ile	Thr	Glu	
		120					125					130				
cta	gag	cac	cac	gca	aac	ttg	gtg	cca	tgg	cag	gag	ctg	tgc	cgt	cga	547
Leu	Glu	His	His	Ala	Asn	Leu	Val	Pro	Trp	Gln	Glu	Leu	Cys	Arg	Arg	
		135				140					145					
acc	ggg	gcg	aca	ttg	aag	tgg	tac	aag	gtg	act	gaa	gat	ggg	cgc	att	595
Thr	Gly	Ala	Thr	Leu	Lys	Trp	Tyr	Lys	Val	Thr	Glu	Asp	Gly	Arg	Ile	
	150				155				160						165	
gat	ctc	gat	tca	ctc	gag	ctt	gat	gaa	act	gtc	aag	gtc	gtt	gcc	ttc	643
Asp	Leu	Asp	Ser	Leu	Glu	Leu	Asp	Glu	Thr	Val	Lys	Val	Val	Ala	Phe	
				170				175						180		
act	cac	cag	tcc	aat	gtg	acc	ggg	gct	gtg	gct	gat	gtt	cca	gag	ttg	691
Thr	His	Gln	Ser	Asn	Val	Thr	Gly	Ala	Val	Ala	Asp	Val	Pro	Glu	Leu	
			185					190					195			
gtt	cgt	cgt	gcc	aag	gct	gtc	ggc	gct	ctc	acg	gtg	ctt	gat	gcg	tgc	739
Val	Arg	Arg	Ala	Lys	Ala	Val	Gly	Ala	Leu	Thr	Val	Leu	Asp	Ala	Cys	
		200					205					210				
cag	tct	gtt	cct	cat	atg	cca	gtg	aat	ttc	cac	gag	ctg	gat	gta	gat	787
Gln	Ser	Val	Pro	His	Met	Pro	Val	Asn	Phe	His	Glu	Leu	Asp	Val	Asp	
		215				220					225					
ttc	tct	gca	ttc	tct	ggc	cat	aag	atg	ctg	gga	cct	gca	ggc	gtg	ggc	835
Phe	Ser	Ala	Phe	Ser	Gly	His	Lys	Met	Leu	Gly	Pro	Ala	Gly	Val	Gly	
		230			235					240					245	
gtt	gtg	tat	gca	aag	tcc	cca	atc	ttg	gat	gaa	ctg	cca	cca	ttt	ttg	883
Val	Val	Tyr	Ala	Lys	Ser	Pro	Ile	Leu	Asp	Glu	Leu	Pro	Pro	Phe	Leu	
				250				255						260		
act	ggg	ggg	tcc	atg	att	gaa	gtt	gtc	acc	atg	gag	ggg	tcc	acc	tac	931

Thr Gly Gly Ser Met Ile Glu Val Val Thr Met Glu Gly Ser Thr Tyr
 265 270 275
 gct gcc gca cct caa cgt ttt gag gcc ggc acg cag atg acc agc cag 979
 Ala Ala Ala Pro Gln Arg Phe Glu Ala Gly Thr Gln Met Thr Ser Gln
 280 285 290
 gtt gtg ggc ttg ggt gct gcc gtg gac atg ctg aat gaa atc ggt atg
 1027
 Val Val Gly Leu Gly Ala Ala Val Asp Met Leu Asn Glu Ile Gly Met
 295 300 305
 gaa gca atc gca gcg cat gag cac gca ttg act gct tac gcg ttg gaa
 1075
 Glu Ala Ile Ala Ala His Glu His Ala Leu Thr Ala Tyr Ala Leu Glu
 310 315 320 325
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 1123
 Lys Leu Thr Ala Ile Lys Gly Leu Thr Ile Ala Gly Pro Leu Thr Ala
 330 335 340
 gag cag cgc ggc ggt gca atc agc ttc ggt gtc gag ggc att cac cca
 1171
 Glu Gln Arg Gly Gly Ala Ile Ser Phe Gly Val Glu Gly Ile His Pro
 345 350 355
 cac gat cta ggc caa gtg ctt gac gat cag ggc gtg aat atc cgc gtc
 1219
 His Asp Leu Gly Gln Val Leu Asp Asp Gln Gly Val Asn Ile Arg Val
 360 365 370
 ggc cac cac tgc gcg tgg ccc gtg cac cgc agc atg aac gta caa tcg
 1267
 Gly His His Cys Ala Trp Pro Val His Arg Ser Met Asn Val Gln Ser
 375 380 385
 aca gca aga gca tct ttc tat ctc tat aac acc ttc gaa gaa atc gac
 1315
 Thr Ala Arg Ala Ser Phe Tyr Leu Tyr Asn Thr Phe Glu Glu Ile Asp
 390 395 400 405
 cgc ctc gcg gca gcg atc gag aag gcc aag caa ttc ttt gga gtt gag
 1363
 Arg Leu Ala Ala Ala Ile Glu Lys Ala Lys Gln Phe Phe Gly Val Glu
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 1386

<210> 658
 <211> 421
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 658
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 Arg Glu Glu Phe Pro Ile Leu Lys Arg Thr Val Arg Asp Gly Lys Pro

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Leu	Ala	Tyr	Leu	Asp	Ser	Gly	Ala	Thr	Ser	Gln	Arg	Pro	Glu	Arg	Val															
		35					40					45																		
Trp	Arg	Ala	Glu	Glu	His	Phe	Val	Leu	His	Thr	Asn	Ala	Pro	Val	His															
		50				55					60																			
Arg	Gly	Ala	Tyr	Gln	Leu	Ala	Glu	Glu	Ala	Thr	Asp	Ala	Tyr	Glu	Gly															
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Ala	Arg	Glu	Lys	Ile	Ala	Ala	Phe	Val	Gly	Ala	Glu	Gln	His	Glu	Ile															
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Ala	Phe	Thr	Lys	Asn	Ala	Thr	Glu	Ala	Leu	Asn	Leu	Val	Ala	Tyr	Thr															
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Leu	Gly	Asp	Asp	Arg	Ser	Gly	Lys	Tyr	Arg	Val	Gln	Ala	Gly	Asp	Thr															
		115				120					125																			
Val	Val	Ile	Thr	Glu	Leu	Glu	His	His	Ala	Asn	Leu	Val	Pro	Trp	Gln															
		130				135					140																			
Glu	Leu	Cys	Arg	Arg	Thr	Gly	Ala	Thr	Leu	Lys	Trp	Tyr	Lys	Val	Thr															
		145			150					155					160															
Glu	Asp	Gly	Arg	Ile	Asp	Leu	Asp	Ser	Leu	Glu	Leu	Asp	Glu	Thr	Val															
				165				170						175																
Lys	Val	Val	Ala	Phe	Thr	His	Gln	Ser	Asn	Val	Thr	Gly	Ala	Val	Ala															
			180					185					190																	
Asp	Val	Pro	Glu	Leu	Val	Arg	Arg	Ala	Lys	Ala	Val	Gly	Ala	Leu	Thr															
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Val	Leu	Asp	Ala	Cys	Gln	Ser	Val	Pro	His	Met	Pro	Val	Asn	Phe	His															
		210				215					220																			
Glu	Leu	Asp	Val	Asp	Phe	Ser	Ala	Phe	Ser	Gly	His	Lys	Met	Leu	Gly															
		225			230					235					240															
Pro	Ala	Gly	Val	Gly	Val	Val	Tyr	Ala	Lys	Ser	Pro	Ile	Leu	Asp	Glu															
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Leu	Pro	Pro	Phe	Leu	Thr	Gly	Gly	Ser	Met	Ile	Glu	Val	Val	Thr	Met															
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Glu	Gly	Ser	Thr	Tyr	Ala	Ala	Ala	Pro	Gln	Arg	Phe	Glu	Ala	Gly	Thr															
		275				280						285																		
Gln	Met	Thr	Ser	Gln	Val	Val	Gly	Leu	Gly	Ala	Ala	Val	Asp	Met	Leu															
		290				295					300																			
Asn	Glu	Ile	Gly	Met	Glu	Ala	Ile	Ala	Ala	His	Glu	His	Ala	Leu	Thr															
		305			310					315					320															
Ala	Tyr	Ala	Leu	Glu	Lys	Leu	Thr	Ala	Ile	Lys	Gly	Leu	Thr	Ile	Ala															
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Gly	Pro	Leu	Thr	Ala	Glu	Gln	Arg	Gly	Gly	Ala	Ile	Ser	Phe	Gly	Val															
			340					345					350																	

Glu Gly Ile His Pro His Asp Leu Gly Gln Val Leu Asp Asp Gln Gly
 355 360 365
 Val Asn Ile Arg Val Gly His His Cys Ala Trp Pro Val His Arg Ser
 370 375 380
 Met Asn Val Gln Ser Thr Ala Arg Ala Ser Phe Tyr Leu Tyr Asn Thr
 385 390 395 400
 Phe Glu Glu Ile Asp Arg Leu Ala Ala Ala Ile Glu Lys Ala Lys Gln
 405 410 415
 Phe Phe Gly Val Glu
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<210> 659

<211> 570

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(547)

<223> RXA02517

<400> 659

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 Met Asn Leu Glu Gln
 1 5
 atg tac cag gag gtg atc ctg gac cac tac aaa aac cca cag cac aag 163
 Met Tyr Gln Glu Val Ile Leu Asp His Tyr Lys Asn Pro Gln His Lys
 10 15 20
 ggc ctt cgg gat cct ttc gat gct gag gtt cac cac gtc aac cct tct 211
 Gly Leu Arg Asp Pro Phe Asp Ala Glu Val His His Val Asn Pro Ser
 25 30 35
 tgt ggc gac gaa ttg act ctg cgc gtg aag ctg tct gag gac ggc tcc 259
 Cys Gly Asp Glu Leu Thr Leu Arg Val Lys Leu Ser Glu Asp Gly Ser
 40 45 50
 acc gtg gag gac gtc tcc tac gaa gca gtt ggt tgc tca atc agc cag 307
 Thr Val Glu Asp Val Ser Tyr Glu Ala Val Gly Cys Ser Ile Ser Gln
 55 60 65
 gcc tcc acg tcc gtt atg gcc gag gag atc gtg ggc caa ccc gtc gac 355
 Ala Ser Thr Ser Val Met Ala Glu Glu Ile Val Gly Gln Pro Val Asp
 70 75 80 85
 aag gcg ctg gaa aag ctc aca gaa ttt gag aag atg atc gtt tcc cgc 403
 Lys Ala Leu Glu Lys Leu Thr Glu Phe Glu Lys Met Ile Val Ser Arg
 90 95 100
 ggt cag ttt gtt ggc gat gaa gat ctc atc gga gat ggc gtt gct ttc 451
 Gly Gln Phe Val Gly Asp Glu Asp Leu Ile Gly Asp Gly Val Ala Phe
 105 110 115

tcc gga gtc gcc aag tac ccg gca cgc gtg aag tgc gcg ctg ctt ggg 499
 Ser Gly Val Ala Lys Tyr Pro Ala Arg Val Lys Cys Ala Leu Leu Gly
 120 125 130

tgg aag gct ttc cag gcg gca acc gct gac gct gtt gcg cac gca cat 547
 Trp Lys Ala Phe Gln Ala Ala Thr Ala Asp Ala Val Ala His Ala His
 135 140 145

tagccccgctg tattaattgg agg 570

<210> 660

<211> 149

<212> PRT

<213> Corynebacterium glutamicum

<400> 660

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Asn Pro Gln His Lys Gly Leu Arg Asp Pro Phe Asp Ala Glu Val His
 20 25 30

His Val Asn Pro Ser Cys Gly Asp Glu Leu Thr Leu Arg Val Lys Leu
 35 40 45

Ser Glu Asp Gly Ser Thr Val Glu Asp Val Ser Tyr Glu Ala Val Gly
 50 55 60

Cys Ser Ile Ser Gln Ala Ser Thr Ser Val Met Ala Glu Glu Ile Val
 65 70 75 80

Gly Gln Pro Val Asp Lys Ala Leu Glu Lys Leu Thr Glu Phe Glu Lys
 85 90 95

Met Ile Val Ser Arg Gly Gln Phe Val Gly Asp Glu Asp Leu Ile Gly
 100 105 110

Asp Gly Val Ala Phe Ser Gly Val Ala Lys Tyr Pro Ala Arg Val Lys
 115 120 125

Cys Ala Leu Leu Gly Trp Lys Ala Phe Gln Ala Ala Thr Ala Asp Ala
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Val Ala His Ala His
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<210> 661

<211> 1167

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1144)

<223> RXA01747

<400> 661

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ctaaaaatat cactaactcg aaagatgtaa ggttgcat	gtg act atc gca cct	115
	Val Thr Ile Ala Pro	
	1 5	
gaa gga cga cga ctg cta cgc gtc gaa gct cga aac tca gaa acc ccg	163	
Glu Gly Arg Arg Leu Leu Arg Val Glu Ala Arg Asn Ser Glu Thr Pro		
10 15 20		
att gag acg aag cct cga tgg att aga aac cag gtc aaa aac gga cct	211	
Ile Glu Thr Lys Pro Arg Trp Ile Arg Asn Gln Val Lys Asn Gly Pro		
25 30 35		
gag tat cag gat atg aag gaa cgt gtc gct ggc gca tca cta cac act	259	
Glu Tyr Gln Asp Met Lys Glu Arg Val Ala Gly Ala Ser Leu His Thr		
40 45 50		
gtg tgt cag gag gct ggc tgt cct aat atc cat gag tgt tgg gaa tcc	307	
Val Cys Gln Glu Ala Gly Cys Pro Asn Ile His Glu Cys Trp Glu Ser		
55 60 65		
cgt gag gca acc ttc ctc att ggt ggc gcc aac tgc tct cgc cgc tgt	355	
Arg Glu Ala Thr Phe Leu Ile Gly Gly Ala Asn Cys Ser Arg Arg Cys		
70 75 80 85		
gat ttc tgc atg atc aac tcg gct cgc cct gag cca ctc gac cgc ggt	403	
Asp Phe Cys Met Ile Asn Ser Ala Arg Pro Glu Pro Leu Asp Arg Gly		
90 95 100		
gag cca ctg cgt gtc gct gag tct gtt cgt gag atg cag ctg aat tac	451	
Glu Pro Leu Arg Val Ala Glu Ser Val Arg Glu Met Gln Leu Asn Tyr		
105 110 115		
tcc acc atc acc ggt gtt acc cgt gat gat ctg gat gat gaa ggc gca	499	
Ser Thr Ile Thr Gly Val Thr Arg Asp Asp Leu Asp Asp Glu Gly Ala		
120 125 130		
tgg ctg tac tca gaa gtg gtt cgt aag atc cac gag ctg aac cca cac	547	
Trp Leu Tyr Ser Glu Val Val Arg Lys Ile His Glu Leu Asn Pro His		
135 140 145		
acc ggt gtg gaa aac ctg gtg cct gat ttc tcc ggc aag aag gat ctg	595	
Thr Gly Val Glu Asn Leu Val Pro Asp Phe Ser Gly Lys Lys Asp Leu		
150 155 160 165		
ctg cag gaa gtt ttt gaa tcc cgc cca gag gtt ttc gct cac aac gtg	643	
Leu Gln Glu Val Phe Glu Ser Arg Pro Glu Val Phe Ala His Asn Val		
170 175 180		
gaa act gtg cca cgt att ttc aag cgc att cgc cca gca ttc cgc tac	691	
Glu Thr Val Pro Arg Ile Phe Lys Arg Ile Arg Pro Ala Phe Arg Tyr		
185 190 195		
gag cgt tca ctt gat gtg atc cgt cag gct cgc gat ttc ggt ctg gtg	739	
Glu Arg Ser Leu Asp Val Ile Arg Gln Ala Arg Asp Phe Gly Leu Val		
200 205 210		
acc aag tcc aac ctg att ttg ggc atg ggt gaa acc aag gaa gaa atc	787	
Thr Lys Ser Asn Leu Ile Leu Gly Met Gly Glu Thr Lys Glu Glu Ile		
215 220 225		

acc gag gcg ctg cag gat ctg cac gac gct ggc tgt gac atc atc acc 835
 Thr Glu Ala Leu Gln Asp Leu His Asp Ala Gly Cys Asp Ile Ile Thr
 230 235 240 245

atc acc cag tac ctg cgt cct ggt cct ttg ttc cac ccc atc gag cgt 883
 Ile Thr Gln Tyr Leu Arg Pro Gly Pro Leu Phe His Pro Ile Glu Arg
 250 255 260

tgg gtg aag cct gag gag ttc ctc gag cac gct gat gct gca aag gaa 931
 Trp Val Lys Pro Glu Glu Phe Leu Glu His Ala Asp Ala Lys Glu
 265 270 275

atg ggc ttc gct gct gtt atg tcc ggc cca ttg gtt cgt tcc tct tac 979
 Met Gly Phe Ala Ala Val Met Ser Gly Pro Leu Val Arg Ser Ser Tyr
 280 285 290

cgt gca ggc cgt ctg tac gcg cag gcc atg gag ttc cgt ggc gag gaa
 1027
 Arg Ala Gly Arg Leu Tyr Ala Gln Ala Met Glu Phe Arg Gly Glu Glu
 295 300 305

atc cca gca cac ctc gcg cac ctg aag gat act tcc gga gga tcc acc
 1075
 Ile Pro Ala His Leu Ala His Leu Lys Asp Thr Ser Gly Gly Ser Thr
 310 315 320 325

gcc cag gaa gca tct aca ctt ctg gag cgt tac ggt gct tcc gaa gac
 1123
 Ala Gln Glu Ala Ser Thr Leu Leu Glu Arg Tyr Gly Ala Ser Glu Asp
 330 335 340

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 Thr Pro Val Val Ser Phe Asn
 345

<210> 662

<211> 348

<212> PRT

<213> Corynebacterium glutamicum

<400> 662

Val Thr Ile Ala Pro Glu Gly Arg Arg Leu Leu Arg Val Glu Ala Arg
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Asn Ser Glu Thr Pro Ile Glu Thr Lys Pro Arg Trp Ile Arg Asn Gln
 20 25 30

Val Lys Asn Gly Pro Glu Tyr Gln Asp Met Lys Glu Arg Val Ala Gly
 35 40 45

Ala Ser Leu His Thr Val Cys Gln Glu Ala Gly Cys Pro Asn Ile His
 50 55 60

Glu Cys Trp Glu Ser Arg Glu Ala Thr Phe Leu Ile Gly Gly Ala Asn
 65 70 75 80

Cys Ser Arg Arg Cys Asp Phe Cys Met Ile Asn Ser Ala Arg Pro Glu
 85 90 95

Pro Leu Asp Arg Gly Glu Pro Leu Arg Val Ala Glu Ser Val Arg Glu
 100 105 110
 Met Gln Leu Asn Tyr Ser Thr Ile Thr Gly Val Thr Arg Asp Asp Leu
 115 120 125
 Asp Asp Glu Gly Ala Trp Leu Tyr Ser Glu Val Val Arg Lys Ile His
 130 135 140
 Glu Leu Asn Pro His Thr Gly Val Glu Asn Leu Val Pro Asp Phe Ser
 145 150 155 160
 Gly Lys Lys Asp Leu Leu Gln Glu Val Phe Glu Ser Arg Pro Glu Val
 165 170 175
 Phe Ala His Asn Val Glu Thr Val Pro Arg Ile Phe Lys Arg Ile Arg
 180 185 190
 Pro Ala Phe Arg Tyr Glu Arg Ser Leu Asp Val Ile Arg Gln Ala Arg
 195 200 205
 Asp Phe Gly Leu Val Thr Lys Ser Asn Leu Ile Leu Gly Met Gly Glu
 210 215 220
 Thr Lys Glu Glu Ile Thr Glu Ala Leu Gln Asp Leu His Asp Ala Gly
 225 230 235 240
 Cys Asp Ile Ile Thr Ile Thr Gln Tyr Leu Arg Pro Gly Pro Leu Phe
 245 250 255
 His Pro Ile Glu Arg Trp Val Lys Pro Glu Glu Phe Leu Glu His Ala
 260 265 270
 Asp Ala Ala Lys Glu Met Gly Phe Ala Ala Val Met Ser Gly Pro Leu
 275 280 285
 Val Arg Ser Ser Tyr Arg Ala Gly Arg Leu Tyr Ala Gln Ala Met Glu
 290 295 300
 Phe Arg Gly Glu Glu Ile Pro Ala His Leu Ala His Leu Lys Asp Thr
 305 310 315 320
 Ser Gly Gly Ser Thr Ala Gln Glu Ala Ser Thr Leu Leu Glu Arg Tyr
 325 330 335
 Gly Ala Ser Glu Asp Thr Pro Val Val Ser Phe Asn
 340 345

<210> 663

<211> 876

<212> DNA

<213> *Corynebacterium glutamicum*

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<221> CDS

<222> (101)..(853)

<223> RXA01746

<400> 663

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	Met Thr Ala Pro Arg	
	1 5	
gat cct ttt ttc ccc gca gat ctt tct atc cgc gcg tct gca gag ccc	163	
Asp Pro Phe Phe Pro Ala Asp Leu Ser Ile Arg Ala Ser Ala Glu Pro		
10 15 20		
att gaa att cag cgg ttg ggt ttg atc gat tat caa gag gcc tgg gat	211	
Ile Glu Ile Gln Arg Leu Gly Leu Ile Asp Tyr Gln Glu Ala Trp Asp		
25 30 35		
tat caa gca gag ctt gct acc cgt agg gct aat gat gaa atc cct gat	259	
Tyr Gln Ala Glu Leu Ala Thr Arg Arg Ala Asn Asp Glu Ile Pro Asp		
40 45 50		
cag ctg ctt att ttg gag cac ccg tcg gtg tat acc gca ggt aag cgc	307	
Gln Leu Leu Ile Leu Glu His Pro Ser Val Tyr Thr Ala Gly Lys Arg		
55 60 65		
acc cag ccg gaa gat ctt ccc acc aac gga ctg ccg gtg atc aat gct	355	
Thr Gln Pro Glu Asp Leu Pro Thr Asn Gly Leu Pro Val Ile Asn Ala		
70 75 80 85		
gat cgt ggt ggt cgc atc acg tgg cat ggt cct ggc caa ttg gtg atc	403	
Asp Arg Gly Gly Arg Ile Thr Trp His Gly Pro Gly Gln Leu Val Ile		
90 95 100		
tat ccg atc atc aaa tta gcc gat ccg atc gat gtg gtt gat tac gta	451	
Tyr Pro Ile Ile Lys Leu Ala Asp Pro Ile Asp Val Val Asp Tyr Val		
105 110 115		
aga cgc ctc gag gaa gcg ctc atc caa gtt gtc ggc gat atg ggt gtt	499	
Arg Arg Leu Glu Glu Ala Leu Ile Gln Val Val Gly Asp Met Gly Val		
120 125 130		
gcc ggc gct ggg cgc att gat ggg cgt tcg ggt gtg tgg gtg cca gct	547	
Ala Gly Ala Gly Arg Ile Asp Gly Arg Ser Gly Val Trp Val Pro Ala		
135 140 145		
cat gat ggt tgg gtg gac agc aag gtt gcg gcc atc ggc att cga ata	595	
His Asp Gly Trp Val Asp Ser Lys Val Ala Ala Ile Gly Ile Arg Ile		
150 155 160 165		
act cgt ggt gtt gca atg cac ggt gtg gcc atc aac tgc aac aac acg	643	
Thr Arg Gly Val Ala Met His Gly Val Ala Ile Asn Cys Asn Asn Thr		
170 175 180		
ttg gat ttc tat gag cac atc att ccg tgt ggc att gct gat gca ggc	691	
Leu Asp Phe Tyr Glu His Ile Ile Pro Cys Gly Ile Ala Asp Ala Gly		
185 190 195		
ttg agc aca ctc tcg agg gaa ctg aaa agg gac gtt tca gtt gag gaa	739	
Leu Ser Thr Leu Ser Arg Glu Leu Lys Arg Asp Val Ser Val Glu Glu		
200 205 210		
tta gtc gag cca tcg atc cgc gca ttg gat gat gct ttg gct ggt cgg	787	
Leu Val Glu Pro Ser Ile Arg Ala Leu Asp Asp Ala Leu Ala Gly Arg		
215 220 225		

ctg gtt gtt tct gat cat tct ttc ggc agc gcg ccc gac cca act aag 835
 Leu Val Val Ser Asp His Ser Phe Gly Ser Ala Pro Asp Pro Thr Lys
 230 235 240 245

aat ctc cct aaa cgg ggg tagtacgagg aattttgtcg gtg 876
 Asn Leu Pro Lys Arg Gly
 250

<210> 664

<211> 251

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 664

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Ala Ser Ala Glu Pro Ile Glu Ile Gln Arg Leu Gly Leu Ile Asp Tyr
 20 25 30

Gln Glu Ala Trp Asp Tyr Gln Ala Glu Leu Ala Thr Arg Arg Ala Asn
 35 40 45

Asp Glu Ile Pro Asp Gln Leu Leu Ile Leu Glu His Pro Ser Val Tyr
 50 55 60

Thr Ala Gly Lys Arg Thr Gln Pro Glu Asp Leu Pro Thr Asn Gly Leu
 65 70 75 80

Pro Val Ile Asn Ala Asp Arg Gly Gly Arg Ile Thr Trp His Gly Pro
 85 90 95

Gly Gln Leu Val Ile Tyr Pro Ile Ile Lys Leu Ala Asp Pro Ile Asp
 100 105 110

Val Val Asp Tyr Val Arg Arg Leu Glu Glu Ala Leu Ile Gln Val Val
 115 120 125

Gly Asp Met Gly Val Ala Gly Ala Gly Arg Ile Asp Gly Arg Ser Gly
 130 135 140

Val Trp Val Pro Ala His Asp Gly Trp Val Asp Ser Lys Val Ala Ala
 145 150 155 160

Ile Gly Ile Arg Ile Thr Arg Gly Val Ala Met His Gly Val Ala Ile
 165 170 175

Asn Cys Asn Asn Thr Leu Asp Phe Tyr Glu His Ile Ile Pro Cys Gly
 180 185 190

Ile Ala Asp Ala Gly Leu Ser Thr Leu Ser Arg Glu Leu Lys Arg Asp
 195 200 205

Val Ser Val Glu Glu Leu Val Glu Pro Ser Ile Arg Ala Leu Asp Asp
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Ala Leu Ala Gly Arg Leu Val Val Ser Asp His Ser Phe Gly Ser Ala
 225 230 235 240

Pro Asp Pro Thr Lys Asn Leu Pro Lys Arg Gly

250

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<222> (101)..(1156)
<223> RXA02106
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Met Asn Asn His Phe 5																
gag ctc aaa gta cct ggt gga aag ctt gtc gtc gtt gat gtg acc acc 163																
Glu Leu Lys Val Pro Gly Gly Lys Leu Val Val Val Asp Val Thr Thr 10 15 20																
gat ctg gat tcc att gct gac gtg aag att tcc ggc gat ttc ttc ctc 211																
Asp Leu Asp Ser Ile Ala Asp Val Lys Ile Ser Gly Asp Phe Phe Leu 25 30 35																
gaa ccc gat gag gca ttc ttc gcc ctt ggc cgg gcg ctg cag ggg gcg 259																
Glu Pro Asp Glu Ala Phe Phe Ala Leu Gly Arg Ala Leu Gln Gly Ala 40 45 50																
tcg gtg ggt gat aac act gat cgt ttg cag gca aag ttg gat gga gcg 307																
Ser Val Gly Asp Asn Thr Asp Arg Leu Gln Ala Lys Leu Asp Ala Ala 55 60 65																
ttg gcg gaa tat gat gac gtt gag cta cac ggc ttt agc act gcg gat 355																
Leu Ala Glu Tyr Asp Asp Val Glu Leu His Gly Phe Ser Thr Ala Asp 70 75 80 85																
att gct tta gct gtg cgt cgg gca gtc acc ggc gcg caa gat ttc acc 403																
Ile Ala Leu Ala Val Arg Arg Ala Val Thr Gly Ala Gln Asp Phe Thr 90 95 100																
gat tat gaa tgg gaa atc ctg cac cca ggg gtg ctt cct acc cca ctt 451																
Asp Tyr Glu Trp Glu Ile Leu His Pro Gly Val Leu Pro Thr Pro Leu 105 110 115																
aac gtt gcg ttg gat gag ctc ctt ttg gac caa gtt gcc agt ggt cag 499																
Asn Val Ala Leu Asp Glu Leu Leu Leu Asp Gln Val Ala Ser Gly Gln 120 125 130																
cgt ggc ccg acg atg cgc att tgg gat tgg gat gat cgc gcc aca gtg 547																
Arg Gly Pro Thr Met Arg Ile Trp Asp Trp Asp Asp Arg Ala Thr Val 135 140 145																
atc ggt agt ttc cag tca tat gtc aat gaa atc aac caa gaa ggc gtt 595																
Ile Gly Ser Phe Gln Ser Tyr Val Asn Glu Ile Asn Gln Glu Gly Val 150 155 160 165																
aat gaa cat ggt gtg acc gtg gta cga cgc atg tct ggt gcc ggt gca 643																

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Asn Glu His Gly Val Thr Val Val Arg Arg Met Ser Gly Gly Gly Ala
170                               175                               180

atg ttt atg gag ggc ggc aac tgc atc acc tat tcc ctg tat gca ccg      691
Met Phe Met Glu Gly Gly Asn Cys Ile Thr Tyr Ser Leu Tyr Ala Pro
185                               190                               195

gaa tct ctc gtt gct ggt ttg agc tat gag cag tcc tat gaa tat ttg      739
Glu Ser Leu Val Ala Gly Leu Ser Tyr Glu Gln Ser Tyr Glu Tyr Leu
200                               205                               210

gat cgt tgg gtg att gct gcg ctg aag aca cac gat gtt gac gct tgg      787
Asp Arg Trp Val Ile Ala Ala Leu Lys Thr His Asp Val Asp Ala Trp
215                               220                               225

tac gtg cct atc aat gac atc acc tcc acc ggc gga aaa atc ggt ggc      835
Tyr Val Pro Ile Asn Asp Ile Thr Ser Thr Gly Gly Lys Ile Gly Gly
230                               235                               240

gct gca cag aaa cgt cgc agt ggc gca gtc ctc cac cac gtg acc atg      883
Ala Ala Gln Lys Arg Arg Ser Gly Ala Val Leu His His Val Thr Met
250                               255                               260

tcc tat gac atc gat gcg gac atg atg acc cag gtg ttg cgc att gga      931
Ser Tyr Asp Ile Asp Ala Asp Met Met Thr Gln Val Leu Arg Ile Gly
265                               270                               275

aag gtg aag att tcc gac aag ggt ctt cgc agc gca aag aag cgc gtt      979
Lys Val Lys Ile Ser Asp Lys Gly Leu Arg Ser Ala Lys Lys Arg Val
280                               285                               290

gat cct ctg cgc cgc caa aca ggt gca tca cgt gag caa atc atc gac
1027
Asp Pro Leu Arg Arg Gln Thr Gly Ala Ser Arg Glu Gln Ile Ile Asp
295                               300                               305

acc cta aag tcc aca ttc agt gct agg tac ggc gcg caa gaa gta gag
1075
Thr Leu Lys Ser Thr Phe Ser Ala Arg Tyr Gly Ala Gln Glu Val Glu
310                               315                               320                               325

ctc agc gat gaa gat ttc gcg gca ggc cac gac cta gta aaa acc aaa
1123
Leu Ser Asp Glu Asp Phe Ala Ala Gly His Asp Leu Val Lys Thr Lys
330                               335                               340

tac gcc acc gag gag tgg act aag cga gtt caa tagtttctat ggatctgcac
1176
Tyr Ala Thr Glu Glu Trp Thr Lys Arg Val Gln
345                               350

aag
1179

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<210> 666

<211> 352

<212> PRT

<213> Corynebacterium glutamicum

<400> 666

Met Asn Asn His Phe Glu Leu Lys Val Pro Gly Gly Lys Leu Val Val
 1 5 10 15
 Val Asp Val Thr Thr Asp Leu Asp Ser Ile Ala Asp Val Lys Ile Ser
 20 25 30
 Gly Asp Phe Phe Leu Glu Pro Asp Glu Ala Phe Phe Ala Leu Gly Arg
 35 40 45
 Ala Leu Gln Gly Ala Ser Val Gly Asp Asn Thr Asp Arg Leu Gln Ala
 50 55 60
 Lys Leu Asp Ala Ala Leu Ala Glu Tyr Asp Asp Val Glu Leu His Gly
 65 70 75 80
 Phe Ser Thr Ala Asp Ile Ala Leu Ala Val Arg Arg Ala Val Thr Gly
 85 90 95
 Ala Gln Asp Phe Thr Asp Tyr Glu Trp Glu Ile Leu His Pro Gly Val
 100 105 110
 Leu Pro Thr Pro Leu Asn Val Ala Leu Asp Glu Leu Leu Leu Asp Gln
 115 120 125
 Val Ala Ser Gly Gln Arg Gly Pro Thr Met Arg Ile Trp Asp Trp Asp
 130 135 140
 Asp Arg Ala Thr Val Ile Gly Ser Phe Gln Ser Tyr Val Asn Glu Ile
 145 150 155 160
 Asn Gln Glu Gly Val Asn Glu His Gly Val Thr Val Val Arg Arg Met
 165 170 175
 Ser Gly Gly Gly Ala Met Phe Met Glu Gly Gly Asn Cys Ile Thr Tyr
 180 185 190
 Ser Leu Tyr Ala Pro Glu Ser Leu Val Ala Gly Leu Ser Tyr Glu Gln
 195 200 205
 Ser Tyr Glu Tyr Leu Asp Arg Trp Val Ile Ala Ala Leu Lys Thr His
 210 215 220
 Asp Val Asp Ala Trp Tyr Val Pro Ile Asn Asp Ile Thr Ser Thr Gly
 225 230 235 240
 Gly Lys Ile Gly Gly Ala Ala Gln Lys Arg Arg Ser Gly Ala Val Leu
 245 250 255
 His His Val Thr Met Ser Tyr Asp Ile Asp Ala Asp Met Met Thr Gln
 260 265 270
 Val Leu Arg Ile Gly Lys Val Lys Ile Ser Asp Lys Gly Leu Arg Ser
 275 280 285
 Ala Lys Lys Arg Val Asp Pro Leu Arg Arg Gln Thr Gly Ala Ser Arg
 290 295 300
 Glu Gln Ile Ile Asp Thr Leu Lys Ser Thr Phe Ser Ala Arg Tyr Gly
 305 310 315 320
 Ala Gln Glu Val Glu Leu Ser Asp Glu Asp Phe Ala Ala Gly His Asp

325 330 335
 Leu Val Lys Thr Lys Tyr Ala Thr Glu Glu Trp Thr Lys Arg Val Gln
 340 345 350

<210> 667
 <211> 403
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(403)
 <223> RXS01183

<400> 667
 cttgatatga cccgaacacc acacatcaca aattgaatcg gtatcctttg gggtattagt 60
 ttccgtttta acgacacgac ttgcgaggag tcttaaaata atg gcg ttc tcc gta 115
 Met Ala Phe Ser Val
 1 5
 gag atg ccc gag ctg ggc gaa tca gta acc gaa ggc acg atc acc cag 163
 Glu Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln
 10 15 20
 tgg ttg aag tct gtt ggt gac act gtt gag gta gat gag ccg ttg ctc 211
 Trp Leu Lys Ser Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu
 25 30 35
 gag gtc tca act gac aag gtc gac acc gag att ccc tct cct gtc gcc 259
 Glu Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala
 40 45 50
 ggt gtc atc cta gag att aag gct gaa gag gat gac acc gtc gac gtc 307
 Gly Val Ile Leu Glu Ile Lys Ala Glu Glu Asp Asp Thr Val Asp Val
 55 60 65
 ggc ggt gtc att gca ata atc ggc gat gct gat gag act cct gcc aac 355
 Gly Gly Val Ile Ala Ile Ile Gly Asp Ala Asp Glu Thr Pro Ala Asn
 70 75 80 85
 gaa gct cct gcc gac gag gca cca gct cct gcc gaa gag gaa gaa cca 403
 Glu Ala Pro Ala Asp Glu Ala Pro Ala Pro Ala Glu Glu Glu Glu Pro
 90 95 100

<210> 668
 <211> 101
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 668
 Met Ala Phe Ser Val Glu Met Pro Glu Leu Gly Glu Ser Val Thr Glu
 1 5 10 15
 Gly Thr Ile Thr Gln Trp Leu Lys Ser Val Gly Asp Thr Val Glu Val

20	25	30
Asp Glu Pro Leu Leu Glu Val Ser Thr Asp Lys Val Asp Thr Glu Ile		
35	40	45
Pro Ser Pro Val Ala Gly Val Ile Leu Glu Ile Lys Ala Glu Glu Asp		
50	55	60
Asp Thr Val Asp Val Gly Gly Val Ile Ala Ile Ile Gly Asp Ala Asp		
65	70	75
Glu Thr Pro Ala Asn Glu Ala Pro Ala Asp Glu Ala Pro Ala Pro Ala		
85	90	95
Glu Glu Glu Glu Pro		
100		

<210> 669
 <211> 1305
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1282)
 <223> RXS01260

<400> 669
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 ctttaccatcct gagaagaaga ccttcggcat caatggcgaa gtg acc ttc aac tat 115
 Val Thr Phe Asn Tyr
 1 5
 gag gat gct cac aag cgt tcc cgt ggc gtt tcc gac aag atc gtt gga 163
 Glu Asp Ala His Lys Arg Ser Arg Gly Val Ser Asp Lys Ile Val Gly
 10 15 20
 ggc gtt cat tac ttg atg aag aag aac aag atc atc gaa att cat ggt 211
 Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile Ile Glu Ile His Gly
 25 30 35
 ctt gga aac ttc aag gat gct aag act ctt gag gtc acc gac ggt aag 259
 Leu Gly Asn Phe Lys Asp Ala Lys Thr Leu Glu Val Thr Asp Gly Lys
 40 45 50
 gat gct ggc aag acc atc acc ttt gat gac tgc atc atc gca acc ggt 307
 Asp Ala Gly Lys Thr Ile Thr Phe Asp Asp Cys Ile Ile Ala Thr Gly
 55 60 65
 tcg gta gtc aac acc ctc cgt ggc gtt gac ttc tca gag aac gtt gtg 355
 Ser Val Val Asn Thr Leu Arg Gly Val Asp Phe Ser Glu Asn Val Val
 70 75 80 85
 tct ttt gaa gag cag att ctt aac cct gtt gcg cca aag aag atg gtc 403
 Ser Phe Glu Glu Gln Ile Leu Asn Pro Val Ala Pro Lys Lys Met Val
 90 95 100
 att gtt ggt gca ggc gca att gga atg gaa ttc gcc tac gtt ctt ggt 451
 Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe Ala Tyr Val Leu Gly

105					110					115					
aac tac ggt gta gat gta acc gtc atc gag ttc atg gat cgt gtg ctt	499														
Asn Tyr Gly Val Asp Val Thr Val Ile Glu Phe Met Asp Arg Val Leu															
120	125	130													
cca aat gaa gat gct gaa gtc tcc aag gtt att gca aag gcc tac aag	547														
Pro Asn Glu Asp Ala Glu Val Ser Lys Val Ile Ala Lys Ala Tyr Lys															
135	140	145													
aag atg ggc gtt aag ctt ctt cct ggc cat gca acc act gct gtt cgg	595														
Lys Met Gly Val Lys Leu Leu Pro Gly His Ala Thr Thr Ala Val Arg															
150	155	160	165												
gac aac ggt gac ttt gtc gag gtt gat tac cag aag aag ggc tct gac	643														
Asp Asn Gly Asp Phe Val Glu Val Asp Tyr Gln Lys Lys Gly Ser Asp															
	170	175	180												
aag aca gag act ctt act gtt gat cga gtc atg gtt tcc gtt ggt ttc	691														
Lys Thr Glu Thr Leu Thr Val Asp Arg Val Met Val Ser Val Gly Phe															
	185	190	195												
cgt cca cgc gtt gag gga ttt ggt ctt gaa aac act ggc gtt aag ctc	739														
Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn Thr Gly Val Lys Leu															
	200	205	210												
acc gag cgt ggc gca atc gag atc gat gat tac atg cgt acc aac gtc	787														
Thr Glu Arg Gly Ala Ile Glu Ile Asp Asp Tyr Met Arg Thr Asn Val															
	215	220	225												
gat ggc att tac gcc atc ggt gac gtg acc gcc aag ctt cag ctt gct	835														
Asp Gly Ile Tyr Ala Ile Gly Asp Val Thr Ala Lys Leu Gln Leu Ala															
	230	235	240	245											
cac gtc gca gaa gca cag ggc att gtt gcc gca gag act att gct ggt	883														
His Val Ala Glu Ala Gln Gly Ile Val Ala Ala Glu Thr Ile Ala Gly															
	250	255	260												
gca gaa act cag act ctt ggt gat tac atg atg atg cca cgt gca acc	931														
Ala Glu Thr Gln Thr Leu Gly Asp Tyr Met Met Met Pro Arg Ala Thr															
	265	270	275												
ttc tgc aac cca cag gtt tct tcc ttt ggt tac acc gaa gag cag gcc	979														
Phe Cys Asn Pro Gln Val Ser Ser Phe Gly Tyr Thr Glu Glu Gln Ala															
	280	285	290												
aag gag aag tgg cca gat cgt gag atc aag gtt gct tcc ttc cca ttc															
1027															
Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val Ala Ser Phe Pro Phe															
	295	300	305												
tct gca aac ggt aaa gca gtt ggc ctg gca gaa act gat ggt ttc gca															
1075															
Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu Thr Asp Gly Phe Ala															
	310	315	320	325											
aag atc gtt gct gat gca gaa ttc ggt gag ctg ctc ggt gca cac ctg															
1123															
Lys Ile Val Ala Asp Ala Glu Phe Gly Glu Leu Leu Gly Ala His Leu															
	330	335	340												

gtt gga gca aat gca tca gag ctc atc aat gaa ttg gtg ctt gct cag
1171

Val Gly Ala Asn Ala Ser Glu Leu Ile Asn Glu Leu Val Leu Ala Gln
345 350 355

aac tgg gat ctc acc act gaa gag atc tct cgt agc gtc cat att cac
1219

Asn Trp Asp Leu Thr Thr Glu Glu Ile Ser Arg Ser Val His Ile His
360 365 370

cca acg cta tct gag gca gtt aag gaa gct gca cac ggt atc tct gga
1267

Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala His Gly Ile Ser Gly
375 380 385

cac atg atc aac ttc tagaatccac ctcgttggcc ctg
1305

His Met Ile Asn Phe
390

<210> 670

<211> 394

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 670

Val Thr Phe Asn Tyr Glu Asp Ala His Lys Arg Ser Arg Gly Val Ser
1 5 10 15

Asp Lys Ile Val Gly Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile
20 25 30

Ile Glu Ile His Gly Leu Gly Asn Phe Lys Asp Ala Lys Thr Leu Glu
35 40 45

Val Thr Asp Gly Lys Asp Ala Gly Lys Thr Ile Thr Phe Asp Asp Cys
50 55 60

Ile Ile Ala Thr Gly Ser Val Val Asn Thr Leu Arg Gly Val Asp Phe
65 70 75 80

Ser Glu Asn Val Val Ser Phe Glu Glu Gln Ile Leu Asn Pro Val Ala
85 90 95

Pro Lys Lys Met Val Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe
100 105 110

Ala Tyr Val Leu Gly Asn Tyr Gly Val Asp Val Thr Val Ile Glu Phe
115 120 125

Met Asp Arg Val Leu Pro Asn Glu Asp Ala Glu Val Ser Lys Val Ile
130 135 140

Ala Lys Ala Tyr Lys Lys Met Gly Val Lys Leu Leu Pro Gly His Ala
145 150 155 160

Thr Thr Ala Val Arg Asp Asn Gly Asp Phe Val Glu Val Asp Tyr Gln
165 170 175

Lys Lys Gly Ser Asp Lys Thr Glu Thr Leu Thr Val Asp Arg Val Met

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<210> 671
<211> 294
<212> DNA
<213> Corynebacterium glutamicum.
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<220>  
<221> CDS  
<222> (101)..(271)  
<223> RXS01261
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<400> 671
gtgggtgttt ttcattttct tccactctaa aattaagtat ggaaaaccaa ccgcacccgg 60
atgcacgaca atgaccact aaacacgtat ctttgaatgc gtg act gaa cat tat 115
                                     Val Thr Glu His Tyr
                                     1                               5
gac gta gta gta ctc gga gcc ggc ccc ggt ggc tat gtc tcc gcc atc 163
Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly Tyr Val Ser Ala Ile

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10	15	20	
cgt gca gcg cag ctt ggc aag aag gtt gct gta att gag aag cag tac			211
Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val Ile Glu Lys Gln Tyr			
25	30	35	
tgg ggt ggt gtt tgc cta aac gtg ggc tgc att cct tcc aaa gtc tct			259
Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile Pro Ser Lys Val Ser			
40	45	50	
gat caa aaa cgc tgaagttgcc cataccttta ccc			294
Asp Gln Lys Arg			
55			

<210> 672

<211> 57

<212> PRT

<213> Corynebacterium glutamicum

<400> 672

Val Thr Glu His Tyr Asp Val Val Val Leu Gly Ala Gly Pro Gly Gly	
1	5
10	15

Tyr Val Ser Ala Ile Arg Ala Ala Gln Leu Gly Lys Lys Val Ala Val	
20	25
30	

Ile Glu Lys Gln Tyr Trp Gly Gly Val Cys Leu Asn Val Gly Cys Ile	
35	40
45	

Pro Ser Lys Val Ser Asp Gln Lys Arg	
50	55

<210> 673

<211> 1005

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(982)

<223> RXA02717

<400> 673

agggcatgtcc ctaacgaaca tcccagcctc atctcaatgg gcaattagcg acgttttgaa 60

gcgtccttca cccggccgag tacctttttc tgtcgagttt atg cca ccc cgc gac	115
Met Pro Pro Arg Asp	
1	5

gat gca gct gaa gag cgt ctt tac cgc gca gca gag gtc ttc cat gac	163
Asp Ala Ala Glu Glu Arg Leu Tyr Arg Ala Ala Glu Val Phe His Asp	
10	15
20	

ctc ggt gca tcg ttt gtc tcc gtg act tat ggt gct ggc gga tca acc	211
Leu Gly Ala Ser Phe Val Ser Val Thr Tyr Gly Ala Gly Gly Ser Thr	
25	30
35	

cgt gag aga acc tca cgt att gct cga cga tta gcg aaa caa ccg ttg	259
Arg Glu Arg Thr Ser Arg Ile Ala Arg Arg Leu Ala Lys Gln Pro Leu	

40	45	50	
acc act ctg gtg cac ctg acc ctg gtt aac cac act cgc gaa gag atg Thr Thr Leu Val His Leu Thr Leu Val Asn His Thr Arg Glu Glu Met 55 60 65	307		
aag gca att ctt cgg gaa tac cta gag ctg gga tta aca aac ctg ttg Lys Ala Ile Leu Arg Glu Tyr Leu Glu Leu Gly Leu Thr Asn Leu Leu 70 75 80 85	355		
gcg ctt cga gga gat ccg cct gga gac cca tta ggc gat tgg gtg agc Ala Leu Arg Gly Asp Pro Pro Gly Asp Pro Leu Gly Asp Trp Val Ser 90 95 100	403		
acc gat gga gga ctg aac tat gcc tct gag ctc atc gat ctt att aag Thr Asp Gly Gly Leu Asn Tyr Ala Ser Glu Leu Ile Asp Leu Ile Lys 105 110 115	451		
tcc act cct gag ttc cgg gaa ttc gac ctc ggt atc gcc tcc ttc ccc Ser Thr Pro Glu Phe Arg Glu Phe Asp Leu Gly Ile Ala Ser Phe Pro 120 125 130	499		
gaa ggg cat ttc cgg gcg aaa act cta gaa gaa gac acc aaa tac act Glu Gly His Phe Arg Ala Lys Thr Leu Glu Glu Asp Thr Lys Tyr Thr 135 140 145	547		
ctg gcg aag ctg cgt gga ggg gca gag tac tcc atc acg cag atg ttc Leu Ala Lys Leu Arg Gly Gly Ala Glu Tyr Ser Ile Thr Gln Met Phe 150 155 160 165	595		
ttt gat gtg gaa gac tac ctg cga ctt cgt gat cgc ctt gtc gct gca Phe Asp Val Glu Asp Tyr Leu Arg Leu Arg Asp Arg Leu Val Ala Ala 170 175 180	643		
gac ccc att cat ggt gcg aag cca atc att cct ggc atc atg ccc att Asp Pro Ile His Gly Ala Lys Pro Ile Ile Pro Gly Ile Met Pro Ile 185 190 195	691		
acg agc ctg cgg tct gtg cgt cga cag gtc gaa ctc tct ggt gct caa Thr Ser Leu Arg Ser Val Arg Arg Gln Val Glu Leu Ser Gly Ala Gln 200 205 210	739		
ttg ccg agc caa cta gaa gaa tca ctt gtt cga gct gca aac ggc aat Leu Pro Ser Gln Leu Glu Glu Ser Leu Val Arg Ala Ala Asn Gly Asn 215 220 225	787		
gaa gaa gcg aac aaa gac gag atc cgc aag gtg ggc att gaa tat tcc Glu Glu Ala Asn Lys Asp Glu Ile Arg Lys Val Gly Ile Glu Tyr Ser 230 235 240 245	835		
acc aat atg gca gag cga ctc att gcc gaa ggt gcg gaa gat ctg cac Thr Asn Met Ala Glu Arg Leu Ile Ala Glu Gly Ala Glu Asp Leu His 250 255 260	883		
ttc atg acg ctt aac ttc acc cgt gca acc caa gaa gtg ttg tac aac Phe Met Thr Leu Asn Phe Thr Arg Ala Thr Gln Glu Val Leu Tyr Asn 265 270 275	931		
ctt ggc atg gcg cct gct tgg gga gca gag cac ggc caa gac gcg gtg Leu Gly Met Ala Pro Ala Trp Gly Ala Glu His Gly Gln Asp Ala Val 280 285 290	979		

cgt taagccctct taggaatcat gaa
 1005
 Arg

<210> 674
 <211> 294
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 674
 Met Pro Pro Arg Asp Asp Ala Ala Glu Glu Arg Leu Tyr Arg Ala Ala
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 Glu Val Phe His Asp Leu Gly Ala Ser Phe Val Ser Val Thr Tyr Gly
 20 25 30
 Ala Gly Gly Ser Thr Arg Glu Arg Thr Ser Arg Ile Ala Arg Arg Leu
 35 40 45
 Ala Lys Gln Pro Leu Thr Thr Leu Val His Leu Thr Leu Val Asn His
 50 55 60
 Thr Arg Glu Glu Met Lys Ala Ile Leu Arg Glu Tyr Leu Glu Leu Gly
 65 70 75 80
 Leu Thr Asn Leu Leu Ala Leu Arg Gly Asp Pro Pro Gly Asp Pro Leu
 85 90 95
 Gly Asp Trp Val Ser Thr Asp Gly Gly Leu Asn Tyr Ala Ser Glu Leu
 100 105 110
 Ile Asp Leu Ile Lys Ser Thr Pro Glu Phe Arg Glu Phe Asp Leu Gly
 115 120 125
 Ile Ala Ser Phe Pro Glu Gly His Phe Arg Ala Lys Thr Leu Glu Glu
 130 135 140
 Asp Thr Lys Tyr Thr Leu Ala Lys Leu Arg Gly Gly Ala Glu Tyr Ser
 145 150 155 160
 Ile Thr Gln Met Phe Phe Asp Val Glu Asp Tyr Leu Arg Leu Arg Asp
 165 170 175
 Arg Leu Val Ala Ala Asp Pro Ile His Gly Ala Lys Pro Ile Ile Pro
 180 185 190
 Gly Ile Met Pro Ile Thr Ser Leu Arg Ser Val Arg Arg Gln Val Glu
 195 200 205
 Leu Ser Gly Ala Gln Leu Pro Ser Gln Leu Glu Glu Ser Leu Val Arg
 210 215 220
 Ala Ala Asn Gly Asn Glu Glu Ala Asn Lys Asp Glu Ile Arg Lys Val
 225 230 235 240
 Gly Ile Glu Tyr Ser Thr Asn Met Ala Glu Arg Leu Ile Ala Glu Gly
 245 250 255

Ala Glu Asp Leu His Phe Met Thr Leu Asn Phe Thr Arg Ala Thr Gln
 260 265 270

Glu Val Leu Tyr Asn Leu Gly Met Ala Pro Ala Trp Gly Ala Glu His
 275 280 285

Gly Gln Asp Ala Val Arg
 290

<210> 675

<211> 601

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(601)

<223> RXN02027

<400> 675

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tcgtcgtacc cctccgaaaa taacgggttat ccttagattt atg agc caa act aag 115
 Met Ser Gln Thr Lys
 1 5

cag gaa ctg cgc acg aag ctt cgg gaa gcg cgc acc aat atg gat gag 163
 Gln Glu Leu Arg Thr Lys Leu Arg Glu Ala Arg Thr Asn Met Asp Glu
 10 15 20

gct tct cgc acg cga gaa aac gca gcc atc att gcc aac gtt tct tat 211
 Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile Ala Asn Val Ser Tyr
 25 30 35

tac atc cgc tca aag cag cca aaa agg att gcc gct tac gtg ccg gtg 259
 Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala Ala Tyr Val Pro Val
 40 45 50

cgt acc gaa cct ggt ggg cga ttg ctt ctt gac gcc ctc cac gcc gaa 307
 Arg Thr Glu Pro Gly Gly Arg Leu Leu Leu Asp Ala Leu His Ala Glu
 55 60 65

act tcc gcg ctt att ttg cca gtc tcc ctc gag gat cga cgc ctc gac 355
 Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu Asp Arg Arg Leu Asp
 70 75 80 85

tgg gct ctt tat gaa ggc cca acc agc ctt gtt cct ggc gca ttt ggc 403
 Trp Ala Leu Tyr Glu Gly Pro Thr Ser Leu Val Pro Gly Ala Phe Gly
 90 95 100

atc cag gaa ccc ggt ggc act cgc ctt gga cct gaa gct ctc aac ttc 451
 Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro Glu Ala Leu Asn Phe
 105 110 115

tgc gac ctt gtc atc gcc ccc gca ctg gca tgc acc ccc agt gga atc 499
 Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys Thr Pro Ser Gly Ile
 120 125 130

agg cta ggt aaa ggt ggc ggt ttc tac gac cgc gct cta gcc acc gga 547
 Arg Leu Gly Lys Gly Gly Gly Phe Tyr Asp Arg Ala Leu Ala Thr Gly

135 140 145
 gtc aag gct gac gtg att act ttg ctc ttc aac gga gaa atc cgc gac 595
 Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn Gly Glu Ile Arg Asp
 150 155 160 165

 gat atc 601
 Asp Ile

<210> 676
 <211> 167
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 676
 Met Ser Gln Thr Lys Gln Glu Leu Arg Thr Lys Leu Arg Glu Ala Arg
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 Thr Asn Met Asp Glu Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile
 20 25 30
 Ala Asn Val Ser Tyr Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala
 35 40 45
 Ala Tyr Val Pro Val Arg Thr Glu Pro Gly Gly Arg Leu Leu Leu Asp
 50 55 60
 Ala Leu His Ala Glu Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu
 65 70 75 80
 Asp Arg Arg Leu Asp Trp Ala Leu Tyr Glu Gly Pro Thr Ser Leu Val
 85 90 95
 Pro Gly Ala Phe Gly Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro
 100 105 110
 Glu Ala Leu Asn Phe Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys
 115 120 125
 Thr Pro Ser Gly Ile Arg Leu Gly Lys Gly Gly Gly Phe Tyr Asp Arg
 130 135 140
 Ala Leu Ala Thr Gly Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn
 145 150 155 160
 Gly Glu Ile Arg Asp Asp Ile
 165

<210> 677
 <211> 595
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(595)
 <223> FRXA02027

<400> 677

tcacgtgctc atcgataggc aaactcatgg aaccaagagt acctgcccc gcaaccccaa 60

tcgtcgtagc cctccgaaaa taacgggttat ccttagatatt atg agc caa act aag 115
 Met Ser Gln Thr Lys
 1 5

cag gaa ctg cgc acg aag ctt cgg gaa gcg cgc acc aat atg gat gag 163
 Gln Glu Leu Arg Thr Lys Leu Arg Glu Ala Arg Thr Asn Met Asp Glu
 10 15 20

gct tct cgc acg cga gaa aac gca gcc atc att gcc aac gtt tct tat 211
 Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile Ala Asn Val Ser Tyr
 25 30 35

tac atc cgc tca aag cag cca aaa agg att gcc gct tac gtg cgc gtg 259
 Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala Ala Tyr Val Pro Val
 40 45 50

cgt acc gaa cct ggt ggg cga ttg ctt ctt gac gcc ctc cac gcc gaa 307
 Arg Thr Glu Pro Gly Gly Arg Leu Leu Leu Asp Ala Leu His Ala Glu
 55 60 65

act tcc gcg ctt att ttg cca gtc tcc ctc gag gat cga cgc ctc gac 355
 Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu Asp Arg Arg Leu Asp
 70 75 80 85

tgg gct ctt tat gaa ggc cca acc agc ctt gtt cct ggc gca ttt ggc 403
 Trp Ala Leu Tyr Glu Gly Pro Thr Ser Leu Val Pro Gly Ala Phe Gly
 90 95 100

atc cag gaa ccc ggt ggc act cgc ctt gga cct gaa gct ctc aac ttc 451
 Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro Glu Ala Leu Asn Phe
 105 110 115

tgc gac ctt gtc atc gcc ccc gca ctg gca tgc acc ccc agt gga atc 499
 Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys Thr Pro Ser Gly Ile
 120 125 130

agg cta ggt aaa ggt ggc ggt ttc tac gac cgc gct cta gcc acc gga 547
 Arg Leu Gly Lys Gly Gly Gly Phe Tyr Asp Arg Ala Leu Ala Thr Gly
 135 140 145

gtc aag gct gac gtg att act ttg ctc ttc aac gga gaa atc cgc gac 595
 Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn Gly Glu Ile Arg Asp
 150 155 160 165

<210> 678

<211> 165

<212> PRT

<213> Corynebacterium glutamicum

<400> 678

Met Ser Gln Thr Lys Gln Glu Leu Arg Thr Lys Leu Arg Glu Ala Arg
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Thr Asn Met Asp Glu Ala Ser Arg Thr Arg Glu Asn Ala Ala Ile Ile
 20 25 30

Ala Asn Val Ser Tyr Tyr Ile Arg Ser Lys Gln Pro Lys Arg Ile Ala

35	40	45
Ala Tyr Val Pro Val Arg Thr Glu Pro Gly Gly Arg Leu Leu Leu Asp		
50	55	60
Ala Leu His Ala Glu Thr Ser Ala Leu Ile Leu Pro Val Ser Leu Glu		
65	70	75
Asp Arg Arg Leu Asp Trp Ala Leu Tyr Glu Gly Pro Thr Ser Leu Val		
85	90	95
Pro Gly Ala Phe Gly Ile Gln Glu Pro Gly Gly Thr Arg Leu Gly Pro		
100	105	110
Glu Ala Leu Asn Phe Cys Asp Leu Val Ile Ala Pro Ala Leu Ala Cys		
115	120	125
Thr Pro Ser Gly Ile Arg Leu Gly Lys Gly Gly Gly Phe Tyr Asp Arg		
130	135	140
Ala Leu Ala Thr Gly Val Lys Ala Asp Val Ile Thr Leu Leu Phe Asn		
145	150	155
Gly Glu Ile Arg Asp		
165		

<210> 679

<211> 579

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(556)

<223> RXA00106

<400> 679

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gctacgatcc acaccattg atccgcggca aggtcgccgt atg atc ggt gcg att	115
	Met Ile Gly Ala Ile
	1 5
tgg gca caa ggc cgt gac ggc atc atc ggc gac ggc acc gac atg ccc	163
Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp Gly Thr Asp Met Pro	
	10 15 20
tgg cac atc ccg gaa gac ctc aaa cac ttc aag aaa acc acc atg ggc	211
Trp His Ile Pro Glu Asp Leu Lys His Phe Lys Lys Thr Thr Met Gly	
	25 30 35
cag ccg gtc atc atg ggt cgt cgc acg tgg gag tct ttg ccg ttc aag	259
Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu Ser Leu Pro Phe Lys	
	40 45 50
ccg ctt ccc ggc cgc gag aac ttc att ctc tcc tca cgc gag ccc ggc	307
Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser Ser Arg Glu Pro Gly	
	55 60 65
gac tgg tcc gcc ggc ggc aca gtg gtc acc gaa atc cct aaa agc ggc	355

Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu Ile Pro Lys Ser Gly
 70 75 80 85
 tgg atc atg ggc ggc ggc gag gtc tac aag gcc acc gtc ggc agc gcc 403
 Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala Thr Val Gly Ser Ala
 90 95 100
 gac gtt tta gaa ata acg ctt atc gac gcc acc ttc gat gtt tcc act 451
 Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr Phe Asp Val Ser Thr
 105 110 115
 ccc gtc tac gca ccc gaa atc ccg gcg aac ttc aac ctc gat gac gaa 499
 Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe Asn Leu Asp Asp Glu
 120 125 130
 tcc gag tgg ttt acc tca ggc gag tat cgt tac aag ttc cag cgc tac 547
 Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr Lys Phe Gln Arg Tyr
 135 140 145
 atc aag gtt taaggagcaa acaacatgag caa 579
 Ile Lys Val
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<210> 680

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 680

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 Gly Thr Asp Met Pro Trp His Ile Pro Glu Asp Leu Lys His Phe Lys
 20 25 30
 Lys Thr Thr Met Gly Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu
 35 40 45
 Ser Leu Pro Phe Lys Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser
 50 55 60
 Ser Arg Glu Pro Gly Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu
 65 70 75 80
 Ile Pro Lys Ser Gly Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala
 85 90 95
 Thr Val Gly Ser Ala Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr
 100 105 110
 Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe
 115 120 125
 Asn Leu Asp Asp Glu Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr
 130 135 140
 Lys Phe Gln Arg Tyr Ile Lys Val
 145 150

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<222> (101)..(1021)
<223> RXN01321
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							Met	Gln	Arg	Met	Thr					
							1				5					
ccg	agt	tct	cct	gaa	gtt	cgt	aat	cgt	ccg	agc	gct	gcg	cct	gaa	gag	163
Pro	Ser	Ser	Pro	Glu	Val	Arg	Asn	Arg	Pro	Ser	Ala	Ala	Pro	Glu	Glu	
				10					15					20		
cgt	cag	ttt	gtg	ctc	act	ttt	ggc	tgc	cct	gac	tcc	act	gga	att	gtg	211
Arg	Gln	Phe	Val	Leu	Thr	Phe	Gly	Cys	Pro	Asp	Ser	Thr	Gly	Ile	Val	
				25					30					35		
gcg	aag	ttg	tcg	tcg	ttc	cta	gct	gag	cgt	ggg	ggg	tgg	att	act	gag	259
Ala	Lys	Leu	Ser	Ser	Phe	Leu	Ala	Glu	Arg	Gly	Gly	Trp	Ile	Thr	Glu	
				40					45					50		
gct	gga	tat	ttc	acg	gat	cct	gat	tcg	aat	tgg	ttc	ttt	act	cgt	cag	307
Ala	Gly	Tyr	Phe	Thr	Asp	Pro	Asp	Ser	Asn	Trp	Phe	Phe	Thr	Arg	Gln	
				55					60					65		
gcg	att	cgc	gct	gag	tcg	att	gat	acc	acg	att	gag	cag	ttg	cgg	gag	355
Ala	Ile	Arg	Ala	Glu	Ser	Ile	Asp	Thr	Thr	Ile	Glu	Gln	Leu	Arg	Glu	
				70					75					80	85	
gag	ttc	gct	ccg	ctt	gcg	gag	gag	ttc	ggc	ccg	agg	gct	aag	tgg	agt	403
Glu	Phe	Ala	Pro	Leu	Ala	Glu	Glu	Phe	Gly	Pro	Arg	Ala	Lys	Trp	Ser	
				90					95					100		
ttc	act	gac	act	gcg	cag	gtg	aag	aag	gct	gtg	ttg	ttg	gtg	tct	aag	451
Phe	Thr	Asp	Thr	Ala	Gln	Val	Lys	Lys	Ala	Val	Leu	Leu	Val	Ser	Lys	
				105					110					115		
gag	ggc	cac	tgc	ttg	cac	gat	ttg	tta	ggt	cgt	gtg	gct	gag	aat	gat	499
Glu	Gly	His	Cys	Leu	His	Asp	Leu	Leu	Gly	Arg	Val	Ala	Glu	Asn	Asp	
				120					125					130		
tat	ccg	atg	gaa	gtt	gtt	gcg	gtt	gtg	ggt	aac	cat	gag	aac	ttg	cgt	547
Tyr	Pro	Met	Glu	Val	Val	Ala	Val	Val	Gly	Asn	His	Glu	Asn	Leu	Arg	
				135					140					145		
tat	att	gcg	gag	aac	cat	aat	gtt	ccg	ttt	ttc	cat	gtg	ccg	ttt	cct	595
Tyr	Ile	Ala	Glu	Asn	His	Asn	Val	Pro	Phe	Phe	His	Val	Pro	Phe	Pro	
				150					155					160	165	
aag	gat	gcg	gtt	ggt	aag	cgg	aag	gcg	ttt	gac	cag	gtc	gct	gag	att	643
Lys	Asp	Ala	Val	Gly	Lys	Arg	Lys	Ala	Phe	Asp	Gln	Val	Ala	Glu	Ile	
				170					175					180		

gtg aat ggt tat gat ccg gat gcg att gtt ttg gct cgt ttt atg cag 691
 Val Asn Gly Tyr Asp Pro Asp Ala Ile Val Leu Ala Arg Phe Met Gln
 185 190 195

att ttg ccg ccg gat ttg tgt gag atg tgg gct ggt cgt gtg ttg aat 739
 Ile Leu Pro Pro Asp Leu Cys Glu Met Trp Ala Gly Arg Val Leu Asn
 200 205 210

att cat cac agt ttc ttg ccg tcg ttt atg ggt gcg cgc ccg tat cat 787
 Ile His His Ser Phe Leu Pro Ser Phe Met Gly Ala Arg Pro Tyr His
 215 220 225

cag gcg tat agc cgt ggt gtg aag ttg att ggt gcg acc tgc cat tat 835
 Gln Ala Tyr Ser Arg Gly Val Lys Leu Ile Gly Ala Thr Cys His Tyr
 230 235 240 245

gcg act ggg gat ctg gat gat ggt ccg atc att gag cag gat gtt att 883
 Ala Thr Gly Asp Leu Asp Asp Gly Pro Ile Ile Glu Gln Asp Val Ile
 250 255 260

cgt gtg acg cat aag gat acg ccg act gag atg cag cgt ttg ggc cgc 931
 Arg Val Thr His Lys Asp Thr Pro Thr Glu Met Gln Arg Leu Gly Arg
 265 270 275

gat gcg gag aag cag gtg ctg gct cgc ggt ttg cgt ttc cac ttg gag 979
 Asp Ala Glu Lys Gln Val Leu Ala Arg Gly Leu Arg Phe His Leu Glu
 280 285 290

gac cgg gtg ctg gtt tac ggt aac cgc acg gtt gtc ttt gat
 1021
 Asp Arg Val Leu Val Tyr Gly Asn Arg Thr Val Val Phe Asp
 295 300 305

taaggctttt tgcttttcga cgc
 1044

<210> 682

<211> 307

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 682

Met Gln Arg Met Thr Pro Ser Ser Pro Glu Val Arg Asn Arg Pro Ser
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Ala Ala Pro Glu Glu Arg Gln Phe Val Leu Thr Phe Gly Cys Pro Asp
 20 25 30

Ser Thr Gly Ile Val Ala Lys Leu Ser Ser Phe Leu Ala Glu Arg Gly
 35 40 45

Gly Trp Ile Thr Glu Ala Gly Tyr Phe Thr Asp Pro Asp Ser Asn Trp
 50 55 60

Phe Phe Thr Arg Gln Ala Ile Arg Ala Glu Ser Ile Asp Thr Thr Ile
 65 70 75 80

Glu Gln Leu Arg Glu Glu Phe Ala Pro Leu Ala Glu Glu Phe Gly Pro
 85 90 95

Arg Ala Lys Trp Ser Phe Thr Asp Thr Ala Gln Val Lys Lys Ala Val
 100 105 110
 Leu Leu Val Ser Lys Glu Gly His Cys Leu His Asp Leu Leu Gly Arg
 115 120 125
 Val Ala Glu Asn Asp Tyr Pro Met Glu Val Val Ala Val Val Gly Asn
 130 135 140
 His Glu Asn Leu Arg Tyr Ile Ala Glu Asn His Asn Val Pro Phe Phe
 145 150 155 160
 His Val Pro Phe Pro Lys Asp Ala Val Gly Lys Arg Lys Ala Phe Asp
 165 170 175
 Gln Val Ala Glu Ile Val Asn Gly Tyr Asp Pro Asp Ala Ile Val Leu
 180 185 190
 Ala Arg Phe Met Gln Ile Leu Pro Pro Asp Leu Cys Glu Met Trp Ala
 195 200 205
 Gly Arg Val Leu Asn Ile His His Ser Phe Leu Pro Ser Phe Met Gly
 210 215 220
 Ala Arg Pro Tyr His Gln Ala Tyr Ser Arg Gly Val Lys Leu Ile Gly
 225 230 235 240
 Ala Thr Cys His Tyr Ala Thr Gly Asp Leu Asp Asp Gly Pro Ile Ile
 245 250 255
 Glu Gln Asp Val Ile Arg Val Thr His Lys Asp Thr Pro Thr Glu Met
 260 265 270
 Gln Arg Leu Gly Arg Asp Ala Glu Lys Gln Val Leu Ala Arg Gly Leu
 275 280 285
 Arg Phe His Leu Glu Asp Arg Val Leu Val Tyr Gly Asn Arg Thr Val
 290 295 300
 Val Phe Asp
 305

<210> 683

<211> 582

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (23)..(559)

<223> FRXA01321

<400> 683

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 Val Ala Glu Asn Asp Tyr Pro Met Glu Val
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 gtt gcg gtt gtg ggt aac cat gag aac ttg cgt tat att gcg gag aac 100
 Val Ala Val Val Gly Asn His Glu Asn Leu Arg Tyr Ile Ala Glu Asn
 15 20 25

cat aat gtt ccg ttt ttc cat gtg ccg ttt cct aag gat gcg gtt ggt 148
 His Asn Val Pro Phe Phe His Val Pro Phe Pro Lys Asp Ala Val Gly
 30 35 40

aag cgg aag gcg ttt gac cag gtc gct gag att gtg aat ggt tat gat 196
 Lys Arg Lys Ala Phe Asp Gln Val Ala Glu Ile Val Asn Gly Tyr Asp
 45 50 55

ccg gat gcg att gtt ttg gct cgt ttt atg cag att ttg ccg ccg gat 244
 Pro Asp Ala Ile Val Leu Ala Arg Phe Met Gln Ile Leu Pro Pro Asp
 60 65 70

ttg tgt gag atg tgg gct ggt cgt gtg ttg aat att cat cac agt ttc 292
 Leu Cys Glu Met Trp Ala Gly Arg Val Leu Asn Ile His His Ser Phe
 75 80 85 90

ttg ccg tcg ttt atg ggt gcg cgc ccg tat cat cag gcg tat agc cgt 340
 Leu Pro Ser Phe Met Gly Ala Arg Pro Tyr His Gln Ala Tyr Ser Arg
 95 100 105

ggt gtg aag ttg att ggt gcg acc tgc cat tat gcg act ggg gat ctg 388
 Gly Val Lys Leu Ile Gly Ala Thr Cys His Tyr Ala Thr Gly Asp Leu
 110 115 120

gat gat ggt ccg atc att gag cag gat gtt att cgt gtg acg cat aag 436
 Asp Asp Gly Pro Ile Ile Glu Gln Asp Val Ile Arg Val Thr His Lys
 125 130 135

gat acg ccg act gag atg cag cgt ttg ggc cgc gat gcg gag aag cag 484
 Asp Thr Pro Thr Glu Met Gln Arg Leu Gly Arg Asp Ala Glu Lys Gln
 140 145 150

gtg ctg gct cgc ggt ttg cgt ttc cac ttg gag gac cgg gtg ctg gtt 532
 Val Leu Ala Arg Gly Leu Arg Phe His Leu Glu Asp Arg Val Leu Val
 155 160 165 170

tac ggt aac cgc acg gtt gtc ttt gat taaggctttt tgcttttcga 579
 Tyr Gly Asn Arg Thr Val Val Phe Asp
 175

cgc 582

<210> 684

<211> 179

<212> PRT

<213> Corynebacterium glutamicum

<400> 684

Val Ala Glu Asn Asp Tyr Pro Met Glu Val Val Ala Val Val Gly Asn
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His Glu Asn Leu Arg Tyr Ile Ala Glu Asn His Asn Val Pro Phe Phe
 20 25 30

His Val Pro Phe Pro Lys Asp Ala Val Gly Lys Arg Lys Ala Phe Asp
 35 40 45

Gln Val Ala Glu Ile Val Asn Gly Tyr Asp Pro Asp Ala Ile Val Leu
 50 55 60

Ala Arg Phe Met Gln Ile Leu Pro Pro Asp Leu Cys Glu Met Trp Ala
65 70 75 80

Gly Arg Val Leu Asn Ile His His Ser Phe Leu Pro Ser Phe Met Gly
85 90 95

Ala Arg Pro Tyr His Gln Ala Tyr Ser Arg Gly Val Lys Leu Ile Gly
100 105 110

Ala Thr Cys His Tyr Ala Thr Gly Asp Leu Asp Asp Gly Pro Ile Ile
115 120 125

Glu Gln Asp Val Ile Arg Val Thr His Lys Asp Thr Pro Thr Glu Met
130 135 140

Gln Arg Leu Gly Arg Asp Ala Glu Lys Gln Val Leu Ala Arg Gly Leu
145 150 155 160

Arg Phe His Leu Glu Asp Arg Val Leu Val Tyr Gly Asn Arg Thr Val
165 170 175

Val Phe Asp

<210> 685
<211> 975
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(952)
<223> RXA00461

<400> 685
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tgattgtaag gccttggaag aggggtggaat aatagcgggc gtg act gca atc aaa 115
Val Thr Ala Ile Lys
1 5

ctt gat gga aac tta tac cgc ggg gaa att ttc gcc gac ttg gaa cag 163
Leu Asp Gly Asn Leu Tyr Arg Gly Glu Ile Phe Ala Asp Leu Glu Gln
10 15 20

cgc gtt gct gcg ttg aag gag aaa ggg att gtg ccg ggg ctt gcc acc 211
Arg Val Ala Ala Leu Lys Glu Lys Gly Ile Val Pro Gly Leu Ala Thr
25 30 35

gtg ctg gtg ggt gat gac cca gcg agc cac tct tac gtg aag atg aag 259
Val Leu Val Gly Asp Asp Pro Ala Ser His Ser Tyr Val Lys Met Lys
40 45 50

cat cgt gac tgt gag cag att ggt gtg aac tcg atc cgt aag gat ctg 307
His Arg Asp Cys Glu Gln Ile Gly Val Asn Ser Ile Arg Lys Asp Leu
55 60 65

cct gct gat gtc acg cag gaa gag ctt ttc gct gtc atc gat gaa ctg 355
Pro Ala Asp Val Thr Gln Glu Glu Leu Phe Ala Val Ile Asp Glu Leu

70	75	80	85	
aac aac gat gat tct tgc act ggt tac att gtg cag ctt cct ttg cct				403
Asn Asn Asp Asp Ser Cys Thr Gly Tyr Ile Val Gln Leu Pro Leu Pro				
	90	95	100	
aag cac ttg gac gaa aac gct gtg ctg gag cgc att gat cca gct aag				451
Lys His Leu Asp Glu Asn Ala Val Leu Glu Arg Ile Asp Pro Ala Lys				
	105	110	115	
gat gct gat ggc ctg cac cct gta aac ctg ggc aag ctt gtg ctc aac				499
Asp Ala Asp Gly Leu His Pro Val Asn Leu Gly Lys Leu Val Leu Asn				
	120	125	130	
gag cca gct cca ctg cca tgc acc ccg aat ggt tcc atc agc ttg ttg				547
Glu Pro Ala Pro Leu Pro Cys Thr Pro Asn Gly Ser Ile Ser Leu Leu				
	135	140	145	
cgt cgt ttc ggc gtt gag ctt gat ggc gcg aag gtt gtt gtc att ggc				595
Arg Arg Phe Gly Val Glu Leu Asp Gly Ala Lys Val Val Val Ile Gly				
	150	155	160	165
cgt ggc gtc acc gtt ggt cgc cca att ggc ctg atg ctg acc cgc cgt				643
Arg Gly Val Thr Val Gly Arg Pro Ile Gly Leu Met Leu Thr Arg Arg				
	170	175	180	
tcc gag aac tcc acg gtt act ttg tgc cac act ggc acg aag gat ctg				691
Ser Glu Asn Ser Thr Val Thr Leu Cys His Thr Gly Thr Lys Asp Leu				
	185	190	195	
gct gcg gag acc cgt gcg gct gac gtc atc att gct gca gct ggt cag				739
Ala Ala Glu Thr Arg Ala Ala Asp Val Ile Ile Ala Ala Ala Gly Gln				
	200	205	210	
ccg cac atg ctg acc gca gac atg gtc aag cca ggc gca gcg gtg ctc				787
Pro His Met Leu Thr Ala Asp Met Val Lys Pro Gly Ala Ala Val Leu				
	215	220	225	
gat gtc ggc gtc tcc cgc aag gac ggc aag ttg ctt ggc gac gtc cac				835
Asp Val Gly Val Ser Arg Lys Asp Gly Lys Leu Leu Gly Asp Val His				
	230	235	240	245
ccc gac gtg tgg gaa gtc gcc ggc gcg gtc tca cca aac cca ggc ggc				883
Pro Asp Val Trp Glu Val Ala Gly Ala Val Ser Pro Asn Pro Gly Gly				
	250	255	260	
gtt ggc cct ctg acc cgt gca ttc ttg gtg cac aat gtt gtc gag cgc				931
Val Gly Pro Leu Thr Arg Ala Phe Leu Val His Asn Val Val Glu Arg				
	265	270	275	
gct gaa aag ctg gct gga ctc taaaaacaca tgactaatcc cgg				975
Ala Glu Lys Leu Ala Gly Leu				
	280			

<210> 686

<211> 284

<212> PRT

<213> Corynebacterium glutamicum

<400> 686

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 Ala Asp Leu Glu Gln Arg Val Ala Ala Leu Lys Glu Lys Gly Ile Val
 20 25 30
 Pro Gly Leu Ala Thr Val Leu Val Gly Asp Asp Pro Ala Ser His Ser
 35 40 45
 Tyr Val Lys Met Lys His Arg Asp Cys Glu Gln Ile Gly Val Asn Ser
 50 55 60
 Ile Arg Lys Asp Leu Pro Ala Asp Val Thr Gln Glu Glu Leu Phe Ala
 65 70 75 80
 Val Ile Asp Glu Leu Asn Asn Asp Asp Ser Cys Thr Gly Tyr Ile Val
 85 90 95
 Gln Leu Pro Leu Pro Lys His Leu Asp Glu Asn Ala Val Leu Glu Arg
 100 105 110
 Ile Asp Pro Ala Lys Asp Ala Asp Gly Leu His Pro Val Asn Leu Gly
 115 120 125
 Lys Leu Val Leu Asn Glu Pro Ala Pro Leu Pro Cys Thr Pro Asn Gly
 130 135 140
 Ser Ile Ser Leu Leu Arg Arg Phe Gly Val Glu Leu Asp Gly Ala Lys
 145 150 155 160
 Val Val Val Ile Gly Arg Gly Val Thr Val Gly Arg Pro Ile Gly Leu
 165 170 175
 Met Leu Thr Arg Arg Ser Glu Asn Ser Thr Val Thr Leu Cys His Thr
 180 185 190
 Gly Thr Lys Asp Leu Ala Ala Glu Thr Arg Ala Ala Asp Val Ile Ile
 195 200 205
 Ala Ala Ala Gly Gln Pro His Met Leu Thr Ala Asp Met Val Lys Pro
 210 215 220
 Gly Ala Ala Val Leu Asp Val Gly Val Ser Arg Lys Asp Gly Lys Leu
 225 230 235 240
 Leu Gly Asp Val His Pro Asp Val Trp Glu Val Ala Gly Ala Val Ser
 245 250 255
 Pro Asn Pro Gly Gly Val Gly Pro Leu Thr Arg Ala Phe Leu Val His
 260 265 270
 Asn Val Val Glu Arg Ala Glu Lys Leu Ala Gly Leu
 275 280

<210> 687

<211> 711

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(688)

<223> RXA01514

<400> 687

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gagggcacac aggagaatcc ggaaaatgaa ggagacaacc gtg gat aac cac gct 115
 Val Asp Asn His Ala
 1 5

gca gtt cgc gag ttc gat gag gag cgc gca aca gct gcg att cgt gag 163
 Ala Val Arg Glu Phe Asp Glu Glu Arg Ala Thr Ala Ala Ile Arg Glu
 10 15 20

ttg ctc atc gct gtg ggt gag gat cca gat cgc gaa ggc ctg ttg gaa 211
 Leu Leu Ile Ala Val Gly Glu Asp Pro Asp Arg Glu Gly Leu Leu Glu
 25 30 35

acc cca gct cga gtg gct agg gcg tac aag gaa act ttc gcg ggt ctg 259
 Thr Pro Ala Arg Val Ala Arg Ala Tyr Lys Glu Thr Phe Ala Gly Leu
 40 45 50

cat gag gat ccc acc act gtg ctg gag aag acg ttc tct gag ggc cat 307
 His Glu Asp Pro Thr Thr Val Leu Glu Lys Thr Phe Ser Glu Gly His
 55 60 65

gaa gag ttg gtt ctg gtt cgt gag atc ccg att tac tcc atg tgt gag 355
 Glu Glu Leu Val Leu Val Arg Glu Ile Pro Ile Tyr Ser Met Cys Glu
 70 75 80 85

cac cac ttg gtg ccg ttc ttt ggc gtg gcg cac att ggt tac att ccg 403
 His His Leu Val Pro Phe Phe Gly Val Ala His Ile Gly Tyr Ile Pro
 90 95 100

ggt aag tcc ggc aag gtg act ggc ctg tcc aag ctg gcg cgt tta gcg 451
 Gly Lys Ser Gly Lys Val Thr Gly Leu Ser Lys Leu Ala Arg Leu Ala
 105 110 115

gat atg ttt gct aag cga cct cag gtt cag gag cgc ttg acc tcc caa 499
 Asp Met Phe Ala Lys Arg Pro Gln Val Gln Glu Arg Leu Thr Ser Gln
 120 125 130

att gcg gat gct ctc gtc gaa aag ctt gat gcc cag gcc gtg gcc gtg 547
 Ile Ala Asp Ala Leu Val Glu Lys Leu Asp Ala Gln Ala Val Ala Val
 135 140 145

gtg att gaa gct gag cac ctg tgc atg gcc atg cgc gga atc cgt aag 595
 Val Ile Glu Ala Glu His Leu Cys Met Ala Met Arg Gly Ile Arg Lys
 150 155 160 165

cct ggt gct gtg acc acg acg tct gcg gtg cgc ggc ggt ttt aag aac 643
 Pro Gly Ala Val Thr Thr Thr Ser Ala Val Arg Gly Gly Phe Lys Asn
 170 175 180

aac gct gcc tcc cgc gct gag gtg ttc tcc ctg att cgg ggg cac 688
 Asn Ala Ala Ser Arg Ala Glu Val Phe Ser Leu Ile Arg Gly His
 185 190 195

taaataaacg tatectcttt gac 711

<210> 688
 <211> 196
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 688
 Val Asp Asn His Ala Ala Val Arg Glu Phe Asp Glu Glu Arg Ala Thr
 1 5 10 15
 Ala Ala Ile Arg Glu Leu Leu Ile Ala Val Gly Glu Asp Pro Asp Arg
 20 25 30
 Glu Gly Leu Leu Glu Thr Pro Ala Arg Val Ala Arg Ala Tyr Lys Glu
 35 40 45
 Thr Phe Ala Gly Leu His Glu Asp Pro Thr Thr Val Leu Glu Lys Thr
 50 55 60
 Phe Ser Glu Gly His Glu Glu Leu Val Leu Val Arg Glu Ile Pro Ile
 65 70 75 80
 Tyr Ser Met Cys Glu His His Leu Val Pro Phe Phe Gly Val Ala His
 85 90 95
 Ile Gly Tyr Ile Pro Gly Lys Ser Gly Lys Val Thr Gly Leu Ser Lys
 100 105 110
 Leu Ala Arg Leu Ala Asp Met Phe Ala Lys Arg Pro Gln Val Gln Glu
 115 120 125
 Arg Leu Thr Ser Gln Ile Ala Asp Ala Leu Val Glu Lys Leu Asp Ala
 130 135 140
 Gln Ala Val Ala Val Val Ile Glu Ala Glu His Leu Cys Met Ala Met
 145 150 155 160
 Arg Gly Ile Arg Lys Pro Gly Ala Val Thr Thr Thr Ser Ala Val Arg
 165 170 175
 Gly Gly Phe Lys Asn Asn Ala Ala Ser Arg Ala Glu Val Phe Ser Leu
 180 185 190
 Ile Arg Gly His
 195

<210> 689
 <211> 513
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
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 <222> (101)..(490)
 <223> RXA01516

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											Met	Ala	Asp	Arg	Ile	
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gaa ctt aaa ggc ctt gaa tgc ttc gga cac cac ggt gtg ttc gac ttt	163															
Glu Leu Lys Gly Leu Glu Cys Phe Gly His His Gly Val Phe Asp Phe																
10 15 20																
gaa aaa gag caa ggc cag ccc ttc att gtg gat gtc acc tgc tgg atg	211															
Glu Lys Glu Gln Gly Gln Pro Phe Ile Val Asp Val Thr Cys Trp Met																
25 30 35																
gat ttc gat gcc gca ggt gcc agc gat gac ctt tcc gac acc gta gat	259															
Asp Phe Asp Ala Ala Gly Ala Ser Asp Asp Leu Ser Asp Thr Val Asp																
40 45 50																
tac ggc gcg ttg gca ttg ttg gtt gct gaa atc gtg gaa ggc cca tcc	307															
Tyr Gly Ala Leu Ala Leu Leu Val Ala Glu Ile Val Glu Gly Pro Ser																
55 60 65																
agg gat ttg atc gag acg gtg gcc acg gaa tct gcg gat gct gtg atg	355															
Arg Asp Leu Ile Glu Thr Val Ala Thr Glu Ser Ala Asp Ala Val Met																
70 75 80 85																
gct aaa ttt gat gcg ctt cat gcg gtg gaa gta acc atc cat aag ccc	403															
Ala Lys Phe Asp Ala Leu His Ala Val Glu Val Thr Ile His Lys Pro																
90 95 100																
aaa gca ccg atc cca cgt act ttt gct gac gtc gcg gtg gtt gcc cga	451															
Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val Ala Val Val Ala Arg																
105 110 115																
cgt tcc agg aaa tcc atg gct gct gga agg agc aac gcc taatgcatgc	500															
Arg Ser Arg Lys Ser Met Ala Ala Gly Arg Ser Asn Ala																
120 125 130																
aqtttttqtcc atc	513															

Thr Ile His Lys Pro Lys Ala Pro Ile Pro Arg Thr Phe Ala Asp Val
 100 105 110

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 115 120 125

Asn Ala
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<210> 691

<211> 975

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(952)

<223> RXA01515

<400> 691

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ctcccgcgct gaggtgttct ccctgattcg ggggcactaa atg aac gta tcc tct 115
 Met Asn Val Ser Ser
 1 5

ttg acc atc ccg gga cgc tgt ttg gtc atg gga att gtc aat gtc act 163
 Leu Thr Ile Pro Gly Arg Cys Leu Val Met Gly Ile Val Asn Val Thr
 10 15 20

gag gat tcc ttt tcg gac ggt ggc aag tac att gac gtt gat cag gcg 211
 Glu Asp Ser Phe Ser Asp Gly Gly Lys Tyr Ile Asp Val Asp Gln Ala
 25 30 35

atc gcg cat gcc aag gaa ttg gtg gct gct ggc gcc gac atg att gat 259
 Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly Ala Asp Met Ile Asp
 40 45 50

gtc ggc ggc gag tcc acc cgg cct ggg gca gtg cgc gtc gac gcg tcc 307
 Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val Arg Val Asp Ala Ser
 55 60 65

gtg gaa cgg gac cgg gtt gtg ccg gtc att aag gcg ctt cac gac gcc 355
 Val Glu Arg Asp Arg Val Val Pro Val Ile Lys Ala Leu His Asp Ala
 70 75 80 85

ggc atc cac act tcc gta gac acc atg cgg gcc tcc gtg gcg cag gct 403
 Gly Ile His Thr Ser Val Asp Thr Met Arg Ala Ser Val Ala Gln Ala
 90 95 100

gcc gcg ggc gct ggc gtc tcc atg atc aac gac gtc tct ggc ggt ttg 451
 Ala Ala Gly Ala Gly Val Ser Met Ile Asn Asp Val Ser Gly Gly Leu
 105 110 115

gct gat cct gag atg ttt tct gtc atg gcg gaa gcg caa att ccc gtg 499
 Ala Asp Pro Glu Met Phe Ser Val Met Ala Glu Ala Gln Ile Pro Val
 120 125 130

tgt ttg atg cac tgg cgc acc ctc caa ttc ggt gat gcc gca ggt cag 547

Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly Asp Ala Ala Gly Gln
 135 140 145
 gca gat cac ggt gga gac gtt gta gcc gat gtg cac gca gtg ctt gat 595
 Ala Asp His Gly Gly Asp Val Val Ala Asp Val His Ala Val Leu Asp
 150 155 160 165
 gat ctt gtc gcc cgc gcc acc gct gct ggt gtg gcc gaa aac cag atc 643
 Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val Ala Glu Asn Gln Ile
 170 175 180
 gtg ctt gat cca ggt ttg ggt ttt gcc aaa tca cgt gaa gac aac tgg 691
 Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser Arg Glu Asp Asn Trp
 185 190 195
 cgt ttg ctg caa gca ctg ccc gag ttt att tct gga cct ttc ccc atc 739
 Arg Leu Leu Gln Ala Leu Pro Glu Phe Ile Ser Gly Pro Phe Pro Ile
 200 205 210
 ctg gtg gga gca tcc cgg aag cga ttc ctg gct ggc gtg cgc aaa gac 787
 Leu Val Gly Ala Ser Arg Lys Arg Phe Leu Ala Gly Val Arg Lys Asp
 215 220 225
 cgt ggc cta gat gtc acc ccc att gat gcc gac cca gca acc gca gcg 835
 Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp Pro Ala Thr Ala Ala
 230 235 240 245
 gtg acc gca gtg tct gca cat atg gga gca tgg ggt gtg cgc gtg cac 883
 Val Thr Ala Val Ser Ala His Met Gly Ala Trp Gly Val Arg Val His
 250 255 260
 gat gtc cca gta tca agg gac gct gtt gat gtt gcc gca ttg tgg cga 931
 Asp Val Pro Val Ser Arg Asp Ala Val Asp Val Ala Ala Leu Trp Arg
 265 270 275
 agt gga gga act cac cat ggc tgatcgtatt gaacttaaag gcc 975
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<210> 692

<211> 284

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 692

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 Asp Val Asp Gln Ala Ile Ala His Ala Lys Glu Leu Val Ala Ala Gly
 35 40 45
 Ala Asp Met Ile Asp Val Gly Gly Glu Ser Thr Arg Pro Gly Ala Val
 50 55 60
 Arg Val Asp Ala Ser Val Glu Arg Asp Arg Val Val Pro Val Ile Lys
 65 70 75 80

Ala Leu His Asp Ala Gly Ile His Thr Ser Val Asp Thr Met Arg Ala
85 90 95

Ser Val Ala Gln Ala Ala Ala Gly Ala Gly Val Ser Met Ile Asn Asp
100 105 110

Val Ser Gly Gly Leu Ala Asp Pro Glu Met Phe Ser Val Met Ala Glu
115 120 125

Ala Gln Ile Pro Val Cys Leu Met His Trp Arg Thr Leu Gln Phe Gly
130 135 140

Asp Ala Ala Gly Gln Ala Asp His Gly Gly Asp Val Val Ala Asp Val
145 150 155 160

His Ala Val Leu Asp Asp Leu Val Ala Arg Ala Thr Ala Ala Gly Val
165 170 175

Ala Glu Asn Gln Ile Val Leu Asp Pro Gly Leu Gly Phe Ala Lys Ser
180 185 190

Arg Glu Asp Asn Trp Arg Leu Leu Gln Ala Leu Pro Glu Phe Ile Ser
195 200 205

Gly Pro Phe Pro Ile Leu Val Gly Ala Ser Arg Lys Arg Phe Leu Ala
210 215 220

Gly Val Arg Lys Asp Arg Gly Leu Asp Val Thr Pro Ile Asp Ala Asp
225 230 235 240

Pro Ala Thr Ala Ala Val Thr Ala Val Ser Ala His Met Gly Ala Trp
245 250 255

Gly Val Arg Val His Asp Val Pro Val Ser Arg Asp Ala Val Asp Val
260 265 270

Ala Ala Leu Trp Arg Ser Gly Gly Thr His His Gly
275 280

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<211> 859

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(859)

<223> RXA02024

<400> 693

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Met Ser Ser Leu Pro
1 5

gtc atc atg gcc atc gtc aat cgc acc ccg gat tct ttc tat gac aag 163
Val Ile Met Ala Ile Val Asn Arg Thr Pro Asp Ser Phe Tyr Asp Lys
10 15 20

ggt gcg aca ttt gag gac acc gct gcg cta aac agg gca gcg gag gtc Gly Ala Thr Phe Glu Asp Thr Ala Ala Leu Asn Arg Ala Ala Glu Val 25 30 35	211
att gaa caa ggc gcc ggc att gtc gat atc ggt ggg gtg aaa gcc ggc Ile Glu Gln Gly Ala Gly Ile Val Asp Ile Gly Gly Val Lys Ala Gly 40 45 50	259
ccg ggg gat ttc gtg tcg gcg gag gaa gag atc gac cgc gtg gtg cca Pro Gly Asp Phe Val Ser Ala Glu Glu Glu Ile Asp Arg Val Val Pro 55 60 65	307
atc atc gct gcg gtg cga gaa cgt ttt cct gac att gat att tct gtt Ile Ile Ala Ala Val Arg Glu Arg Phe Pro Asp Ile Asp Ile Ser Val 70 75 80 85	355
gat acc tgg cgg gcg tcg gtg gct gat gtc gca gtg gcg cat gga gca Asp Thr Trp Arg Ala Ser Val Ala Asp Val Ala Val Ala His Gly Ala 90 95 100	403
acg ctg atc aat gac act tgg gcc ggc cat gat cat gag ttg gtg cag Thr Leu Ile Asn Asp Thr Trp Ala Gly His Asp His Glu Leu Val Gln 105 110 115	451
gta gca ggg cag cac aag gtg ggt tat gtc tgc tcg cac acc ggc ggg Val Ala Gly Gln His Lys Val Gly Tyr Val Cys Ser His Thr Gly Gly 120 125 130	499
gtg att cca aga acg cga cca tat cgg gtg cat ttc gat gac atc gtg Val Ile Pro Arg Thr Arg Pro Tyr Arg Val His Phe Asp Asp Ile Val 135 140 145	547
gcc gat gta att acg gag acc acc aaa ttg gca gag caa gct gtt cgt Ala Asp Val Ile Thr Glu Thr Thr Lys Leu Ala Glu Gln Ala Val Arg 150 155 160 165	595
gcc ggg gtg cca gag gaa cgg gtg ttt att gat ccc acc cat gat ttc Ala Gly Val Pro Glu Glu Arg Val Phe Ile Asp Pro Thr His Asp Phe 170 175 180	643
ggg aaa aac acc ttc cac gga ctg gag ctt tta cga cgg atc gat gag Gly Lys Asn Thr Phe His Gly Leu Glu Leu Leu Arg Arg Ile Asp Glu 185 190 195	691
gtg gtt gcc acg ggc tgg ccg gtg ctg atg gcc ttg agt aat aag gat Val Val Ala Thr Gly Trp Pro Val Leu Met Ala Leu Ser Asn Lys Asp 200 205 210	739
ttc att ggg gaa act ttg gaa agg ggc gtc gat aag cgt gtt gct ggc Phe Ile Gly Glu Thr Leu Glu Arg Gly Val Asp Lys Arg Val Ala Gly 215 220 225	787
acg ctt gct gcc act gcc tgg gcg gcg gcg cgc ggc gtt gcg gct ttt Thr Leu Ala Ala Thr Ala Trp Ala Ala Ala Arg Gly Val Ala Ala Phe 230 235 240 245	835
cgc gtg cat gaa gtt gcg gaa acc Arg Val His Glu Val Ala Glu Thr 250	859

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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 694

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Arg	Ala	Ala	Glu	Val	Ile	Glu	Gln	Gly	Ala	Gly	Ile	Val	Asp	Ile	Gly
			35					40						45	
Gly	Val	Lys	Ala	Gly	Pro	Gly	Asp	Phe	Val	Ser	Ala	Glu	Glu	Glu	Ile
			50					55				60			
Asp	Arg	Val	Val	Pro	Ile	Ile	Ala	Ala	Val	Arg	Glu	Arg	Phe	Pro	Asp
65					70					75					80
Ile	Asp	Ile	Ser	Val	Asp	Thr	Trp	Arg	Ala	Ser	Val	Ala	Asp	Val	Ala
				85					90						95
Val	Ala	His	Gly	Ala	Thr	Leu	Ile	Asn	Asp	Thr	Trp	Ala	Gly	His	Asp
			100					105					110		
His	Glu	Leu	Val	Gln	Val	Ala	Gly	Gln	His	Lys	Val	Gly	Tyr	Val	Cys
			115					120					125		
Ser	His	Thr	Gly	Gly	Val	Ile	Pro	Arg	Thr	Arg	Pro	Tyr	Arg	Val	His
			130					135				140			
Phe	Asp	Asp	Ile	Val	Ala	Asp	Val	Ile	Thr	Glu	Thr	Thr	Lys	Leu	Ala
145					150					155					160
Glu	Gln	Ala	Val	Arg	Ala	Gly	Val	Pro	Glu	Glu	Arg	Val	Phe	Ile	Asp
				165					170					175	
Pro	Thr	His	Asp	Phe	Gly	Lys	Asn	Thr	Phe	His	Gly	Leu	Glu	Leu	Leu
			180					185					190		
Arg	Arg	Ile	Asp	Glu	Val	Val	Ala	Thr	Gly	Trp	Pro	Val	Leu	Met	Ala
			195				200						205		
Leu	Ser	Asn	Lys	Asp	Phe	Ile	Gly	Glu	Thr	Leu	Glu	Arg	Gly	Val	Asp
			210				215					220			
Lys	Arg	Val	Ala	Gly	Thr	Leu	Ala	Ala	Thr	Ala	Trp	Ala	Ala	Ala	Arg
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Gly	Val	Ala	Ala	Phe	Arg	Val	His	Glu	Val	Ala	Glu	Thr			
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 <212> DNA
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<222> (101)..(556)

<223> RXA00106

<400> 695

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Met Ile Gly Ala Ile
1 5

tgg gca caa ggc cgt gac ggc atc atc ggc gac ggc acc gac atg ccc 163
Trp Ala Gln Gly Arg Asp Gly Ile Ile Gly Asp Gly Thr Asp Met Pro
10 15 20

tgg cac atc ccg gaa gac ctc aaa cac ttc aag aaa acc acc atg ggc 211
Trp His Ile Pro Glu Asp Leu Lys His Phe Lys Lys Thr Thr Met Gly
25 30 35

cag ccg gtc atc atg ggt cgt cgc acg tgg gag tct ttg ccg ttc aag 259
Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu Ser Leu Pro Phe Lys
40 45 50

ccg ctt ccc ggc cgc gag aac ttc att ctc tcc tca cgc gag ccc ggc 307
Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser Ser Arg Glu Pro Gly
55 60 65

gac tgg tcc gcc ggc ggc aca gtg gtc acc gaa atc cct aaa agc ggc 355
Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu Ile Pro Lys Ser Gly
70 75 80 85

tgg atc atg ggc ggc ggc gag gtc tac aag gcc acc gtc ggc agc gcc 403
Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala Thr Val Gly Ser Ala
90 95 100

gac gtt tta gaa ata acg ctt atc gac gcc acc ttc gat gtt tcc act 451
Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr Phe Asp Val Ser Thr
105 110 115

ccc gtc tac gca ccc gaa atc ccg gcg aac ttc aac ctc gat gac gaa 499
Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe Asn Leu Asp Asp Glu
120 125 130

tcc gag tgg ttt acc tca ggc gag tat cgt tac aag ttc cag cgc tac 547
Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr Lys Phe Gln Arg Tyr
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<210> 696

<211> 152

<212> PRT

<213> Corynebacterium glutamicum

<400> 696

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 Lys Thr Thr Met Gly Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu
 35 40 45
 Ser Leu Pro Phe Lys Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser
 50 55 60
 Ser Arg Glu Pro Gly Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu
 65 70 75 80
 Ile Pro Lys Ser Gly Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala
 85 90 95
 Thr Val Gly Ser Ala Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr
 100 105 110
 Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe
 115 120 125
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 <212> DNA
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 <223> RXA00989

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 gat gac atc acc gta ggc gat gtc acg ttg ggc gag act gga ctg tct 96
 Asp Asp Ile Thr Val Gly Asp Val Thr Leu Gly Glu Thr Gly Leu Ser
 20 25 30
 ttg ccc atc gat ctc gcc ggt gag gta gaa gca cct gcc tcc gag gag 144
 Leu Pro Ile Asp Leu Ala Gly Glu Val Glu Ala Pro Ala Ser Glu Glu
 35 40 45
 atc acc caa gaa gat ttg ctg cgc ctt gcc cag gtg gaa gca gag ttg 192
 Ile Thr Gln Glu Asp Leu Leu Arg Leu Ala Gln Val Glu Ala Glu Leu
 50 55 60
 gat caa cgt tgg ttg gaa acc aaa att gat ccc act ttc cga cgc atg 240
 Asp Gln Arg Trp Leu Glu Thr Lys Ile Asp Pro Thr Phe Arg Arg Met
 65 70 75 80
 agc tac atg atg gat ctc atg ggc caa cca cag aat tcc ttc cca gca 288
 Ser Tyr Met Met Asp Leu Met Gly Gln Pro Gln Asn Ser Phe Pro Ala

325	330	335
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Ala Leu Ala Ala Val Glu Ala Phe Phe Gly Ala Ser Ala Gly Arg Pro 340 345 350		
ttg gat atc gac acg gtg cgc gaa ggc ttc gca caa gtt cag tcc cca 1104		
Leu Asp Ile Asp Thr Val Arg Glu Gly Phe Ala Gln Val Gln Ser Pro 355 360 365		
ggt cgc ctc gag cgc ctg cgc tct gca cca acc gtg ttc atc gac gca 1152		
Gly Arg Leu Glu Arg Leu Arg Ser Ala Pro Thr Val Phe Ile Asp Ala 370 375 380		
gct cac aac cca cac ggt gcc gca gca ctt ggt gca gca cta gac cgt 1200		
Ala His Asn Pro His Gly Ala Ala Ala Leu Gly Ala Ala Leu Asp Arg 385 390 395 400		
gac ttt gag ttc cgt cgc ctc atc ggt gtc atc gga gtg ctc tgc gac 1248		
Asp Phe Glu Phe Arg Arg Leu Ile Gly Val Ile Gly Val Leu Cys Asp 405 410 415		
aag gat gcc cgc ggc atc ttg gaa tca ctt gag cca tac ctg cat gaa 1296		
Lys Asp Ala Arg Gly Ile Leu Glu Ser Leu Glu Pro Tyr Leu His Glu 420 425 430		
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Ile Val Cys Thr Gln Thr Ala Ser Glu Arg Ala Leu Asp Ala Tyr Asp 435 440 445		
tta gct gaa tat gct cga gag atc tac ggc gat gag cgt gtg cac gtc 1392		
Leu Ala Glu Tyr Ala Arg Glu Ile Tyr Gly Asp Glu Arg Val His Val 450 455 460		
caa gaa gat ctt gct ggc gcg gta gaa ctc gct att gaa cta gca gaa 1440		
Gln Glu Asp Leu Ala Gly Ala Val Glu Leu Ala Ile Glu Leu Ala Glu 465 470 475 480		
gac acc gat gta cag tcc gga tca ggt gtt gtg atc acc ggt tca atc 1488		
Asp Thr Asp Val Gln Ser Gly Ser Gly Val Val Ile Thr Gly Ser Ile 485 490 495		
gtg acc gcc ggc gat gcg cgc acg ctg ttt gga aag gaa cct gca 1533		
Val Thr Ala Gly Asp Ala Arg Thr Leu Phe Gly Lys Glu Pro Ala 500 505 510		
tgagcaagcg tgaagaatca att 1556		

290	295	300	
Gly Gly Gln Gln Leu Thr Leu Lys Gly Leu Gly Gly Glu Tyr Thr Asp			
305	310	315	320
Ile Phe Leu Pro Leu Ser Gly Ala His Gln Ala Asp Asn Ala Ala Val			
	325	330	335
Ala Leu Ala Ala Val Glu Ala Phe Phe Gly Ala Ser Ala Gly Arg Pro			
	340	345	350
Leu Asp Ile Asp Thr Val Arg Glu Gly Phe Ala Gln Val Gln Ser Pro			
	355	360	365
Gly Arg Leu Glu Arg Leu Arg Ser Ala Pro Thr Val Phe Ile Asp Ala			
	370	375	380
Ala His Asn Pro His Gly Ala Ala Ala Leu Gly Ala Ala Leu Asp Arg			
	385	390	395
Asp Phe Glu Phe Arg Arg Leu Ile Gly Val Ile Gly Val Leu Cys Asp			
	405	410	415
Lys Asp Ala Arg Gly Ile Leu Glu Ser Leu Glu Pro Tyr Leu His Glu			
	420	425	430
Ile Val Cys Thr Gln Thr Ala Ser Glu Arg Ala Leu Asp Ala Tyr Asp			
	435	440	445
Leu Ala Glu Tyr Ala Arg Glu Ile Tyr Gly Asp Glu Arg Val His Val			
	450	455	460
Gln Glu Asp Leu Ala Gly Ala Val Glu Leu Ala Ile Glu Leu Ala Glu			
	465	470	475
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Met His Ala Val Leu			
1 5			
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Ser Ile Gly Ser Asn Met Asp Asp Arg Tyr Ala Leu Leu Asn Thr Val			

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Ile Glu Glu Phe Lys Asp Glu Ile Val Ala Gln Ser Ala Ile Tyr Ser				
	25	30	35	
acc cca ccg tgg ggc att gag gat cag gat gaa ttc ctc aac gca gtg				259
Thr Pro Pro Trp Gly Ile Glu Asp Gln Asp Glu Phe Leu Asn Ala Val				
	40	45	50	
ctc gtt gtt gag gtt gaa gaa acc ccc atc gag ttg ctg cgc cgt ggc				307
Leu Val Val Glu Val Glu Glu Thr Pro Ile Glu Leu Leu Arg Arg Gly				
	55	60	65	
caa aaa ctc gaa gaa gcc gcc gag cgg gtc cgc gtc cgc aaa tgg ggg				355
Gln Lys Leu Glu Glu Ala Ala Glu Arg Val Arg Val Arg Lys Trp Gly				
	70	75	80	85
cca cgc acc ctc gat gtg gat atc gtg cag atc att aaa gat ggg gaa				403
Pro Arg Thr Leu Asp Val Asp Ile Val Gln Ile Ile Lys Asp Gly Glu				
	90	95	100	
gag atc ctt tct gag gat ccc gaa ctg acc ttg cca cac cct tgg gct				451
Glu Ile Leu Ser Glu Asp Pro Glu Leu Thr Leu Pro His Pro Trp Ala				
	105	110	115	
tgg cag cgt gcc ttc gtg ttg atc cct tgg ttg gaa gca gaa cct gat				499
Trp Gln Arg Ala Phe Val Leu Ile Pro Trp Leu Glu Ala Glu Pro Asp				
	120	125	130	
gcc gtc ctg cac ggc acg acc att gca gaa cat gtg gat aat ctt gat				547
Ala Val Leu His Gly Thr Thr Ile Ala Glu His Val Asp Asn Leu Asp				
	135	140	145	
ccc aca gac att gaa ggt gtc acc aag att taaggagtcg tggctttcat				597
Pro Thr Asp Ile Glu Gly Val Thr Lys Ile				
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gca				600
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Leu Leu Asn Thr Val Ile Glu Glu Phe Lys Asp Glu Ile Val Ala Gln				
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Ser Ala Ile Tyr Ser Thr Pro Pro Trp Gly Ile Glu Asp Gln Asp Glu				
	35	40	45	
Phe Leu Asn Ala Val Leu Val Val Glu Val Glu Glu Thr Pro Ile Glu				
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Leu Leu Arg Arg Gly Gln Lys Leu Glu Glu Ala Ala Glu Arg Val Arg				
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				Met	Arg	Val	Leu	Ile								
				1				5								
att gat aat tat gat tct ttc acg ttt aat ctc gcc acc tat gtg gaa	163															
Ile Asp Asn Tyr Asp Ser Phe Thr Phe Asn Leu Ala Thr Tyr Val Glu																
	10							15						20		
gag gtt acg ggt cag gca cct gtg gtg gtg cct aat gat caa gaa ata	211															
Glu Val Thr Gly Gln Ala Pro Val Val Val Pro Asn Asp Gln Glu Ile																
	25							30						35		
gat gag atg ctt ttc gac gcc gtc atc ctc tca cct ggc ccg ggc cac	259															
Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser Pro Gly Pro Gly His																
	40							45					50			
gcc gcc gtt gcg gct gat ttt ggt atc tgt gca gcc gtc att gag cgt	307															
Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala Gly Val Ile Glu Arg																
	55						60					65				
gca cgc gtt ccg att ttg ggt gtg tgt tta ggc cac cag gcc att gcg	355															
Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly His Gln Gly Ile Ala																
	70					75				80				85		
ttg gcc tat ggc ggt gat gtt gat ttg gcg ccc agg ccg gtc cac ggt	403															
Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro Arg Pro Val His Gly																
					90				95					100		
gag gtt tcg cag atc acc cat gat ggt tca ggt tta ttt gca gcc atc	451															
Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly Leu Phe Ala Gly Ile																
	105							110					115			

cct gaa acg ttt gag gcg gtg cgt tat cac tcg atg gtg gca acc cgc	499
Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser Met Val Ala Thr Arg	
120 125 130	
ttg ccg gag tca ttg aaa gct aca gct acc agc gat gat ggt ttg atc	547
Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser Asp Asp Gly Leu Ile	
135 140 145	
atg gca ttg gca cat gaa gtg ctt ccg cag tgg ggt gtg caa ttt cat	595
Met Ala Leu Ala His Glu Val Leu Pro Gln Trp Gly Val Gln Phe His	
150 155 160 165	
ccg gaa tct att ggt gga caa ttc ggc cat cag atc att aag aac ttc	643
Pro Glu Ser Ile Gly Gln Phe Gly His Gln Ile Ile Lys Asn Phe	
170 175 180	
ctt aat tta gcg cgc aca tat cgc tgg caa ctc acg gag aaa act att	691
Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu Thr Glu Lys Thr Ile	
185 190 195	
ccg ctc agc gtt gat tca gca gcg gtt ttt gaa aca ttc ttt gcc cat	739
Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu Thr Phe Phe Ala His	
200 205 210	
tcc tcc cat gct ttt tgg ctc gat gat gcc caa gga acc agc tat ctt	787
Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln Gly Thr Ser Tyr Leu	
215 220 225	
ggt gat gcc agc ggt cct ctc gca gcg aca aaa acc cat aat gtc ggc	835
Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys Thr His Asn Val Gly	
230 235 240 245	
gag ggg gat ttc ttc acc tgg cta aag gag gat ctc gcc gcc aac tca	883
Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp Leu Ala Ala Asn Ser	
250 255 260	
gtt gcg ccc ggt caa ggt ttt cgt ctt ggc tgg gtt ggt tac gtt ggt	931
Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp Val Gly Tyr Val Gly	
265 270 275	
tat gag ctt aaa gcg gaa gct ggc gca cgg gct gcg cac act tcg agt	979
Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala Ala His Thr Ser Ser	
280 285 290	
ctt ccg gat gcg cac ctc att ttt gcc gat cgc gcc atc gca gtg gaa	
1027	
Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg Ala Ile Ala Val Glu	
295 300 305	
tcg gat cag gtt cgg ttg ctg gcg ttg ggg gag cag gac gag tgg ttt	
1075	
Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu Gln Asp Glu Trp Phe	
310 315 320 325	
gaa gaa acc atc aag aag ctg cat aat ctt gtc gcc ccg cgg ata cct	
1123	
Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val Ala Pro Arg Ile Pro	
330 335 340	

gcg tcc gga cac ctc gct ttg cag gtt cga gat tcc aaa gat gag tat
 1171
 Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp Ser Lys Asp Glu Tyr
 345 350 355

ctc gac aaa att cgc aga gcc cag gag ctg att act cgc ggc gaa tcg
 1219
 Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile Thr Arg Gly Glu Ser
 360 365 370

tat gaa atc tgc ctg acc aca aaa ctt cag ggc acc act gat gtg gcc
 1267
 Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly Thr Thr Asp Val Ala
 375 380 385

cct ctg gct gcc tat cta gca ctg cgt ggg gcc aat ccc acc gca tat
 1315
 Pro Leu Ala Ala Tyr Leu Ala Leu Arg Gly Ala Asn Pro Thr Ala Tyr
 390 395 400 405

ggt gcg tat ctt cag ctg ggg gat acc tct att ttg agt tcc tcg ccg
 1363
 Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile Leu Ser Ser Ser Pro
 410 415 420

gag cgg ttc atc acc att gat tcg gca ggg tat gtg gaa tca aag ccc
 1411
 Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr Val Glu Ser Lys Pro
 425 430 435

att aaa ggc acc agg ccg cgt ggg cga aca gcg caa gaa gac caa gaa
 1459
 Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala Gln Glu Asp Gln Glu
 440 445 450

atc att gct gag ctg cgc agt aat cct aaa gat cgt gca gaa aac ttg
 1507
 Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp Arg Ala Glu Asn Leu
 455 460 465

atg atc gtg gat ttg gtc cgc aac gac tta gcc cgc ggc gct ttg ccc
 1555
 Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala Arg Gly Ala Leu Pro
 470 475 480 485

acc aca gtt aaa aca tcc aag ctt ttc gac gtc gaa acc tac gcc aca
 1603
 Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val Glu Thr Tyr Ala Thr
 490 495 500

gtc cac caa ctt gtc agc acc gtc tct gca gag ttg ggg cca cgc agt
 1651
 Val His Gln Leu Val Ser Thr Val Ser Ala Glu Leu Gly Pro Arg Ser
 505 510 515

ccg att gag tgc gtg cgc gca gca ttc ccc ggt ggt tcg atg act ggt
 1699
 Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly Gly Ser Met Thr Gly
 520 525 530

gcc cca aag ctg cgc acc atg gag atc atc gat gag ctg gag gca gct
1747

Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp Glu Leu Glu Ala Ala
535 540 545

cct cgc ggt att tac tca ggt ggc ttg gga tat ttt tcc ctc gac ggc
1795

Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr Phe Ser Leu Asp Gly
550 555 560 565

gca gtt gat ctc tcc atg gtg atc aga act ctc gtc atc cag aac aat
1843

Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu Val Ile Gln Asn Asn
570 575 580

cac gtg gag tac gga gtg ggc ggt gca ctt ctt gct ctg tct gat ccg
1891

His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu Ala Leu Ser Asp Pro
585 590 595

gag gct gag tgg gag gaa atc cgc gtt aaa tca cgg cct ctg ctg aat
1939

Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser Arg Pro Leu Leu Asn
600 605 610

ttg ttt ggg gtt gaa ttc cca tgacgtacct cgtgtgggac ggt
1983

Leu Phe Gly Val Glu Phe Pro
615 620

<210> 702

<211> 620

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 702

Met Arg Val Leu Ile Ile Asp Asn Tyr Asp Ser Phe Thr Phe Asn Leu
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Ala Thr Tyr Val Glu Glu Val Thr Gly Gln Ala Pro Val Val Val Pro
20 25 30

Asn Asp Gln Glu Ile Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser
35 40 45

Pro Gly Pro Gly His Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala
50 55 60

Gly Val Ile Glu Arg Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly
65 70 75 80

His Gln Gly Ile Ala Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro
85 90 95

Arg Pro Val His Gly Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly
100 105 110

Leu Phe Ala Gly Ile Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser
115 120 125

Met Val Ala Thr Arg Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser
 130 135 140
 Asp Asp Gly Leu Ile Met Ala Leu Ala His Glu Val Leu Pro Gln Trp
 145 150 155 160
 Gly Val Gln Phe His Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln
 165 170 175
 Ile Ile Lys Asn Phe Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu
 180 185 190
 Thr Glu Lys Thr Ile Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu
 195 200 205
 Thr Phe Phe Ala His Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln
 210 215 220
 Gly Thr Ser Tyr Leu Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys
 225 230 235 240
 Thr His Asn Val Gly Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp
 245 250 255
 Leu Ala Ala Asn Ser Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp
 260 265 270
 Val Gly Tyr Val Gly Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala
 275 280 285
 Ala His Thr Ser Ser Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg
 290 295 300
 Ala Ile Ala Val Glu Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu
 305 310 315 320
 Gln Asp Glu Trp Phe Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val
 325 330 335
 Ala Pro Arg Ile Pro Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp
 340 345 350
 Ser Lys Asp Glu Tyr Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile
 355 360 365
 Thr Arg Gly Glu Ser Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly
 370 375 380
 Thr Thr Asp Val Ala Pro Leu Ala Ala Tyr Leu Ala Leu Arg Gly Ala
 385 390 395 400
 Asn Pro Thr Ala Tyr Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile
 405 410 415
 Leu Ser Ser Ser Pro Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr
 420 425 430
 Val Glu Ser Lys Pro Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala
 435 440 445
 Gln Glu Asp Gln Glu Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp

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<210> 703
<211> 747
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(724)  
<223> RXA00958
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<400> 703
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ccattgcgct tgctgctggg tccactttgg aggtcatccg. atg .aca cac gtt gtt 115
Met Thr His Val Val
1 5

ctc att gat aat cac gat tct ttt gtc tac aac ctg gtg gat gcg ttc 163
Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn Leu Val Asp Ala Phe
10 15 20

gcc gtg gcc ggt tat aag tgc acg gtg ttc cgc aat acg gtg cca gtg 211
Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg Asn Thr Val Pro Val
25 30 35

gaa acc att ttg gca gcc aac ccg gac ctg atc tgc ctt tca cct gga 259
Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile Cys Ser Pro Gly
40 45 50

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cct ggt tac cct gcc gat gcg ggc aac atg atg gcg ctg atc gag cgc 307
 Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met Ala Leu Ile Glu Arg
 55 60 65

aca ctc ggc cag att cct tta ctg ggt att tgc ctc ggc tac cag gca 355
 Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys Leu Gly Tyr Gln Ala
 70 75 80 85

ctc atc gaa tac cac ggc ggc aag gtt gag cct tgt ggc cct gtg cac 403
 Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro Cys Gly Pro Val His
 90 95 100

ggc acc acc gac aac atg atc ctt act gat gca ggt gtg cag agc cct 451
 Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala Gly Val Gln Ser Pro
 105 110 115

gtt ttt gca ggt ctt gcc act gat gtt gag cct gat cat cca gaa atc 499
 Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro Asp His Pro Glu Ile
 120 125 130

cca ggc cgc aag gtt cca att ggc cgt tat cac tca ctg ggc tgc gtg 547
 Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His Ser Leu Gly Cys Val
 135 140 145

gtt gcc cca gac ggt att gaa tca cta ggt acc tgt tcc tcg gag att 595
 Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr Cys Ser Ser Glu Ile
 150 155 160 165

ggt gat gtc atc atg gcg gca cgc acc acc gat gga aag gcc att ggc 643
 Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp Gly Lys Ala Ile Gly
 170 175 180

ctg cag ttt cac cct gag tca gtg cta agc cca acg ggt cct gtc att 691
 Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro Thr Gly Pro Val Ile
 185 190 195

ttg tcc cgc tgt gtc gaa cag ctt ctc gcg aac taataaaaaa aggatttgat 744
 Leu Ser Arg Cys Val Glu Gln Leu Ala Asn
 200 205

tca 747

<210> 704

<211> 208

<212> PRT

<213> Corynebacterium glutamicum

<400> 704

Met Thr His Val Val Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn
 1 5 10 15

Leu Val Asp Ala Phe Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg
 20 25 30

Asn Thr Val Pro Val Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile
 35 40 45

Cys Leu Ser Pro Gly Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met
 50 55 60

Ala Leu Ile Glu Arg Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys
65 70 75 80

Leu Gly Tyr Gln Ala Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro
85 90 95

Cys Gly Pro Val His Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala
100 105 110

Gly Val Gln Ser Pro Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro
115 120 125

Asp His Pro Glu Ile Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His
130 135 140

Ser Leu Gly Cys Val Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr
145 150 155 160

Cys Ser Ser Glu Ile Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp
165 170 175

Gly Lys Ala Ile Gly Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro
180 185 190

Thr Gly Pro Val Ile Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn
195 200 205

<210> 705
<211> 1266
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1243)
<223> RXA02790

<400> 705
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agggaaat ttt cccaggatga accaaatccg aaaccgccgg atg gag ccc gtc tac 115
Met Glu Pro Val Tyr
1 5

gta aag cgc cgc caa cgg ttt att gcc gtg acg atc gct tca ctc atc 163
Val Lys Arg Arg Gln Arg Phe Ile Ala Val Thr Ile Ala Ser Leu Ile
10 15 20

ctc att atc ggt gcc atc atc tat atc ggt gta gcc acc tca aac cgg 211
Leu Ile Ile Gly Ala Ile Ile Tyr Ile Gly Val Ala Thr Ser Asn Arg
25 30 35

acg cca cat gac tat gaa ggc tcc gga aac ggt gtg gtt cag ctg gtc 259
Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly Val Val Gln Leu Val
40 45 50

gaa atc cct gaa ggt tcc tcc ata tca gag ctc ggc cca gag ttg gaa	307
Glu Ile Pro Glu Gly Ser Ser Ile Ser Glu Leu Gly Pro Glu Leu Glu	
55 60 65	
gaa cga gat atc gtg gcc acc aac tca gcg ttc caa aca gcg gcc agc	355
Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe Gln Thr Ala Ala Ser	
70 75 80 85	
aac aac ccc aac gcg ggt agt gta cag cca ggt ttc tac cgt ctg cag	403
Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly Phe Tyr Arg Leu Gln	
90 95 100	
gaa caa atg aac gca gca gct gca gtg tcg gct ctg ctt gat cca gac	451
Glu Gln Met Asn Ala Ala Ala Val Ser Ala Leu Leu Asp Pro Asp	
105 110 115	
aac cag gtt gat ctc ctc gac att cac ggc ggc gcc acc ttg atg gac	499
Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly Ala Thr Leu Met Asp	
120 125 130	
gtc act gtt gtc ggc gga aac acc cgc gcg gga atc tac tcc cag atc	547
Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly Ile Tyr Ser Gln Ile	
135 140 145	
gca gcc gtg acc tgc acc gaa ggc tcc gcc aac tgc atc acc gct gag	595
Ala Ala Val Thr Cys Thr Glu Gly Ser Ala Asn Cys Ile Thr Ala Glu	
150 155 160 165	
gat ttg cag cag gtt gcc tcc acc gtg tcg cct gca gaa ttg ggt gtc	643
Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro Ala Glu Leu Gly Val	
170 175 180	
cca gat tgg gca atc gct gct gtg gaa gct cgc gga act gat cca aag	691
Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg Gly Thr Asp Pro Lys	
185 190 195	
cgc ctc gaa ggc ctg atc atg cct ggc caa tac gtg gtg gat cca tcc	739
Arg Leu Glu Gly Leu Ile Met Pro Gly Gln Tyr Val Val Asp Pro Ser	
200 205 210	
aac gac gcc cag gga atc ctc acc gat ctg atc acg cga tca gca aac	787
Asn Asp Ala Gln Gly Ile Leu Thr Asp Leu Ile Thr Arg Ser Ala Asn	
215 220 225	
cat ttc caa gaa acc gac atc acg ggc cgt gca gat gcc atc gga ctt	835
His Phe Gln Glu Thr Asp Ile Thr Gly Arg Ala Asp Ala Ile Gly Leu	
230 235 240 245	
act cca tat gag ctg gtc acc gca gca tct tta atc gag cgc gaa gca	883
Thr Pro Tyr Glu Leu Val Thr Ala Ala Ser Leu Ile Glu Arg Glu Ala	
250 255 260	
cca gca gga gat ttt gat aag gtc gcc cgc gtc atc ttg aac cgt ctc	931
Pro Ala Gly Asp Phe Asp Lys Val Ala Arg Val Ile Leu Asn Arg Leu	
265 270 275	
gcc gag cca atg cag ctg caa ttc gac tcc acc gtc aac tac ggt ctg	979
Ala Glu Pro Met Gln Leu Gln Phe Asp Ser Thr Val Asn Tyr Gly Leu	
280 285 290	

tct gaa caa gaa gta gca acc acc gac gaa gac cgt cag acc gtc acc
1027

Ser Glu Gln Glu Val Ala Thr Thr Asp Glu Asp Arg Gln Thr Val Thr
295 300 305

cca tgg aac act tac gcc atg gac ggc ctg cca caa acc ccc atc gcc
1075

Pro Trp Asn Thr Tyr Ala Met Asp Gly Leu Pro Gln Thr Pro Ile Ala
310 315 320 325

gca gta tcc acc gaa gca ctc caa gcc atg gaa aac cct gca gaa gga
1123

Ala Val Ser Thr Glu Ala Leu Gln Ala Met Glu Asn Pro Ala Glu Gly
330 335 340

aac tgg ctg tac ttt gtc acc atc gac acc gat gga acc acc gtg ttc
1171

Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp Gly Thr Thr Val Phe
345 350 355

aac gac acc ttc gaa gag cac gaa gcc gac att gag caa gct ttg aac
1219

Asn Asp Thr Phe Glu Glu His Glu Ala Asp Ile Glu Gln Ala Leu Asn
360 365 370

agt ggc gtt cta gac agc aac cga taaggatcag cgaataaaaat tgg
1266

Ser Gly Val Leu Asp Ser Asn Arg
375 380

<210> 706

<211> 381

<212> PRT

<213> Corynebacterium glutamicum

<400> 706

Met Glu Pro Val Tyr Val Lys Arg Arg Gln Arg Phe Ile Ala Val Thr
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Ile Ala Ser Leu Ile Leu Ile Ile Gly Ala Ile Ile Tyr Ile Gly Val
20 25 30

Ala Thr Ser Asn Arg Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly
35 40 45

Val Val Gln Leu Val Glu Ile Pro Glu Gly Ser Ser Ile Ser Glu Leu
50 55 60

Gly Pro Glu Leu Glu Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe
65 70 75 80

Gln Thr Ala Ala Ser Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly
85 90 95

Phe Tyr Arg Leu Gln Glu Gln Met Asn Ala Ala Ala Val Ser Ala
100 105 110

Leu Leu Asp Pro Asp Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly
115 120 125

Ala Thr Leu Met Asp Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly
 130 135 140

Ile Tyr Ser Gln Ile Ala Ala Val Thr Cys Thr Glu Gly Ser Ala Asn
 145 150 155 160

Cys Ile Thr Ala Glu Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro
 165 170 175

Ala Glu Leu Gly Val Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg
 180 185 190

Gly Thr Asp Pro Lys Arg Leu Glu Gly Leu Ile Met Pro Gly Gln Tyr
 195 200 205

Val Val Asp Pro Ser Asn Asp Ala Gln Gly Ile Leu Thr Asp Leu Ile
 210 215 220

Thr Arg Ser Ala Asn His Phe Gln Glu Thr Asp Ile Thr Gly Arg Ala
 225 230 235 240

Asp Ala Ile Gly Leu Thr Pro Tyr Glu Leu Val Thr Ala Ala Ser Leu
 245 250 255

Ile Glu Arg Glu Ala Pro Ala Gly Asp Phe Asp Lys Val Ala Arg Val
 260 265 270

Ile Leu Asn Arg Leu Ala Glu Pro Met Gln Leu Gln Phe Asp Ser Thr
 275 280 285

Val Asn Tyr Gly Leu Ser Glu Gln Glu Val Ala Thr Thr Asp Glu Asp
 290 295 300

Arg Gln Thr Val Thr Pro Trp Asn Thr Tyr Ala Met Asp Gly Leu Pro
 305 310 315 320

Gln Thr Pro Ile Ala Ala Val Ser Thr Glu Ala Leu Gln Ala Met Glu
 325 330 335

Asn Pro Ala Glu Gly Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp
 340 345 350

Gly Thr Thr Val Phe Asn Asp Thr Phe Glu Glu His Glu Ala Asp Ile
 355 360 365

Glu Gln Ala Leu Asn Ser Gly Val Leu Asp Ser Asn Arg
 370 375 380

<210> 707

<211> 579

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(556)

<223> RXA00106

<400> 707

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Gly Thr Asp Met Pro Trp His Ile Pro Glu Asp Leu Lys His Phe Lys
          20             25             30

Lys Thr Thr Met Gly Gln Pro Val Ile Met Gly Arg Arg Thr Trp Glu
      35             40             45

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Ser Leu Pro Phe Lys Pro Leu Pro Gly Arg Glu Asn Phe Ile Leu Ser
50 55 60

Ser Arg Glu Pro Gly Asp Trp Ser Ala Gly Gly Thr Val Val Thr Glu
65 70 75 80

Ile Pro Lys Ser Gly Trp Ile Met Gly Gly Gly Glu Val Tyr Lys Ala
85 90 95

Thr Val Gly Ser Ala Asp Val Leu Glu Ile Thr Leu Ile Asp Ala Thr
100 105 110

Phe Asp Val Ser Thr Pro Val Tyr Ala Pro Glu Ile Pro Ala Asn Phe
115 120 125

Asn Leu Asp Asp Glu Ser Glu Trp Phe Thr Ser Gly Glu Tyr Arg Tyr
130 135 140

Lys Phe Gln Arg Tyr Ile Lys Val
145 150

<210> 709

<211> 2599

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(2599)

<223> RXN02198

<400> 709

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agttcggggaa ttgtctaatac cgtactaagc tgtctacaca atg tct act tca gtt 115
Met Ser Thr Ser Val
1 5

act tca cca gcc cac aac aac gca cat tcc tcc gaa ttt ttg gat gcg 163
Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala
10 15 20

ttg gca aac cat gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc 211
Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu
25 30 35

caa ggc ttt gac ctg gac gtg gaa aag gat ttc ctt gat ctg gag ggg 259
Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe Leu Asp Leu Glu Gly
40 45 50

tgt aat gag att ctc aac gac acc cgc cct gat gtg ttg agg cag att 307
Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile
55 60 65

cac cgc gcc tac ttt gag gcg gga gct gac ttg gtt gag acc aat act 355
His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu Val Glu Thr Asn Thr
70 75 80 85

ttt ggt tgc aac ctg ccg aac ttg gcg gat tat gac atc gct gat cgt 403
Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg

	90	95	100	
tgc cgt gag ctt gcc tac aag ggc act gca gtg gct agg gaa gtg gct				451
Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val Ala Arg Glu Val Ala				
	105	110	115	
gat gag atg ggg ccg ggc cga aac ggc atg cgg cgt ttc gtg gtt ggt				499
Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg Arg Phe Val Val Gly				
	120	125	130	
tcc ctg gga cct gga acg aag ctt cca tcg ctg ggc cat gca ccg tat				547
Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu Gly His Ala Pro Tyr				
	135	140	145	
gca gat ttg cgt ggg cac tac aag gaa gca gcg ctt ggc atc atc gac				595
Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala Leu Gly Ile Ile Asp				
	150	155	160	165
ggg ggt ggc gat gcc ttt ttg att gag act gct cag gac ttg ctt cag				643
Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala Gln Asp Leu Leu Gln				
	170	175	180	
gtc aag gct gcg gtt cac ggc gtt caa gat gcc atg gct gaa ctt gat				691
Val Lys Ala Ala Val His Gly Val Gln Asp Ala Met Ala Glu Leu Asp				
	185	190	195	
aca ttc ttg ccc att att tgc cac gtc acc gta gag acc acc ggc acc				739
Thr Phe Leu Pro Ile Ile Cys His Val Thr Val Glu Thr Thr Gly Thr				
	200	205	210	
atg ctc atg ggt tct gag atc ggt gcc gcg ttg aca gcg ctg cag cca				787
Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu Thr Ala Leu Gln Pro				
	215	220	225	
ctg ggt atc gac atg att ggt ctg aac tgc gcc acc ggc cca gat gag				835
Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala Thr Gly Pro Asp Glu				
	230	235	240	245
atg agc gag cac ctg cgt tac ctg tcc aag cac gcc gat att cct gtg				883
Met Ser Glu His Leu Arg Tyr Leu Ser Lys His Ala Asp Ile Pro Val				
	250	255	260	
tcg gtg atg cct aac gca ggt ctt cct gtc ctg ggt aaa aac ggt gca				931
Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu Gly Lys Asn Gly Ala				
	265	270	275	
gaa tac cca ctt gag gct gag gat ttg gcg cag gcg -ctg gct gga ttc				979
Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln Ala Leu Ala Gly Phe				
	280	285	290	
gtc tcc gaa tat ggc ctg tcc atg gtg ggt ggt tgt tgt ggc acc aca				
1027				
Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly Cys Cys Gly Thr Thr				
	295	300	305	
cct gag cac atc cgt gcg gtc -cgc gat gcg gtg gtt ggt gtt cca gag				
1075				
Pro Glu His Ile Arg Ala Val Arg Asp Ala Val Val Gly Val Pro Glu				
	310	315	320	325

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 Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala Gly Pro Val Glu Gln
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 Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val Ala Ser Leu Tyr Thr
 345 350 355
 tcg gtg cca ttg tcc cag gaa acc ggc att tcc atg atc ggt gag cgc
 1219
 Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser Met Ile Gly Glu Arg
 360 365 370
 acc aac tcc aac ggt tcc aag gca ttc cgt gag gca atg ctg tct ggc
 1267
 Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu Ala Met Leu Ser Gly
 375 380 385
 gat tgg gaa aag tgt gtg gat att gcc aag cag caa acc cgc gat ggt
 1315
 Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln Gln Thr Arg Asp Gly
 390 395 400 405
 gca cac atg ctg gat ctt tgt gtg gat tac gtg gga cga gac ggc acc
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 Ala His Met Leu Asp Leu Cys Val Asp Tyr Val Gly Arg Asp Gly Thr
 410 415 420
 gcc gat atg gcg acc ttg gca gca ctt ctt gct acc agc tcc act ttg
 1411
 Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala Thr Ser Ser Thr Leu
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 cca atc atg att gac tcc acc gag cca gag gtt att cgc aca ggc ctt
 1459
 Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val Ile Arg Thr Gly Leu
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 Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser Val Asn Phe Glu Asp
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 Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile Met Lys Leu Val Lys
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 Gln His Gly Ala Ala Val Val Ala Leu Thr Ile Asp Glu Glu Gly Gln
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 Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp
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Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp
520 525 530

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1747
Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu Glu Thr Arg Arg Asp
535 540 545

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Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu Lys Lys Leu Tyr Pro
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Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn
570 575 580

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1891
Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe Leu Asn Glu Cys Ile
585 590 595

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1939
Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro
600 605 610

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1987
Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val Ala Leu Asp Met Val
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Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu Gln Glu Phe Met Gln
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2083
Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys Asp Ala Arg Ala Glu
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2131
Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile
665 670 675

gac ggc gat aag aat ggc ctt gag gat gat ctg gaa gca ggc atg aag
2179
Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu Glu Ala Gly Met Lys
680 685 690

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2227
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695 700 705

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 2323
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 745 750 755
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 760 765 770
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 2467
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 2563
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<212> PRT

<213> *Corynebacterium glutamicum*

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 20 25 30
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 35 40 45
 Leu Asp Leu Glu Gly Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp
 50 55 60
 Val Leu Arg Gln Ile His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu
 65 70 75 80

992

Gln Thr Arg Asp Gly Ala His Met Leu Asp Leu Cys Val Asp Tyr Val
 405 410 415
 Gly Arg Asp Gly Thr Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala
 420 425 430
 Thr Ser Ser Thr Leu Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val
 435 440 445
 Ile Arg Thr Gly Leu Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser
 450 455 460
 Val Asn Phe Glu Asp Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile
 465 470 475 480
 Met Lys Leu Val Lys Gln His Gly Ala Ala Val Val Ala Leu Thr Ile
 485 490 495
 Asp Glu Glu Gly Gln Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala
 500 505 510
 Lys Arg Leu Ile Asp Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys
 515 520 525
 Asp Ile Val Val Asp Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu
 530 535 540
 Glu Thr Arg Arg Asp Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu
 545 550 555 560
 Lys Lys Leu Tyr Pro Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile
 565 570 575
 Ser Phe Gly Leu Asn Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe
 580 585 590
 Leu Asn Glu Cys Ile Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser
 595 600 605
 Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val
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 Ala Leu Asp Met Val Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu
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 645 650 655
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 Glu Ala Gly Met Lys Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp
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Met Ser Thr Ser Val																	
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Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala																	
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Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu																	
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Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe Leu Asp Leu Glu Gly																	
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Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile																	
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His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu Val Glu Thr Asn Thr																	
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ttt ggt tgc aac ctg ccg aac ttg gcg gat tat gac atc gct gat cgt	403
Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg	
90 95 100	
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Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val Ala Arg Glu Val Ala	
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Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg Arg Phe Val Val Gly	
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Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu Gly His Ala Pro Tyr	
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Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala Leu Gly Ile Ile Asp	
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Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala Gln Asp Leu Leu Gln	
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Val Lys Ala Ala Val His Gly Val Gln Asp Ala Met Ala Glu Leu Asp	
185 190 195	
aca ttc ttg ccc att att tgc cac gtc acc gta gag acc acc ggc acc	739
Thr Phe Leu Pro Ile Ile Cys His Val Thr Val Glu Thr Thr Gly Thr	
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Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu Thr Ala Leu Gln Pro	
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Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala Thr Gly Pro Asp Glu	
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Met Ser Glu His Leu Arg Tyr Leu Ser Lys His Ala Asp Ile Pro Val	
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tcg gtg atg cct aac gca ggt ctt cct gtc ctg ggt aaa aac ggt gca	931
Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu Gly Lys Asn Gly Ala	
265 270 275	
gaa tac cca ctt gag gct gag gat ttg gcg cag gcg ctg gct gga ttc	979
Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln Ala Leu Ala Gly Phe	
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gtc tcc gaa tat ggc ctg tcc atg gtg ggt ggt tgt tgt ggc acc aca	1027
Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly Cys Cys Gly Thr Thr	
295 300 305	
cct gag cac atc cgt gcg gtc cgc gat gcg gtg gtt ggt gtt cca gag	1075
Pro Glu His Ile Arg Ala Val Arg Asp Ala Val Val Gly Val Pro Glu	
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 Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala Gly Pro Val Glu Gln
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 1171
 Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val Ala Ser Leu Tyr Thr
 345 350 355
 tcg gtg cca ttg tcc cag gaa acc ggc att tcc atg atc ggt gag cgc
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 585 590 595

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 Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro
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 Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val Ala Leu Asp Met Val
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 680 685 690

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 Pro Phe Met Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu
 745 750 755

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 760 765 770

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 Val Leu Arg Gln Ile His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu
 65 70 75 80

999

Gln Thr Arg Asp Gly Ala His Met Leu Asp Leu Cys Val Asp Tyr Val
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 Gly Arg Asp Gly Thr Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala
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 Ile Arg Thr Gly Leu Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser
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 Met Lys Leu Val Lys Gln His Gly Ala Ala Val Val Ala Leu Thr Ile
 485 490 495
 Asp Glu Glu Gly Gln Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala
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 Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val
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 690 695 700
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Ser Ala Gln Ala Glu Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys 755 760 765		
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Asn Asn Gly Tyr Asp Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser 785 790 795 800		
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ctt gcg cag acc gcc cgc caa ttg gtc aac act gca tgc gat tct ttg 259 Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu 40 45 50		
tct gga ttg gat tcc gtt ccg ttt gca gga cgt tcc tac tac gac gca 307 Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala 55 60 65		
atg ctc gat acc gcc gct att ttg ggt gtg ctg ccg gag cgt ttt gat 355 Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp 70 75 80 85		
gac atc gct gat cat gaa aac gat ggt ctc cca ctg tgg att gac cgc 403 Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg 90 95 100		

tac ttt ggc gct gct cgc ggt act gag acc ctg cct gca cag gca atg 451
 Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met
 105 110 115

acc aag tgg ttt gat acc aac tac cac tac ctc gtg ccg gag ttg tct 499
 Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser
 120 125 130

gcg gat aca cgt ttc gtt ttg gat gcg tcc gcg ctg att gag gat ctc 547
 Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu
 135 140 145

cgt tgc cag cag gtt cgt ggc gtt aat gcc cgc cct gtt ctg gtt ggt 595
 Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly
 150 155 160 165

cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct 643
 Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro
 170 175 180

ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag 691
 Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys
 185 190 195

tct ttc gat act gag tgg gtt cag atc gat gag cct gcg ttg gtc acc 739
 Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr
 200 205 210

gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act 787
 Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr
 215 220 225

ttg gct aag cgc gat ggc gtg ttt gtc aat act tac ttc ggc tct ggc 835
 Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly
 230 235 240 245

gat cag gcg ctg aac act ctt gcg ggc atc ggc ctt ggc gcg att ggc 883
 Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly
 250 255 260

gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt 931
 Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly
 265 270 275

gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc 979
 Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg
 280 285 290

acc gac ctg tgt gct gct ctt gct tcc ctg aag cgc ctg gca gct cgc
 1027
 Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg
 295 300 305

ggc cca atc gca gtg tct acc tct tgt tca ctg ctg cac gtt cct tac
 1075
 Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr
 310 315 320 325

acc ctc gag gct gag aac att gag cct gag gtc cgc gac tgg ctt gcc
 1123